BAT RESEARCH NEWS

VOLUME 60: NO. 1 SPRING 2019

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Gray Bats (*Myotis grisescens*) in Bat Cave, Shannon County, Missouri. Photo by Lynn Robbins.

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Use of an Underground Cavity for Roosting by the Pygmy Round-eared Bat (*Lophostoma brasiliense*) in Costa Rica

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The use of small, underground holes for roosting is known for few species of bats, with most occupying burrows created by other animals, including birds, agoutis, rabbits, aardvarks, and ground squirrels (Brack and Carter, 1985; Hill and Smith, 1984). Whether this paucity of records is due to rarity of use or difficulty of detection is unclear. Bats using belowground holes for occasional roosting include silver-haired bats (*Lasionycteris noctivagans*), little big-eared bats (*Micronycteris megalotis*), and lesser short-tailed bats (*Mystacina tuberculata*—Allen, 1939; Brack and Carter, 1985; Hall and Dalquest, 1963; Daniel, 1979).

During a university class trip to La Selva Biological Station, near Puerto Viejo, Heredia Province, Costa Rica, a student noticed, through a hole in the ground, several bats flying in a small, subterranean chamber. Staff members of La Selva indicated that the hole led into an old nest of leaf cutter ants (*Atta cephalotes*). The surface opening was about 50-cm long and 30-cm wide, but expanded into a larger space belowground that was about 1-m deep and wider than the opening in the portion that we could see. The hole was located near the center of an elevated mound that was 20–30-cm high and 4–5-m wide (Fig. 1). The opening was located in a mowed area near cabins used by faculty members, on the edge of second-growth tropical forest, along the Puerto Viejo River.

On 3 and 5 January 2012, the class placed mist nets (6-m long, 2.3-m high; Avinet, Dryden, NY) in a "V" configuration next to the hole. We opened nets shortly before sunset and operated them for 2 h each night. Nets were not monitored continuously on the first night, but on the second night, we placed nets closer to the hole and stationed observers to watch the opening, which was backlit by lights from a nearby building. For each bat captured, we recorded sex, age, and reproductive condition and determined identity, using Timm and LaVal (1998) and LaVal and Rodríguez-H. (2002).

At 1754 hours on 3 January, we discovered a pygmy round-eared bat (*Lophostoma brasiliense*) entangled in the net. Although we did not observe emergence, it seemed likely that the bat, a nonreproductive adult female, had exited the hole, based on the animal's location in the net. On 5 January, we watched the opening from 1715 to 1840 hours and observed five bats leaving, four of which were captured. These four bats also were identified as *L. brasiliense*, two of which were adult females and two were adult males; none was in reproductive condition. The size, gender, and reproductive condition of the bat caught on 3 January is the same as an individual captured on 5 January, so we can be confident of catching only four different bats during the two nights.

Lophostoma brasiliense typically roosts in aboveground termite nests (Kalko et al., 2006; York et al., 2007), as do other members of the genus (Williams and Genoways, 2007). Although *L. brasiliense* also has been recorded using hollow logs on the ground (LaVal and Rodriguez-H., 2002), this is the first report of the species using a belowground roost. One proposed benefit gained by *Lophostoma* from roosting in termite mounds

Figure 1. Entrance to the belowground cavity where *Lophostoma* were captured.

is a reduction in ectoparasites because of chemicals secreted by the termites (Dechmann and Kerth, 2008). *L. brasiliense* may roost in nests of *Atta* to gain similar benefits, although this suggestion is highly speculative. Given that the nest was no longer occupied by ants, we suggest that a more reasonable explanation is that the bats adopted the hole after the insects left simply because the cavity offered a large, protected space for roosting. Other researchers should monitor mounds of *Atta* or other holes to determine if our observation was an isolated incident or a common occurrence for this or other species of bats.

Acknowledgments.—I thank the students of the 2011 Tropical Ecology Class from Central College, including R. Connelly Atherton, R. Barrett Baker, H. Corbin, N. Crawford (first to notice bats), N. Curran, M. Strait Eeling, K. Freischlag, M. Louis, M. Cain Newton, A. Phipps, R. Schmidt, G. Severns, C. Steward Shimp, A. Vaage, and J. Boat Wilson, as well as faculty members P. Mena and N. Palenske. Additional thanks go to the staff of La Selva, especially K. Alfaro Gonzalez.

Literature Cited

Allen, G. M. 1939. Bats. Dover Publications, New York, New York.

Brack, V., and J. C. Carter. 1985. Use of an underground burrow by *Lasionycteris*. Bat Research News, 26:28–29.

Daniel, M. J. 1979. The New Zealand short-tailed bat, *Mystacina tuberculata*; a review of present knowledge. New Zealand Journal of Zoology, 6:357–370.

Dechmann, D. K. N., and G. Kerth. 2008. My home is your castle: roost making is sexually selected in the bat *Lophostoma silvicolum*. Journal of Mammalogy, 89:1379–1390.

Hall, E. R., and W. W. Dalquest. 1963. The mammals of Veracruz. University of Kansas Publications, Museum of Natural History, 14:165–363.

Hill, J. E., and J. D. Smith. 1984. Bats: a natural history. University of Texas Press, Austin, Texas.

Kalko, E. K. V., K. Ueberschaer, and D. Dechmann. 2006. Roost structure, modification, and availability in the white-throated round-eared bat, *Lophostoma silvicolum* (Phyllostomidae) living in active termite nests. Biotropica, 38:398–404.

LaVal, R. K., and B. Rodríguez-H. 2002. Costa Rica bats. Instituto Nacional de Biodiversidad, Santa Domingo de Heredia, Costa Rica.

Timm, R. M., and R. K. LaVal. 1998. A field key to the bats of Costa Rica. University of Kansas, Center of Latin American Studies, Occasional Publication Series, 22:1–30.

Williams, S. L., and H. H. Genoways. 2007. Subfamily Phyllostominae Gray, 1825. Pp. 255–300 in Mammals of South America. 1. Marsupials, xenarthrans, shrews, and bats (A. L. Gardner, ed.). University of Chicago Press. Chicago, Illinois.

York, H. A., P. F. Foster, M. F. Jones, W. H. Schwarz, A. L. Vezeau, and M. S. Zerwekh. 2007. Observations of cavity-roosting behavior in Costa Rican *Lophostoma brasiliense* (Chiroptera: Phyllostomidae). Mammalian Biology, 73:230–232.

Abstracts of Papers Presented at the

48th Annual Symposium of the
North American Society for Bat Research
Puerto Vallarta, JA, Mexico
October 24th – 27th, 2018

The following abstracts are from papers presented at the 48th Annual Symposium of the North American Society for Bat Research (NASBR). The local hosts for the meeting were Jorge Ortega and Rodrigo Medellín. Meeting abstracts were submitted by Gary Kwiecinski, Shahroukh Mistry, Riley Bernard, Luis Viquez-R., and Emma Wilcox, Program Directors for NASBR. Abstracts are arranged in alphabetical order by first author and, except for minor formatting changes, are published as received. **Student award recipients** are indicated by an asterisk (*****) next to the title of their paper. E-mail contact information for authors is not available.

Acoustic Suppression of Pulse Emissions in a Solitary Bat Species
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How bats mitigate mutual interference is a longstanding question that has both ecological and technological implications as biosonar systems continue to outperform man-made sonar systems in noisy, cluttered environments. Echolocating free-tailed bats display a mutual suppression response, slowing their pulse emission rates when flying in groups to gain a net improvement in sonar performance. We hypothesized that mutual suppression is an adaptation for bats that roost and swarm in high densities. To test this hypothesis, we looked for the behavior in the tri-colored bat, *Perimyotis subflavus*, that is mostly solitary and roosts alone, predicting that it would not decrease pulse emission rates in the presence of echolocation from other bats. We recorded the echolocation of tri-colored bats and measured their emission rates as they flew through an open and cluttered flight room with and without artificial playback mimicking the calls of other bats. The results disproved our hypothesis, showing the same suppression of pulse emission rates with tri-colored bats as we did with free-tails, *Tadarida brasiliensis*. Instead, mutual suppression appears to be a common mechanism for mitigating interference in laryngeal-echolocating bats. In addition, we recorded emission rates as the echolocation of the bats triggered an artificial stimulus and found that there was a decreased emission rate during the stimulus compared to the rate immediately before the stimulus was played. These findings indicate that a similar mechanism for mutual suppression of echolocation exists among different bat species and may be a used by all bats to cope with interference from conspecifics.

Black-tailed Prairie Dog Colonies Attract Bats
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Black-tailed prairie dogs, BTPD (*Cynomys ludovicianus*), are purported to be keystone species in grassland ecosystems and to support as many as 250 plant and animal species. To test if bats were attracted to BTPD colonies throughout the night, SM2BAT sonar detectors were placed within four colonies in montane meadow habitat with edges at least 200 m from nearest forest stands. In addition, SM2s were simultaneously placed at reference sites (montane meadow without BTPD burrows) about 100m from the edge of each colony. Eleven locations in BTPD colonies were sampled over 124 detector nights with 11 reference sites over 122 detector nights in June, July and August. After adjusting all data to passes per night, bat activity was significantly higher in all BTPD colonies than at reference sites (NHCA, $P = 0.0001$; SHCA, $P = 0.0002$; HVR, $P = 0.0006$; and HALL, $P = 0.0001$). Sonar analysis showed that all nine foothills species passed through BTPD colonies during the night but were not equally present. Most pervasive was *Myotis ciliolabrum* for whom 75.8% of passes where recorded in BTPD colonies with 24.2% at reference sites. Perhaps even more surprisingly, *M. thysanodes,* which typically forages within forested stands, showed 58% of their passes within BTPD colonies. *Eptesicus fuscus* and *Lasiurus cinereus* were also consistently prevalent in BTPD colonies. Pass frequency by the other species varied by site. It appears that BTPD colonies have significant positive effects on activity patterns of bats in the eastern foothills of Colorado.

Learning How to Share: Bat-pollinated Bromeliads from Mexico
Pedro Adrián Aguilar-Rodríguez[1,2], Marco Tschapka[3,4], José G. García-Franco[5], Thorsten Krömer[1] and M. Cristina MacSwiney González[1]
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Competition for pollinators among sympatric plant species is crucial to determine the reproductive success of those species, especially in pollinator-dependent ones. Bats are considered one of the main vertebrate pollinator groups in the Neotropics, and their relationship with some plant families is well known. Members of the Bromeliaceae are commonly reported to be visited by nectarivorous bats, but only a handful of night-blooming bromeliads have been studied. In this work, we studied the strategies that allow four sympatric night-blooming bromeliads to avoid competition at sharing bat-pollinators. The study was conducted at Los Tuxtlas reserve, Mexico. We carried out *ex-situ* and *in situ* manual pollination treatments to determine the breeding system of the plants. We sampled bat-visitors by using mist-nets and also infrared cameras. In addition, we determined the nectar production pattern over the night, estimating the energetic content of this reward. All four bromeliads are self-compatible but only one is pollinator-dependent. The blooming season of each species is staggered between them, and the floral morphology segregates the places of pollen placement over the bat´s body. The species that provides the most abundant nectar is visited by three bat species, but the xenogamous species is the one that offers the best reward accounting for the density of flowering plants. Staggered flowering, different pollen deposition on the pollinator´s body and differences in the offered reward might be sufficient to isolate these bromeliads, while facilitating a constant supply of food to maintain a stable nectarivorous bat community.

Roost Size/Type, Microbiota Diversity, and Conservation Status: A Meta-analysis of Mexican Chiroptera
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Larger groups increase the probability of social interaction and its benefits, but also that of pathogen exchange. However, large associations are often socially structured and partner choice can lead to social assortment, reducing the breadth of interactions and microbial exchange. Therefore, species observed in smaller groups should show less diverse microbiota, i.e., the community of microbes at a particular site in a macroorganism, but higher microbial similarity between individuals. Here, we analyse published data on roost size/type and alpha diversity of Mexican Chiropteran´s microbiota, testing for associations between these variables. Our results (1) describe a correlation between microbiota diversity and roost type/size across species; (2) highlight the still relatively low number of publications including the necessary data on microbiota diversity in these species; (3) mention the lower number of studies focused on bat sociality and their microbiota; (4) describe reported diet and habitat diversity as well as (5) the breadth of interspecies interactions, as variables that could explain the above relationships or aid in their conservation. We conclude that due to the diversity of their roosting behavior, that of their habitats and abundances, together with the relatively low number of studies on their microbiota, this order can be a fruitful model for testing hypotheses on the link between microbial diversity, sociality, and habitat use, while providing novel information for implementing particular conservation strategies. We suggest that through the development of such studies we could promote a "multilevel conservation": both of this mammalian order and its microbiota.

Identification and Localization of Gonadotropin Inhibitory Hormone (GnIH) in Brain of Big Brown Bats
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Animals rely on environmental cues to ensure appropriate timing of behavior and physiology essential to successful reproduction. These cues are translated through neuroendocrine signaling in the brain by the hypothalamic-pituitary-gonadal (HPG) axis. When environmental conditions permit, gonadotropin releasing hormone (GnRH) is produced within the hypothalamus and secreted to the anterior pituitary where hormones promoting sex steroid production in the gonads are released into the circulation. The more recently discovered gonadotropin inhibitory hormone (GnIH)

has been found to suppress the HPG axis across vertebrate species examined, but much remains unknown about its function and responsiveness to environmental stimuli. Many temperate bat species exhibit interesting annual reproductive life history strategies, including the separation of mating and gestation by winter hibernation and delayed ovulation; however, the neuroendocrine mechanisms involved, and which environmental cues are important to their timing, remains wholly unknown. We aimed to determine whether, and where, bats produce GnIH in the brain and how it may serve to fine-tune signals within the HPG axis through interaction with other cell populations. In-tact brains were collected from 6 female and 4 male *Eptesicus fuscus* from a wild-caught captive colony housed/maintained at McMaster University. Brains were sectioned and localization and number of GnRH- and GnIH-containing neurons, as well as fiber density, was determined by floating immunohistochemistry. These preliminary results provide the first evidence of GnIH in the brain of any bat species and is a first step toward identifying key neuroendocrine mediators in bats involved in the response to predictable, and unpredictable, environmental conditions.

Fifteen Years of Acoustic Bat Monitoring in the Missouri Ozarks

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Climate change, human-induced land-use change, wind energy development, and introduced disease all threaten bat populations and underscore the need to detect population changes. We used acoustic detection of bats to estimate probability of detection and site occupancy of forest bats in the Ozark Region of Missouri in 2001–2003 (pre-WNS) and resampled sites in 2010–2012 (2010 first WNS) and 2014–2016 (>3 yrs since detection) to evaluate differences. We fit single-species and multi-species site occupancy models to estimate detection probability and site occupancy with "Unmarked" in R and with a Bayesian approach. Eight species were detected at 20% or more of the sites in the 2001–2003 sample and only five species in the resample years. Detection probabilities varied among species but were similar within species across time. Species responded to landscape pattern at different spatial scales (2, 8, and 16 km). Site, patch and landscape characteristics were important covariates in estimates of site occupancy for most species. Riparian features, aquatic habitats, and bottomland forests were important to most species. All species used landscapes with high percentages of forest. We found more consistent and larger effect sizes for landscape- than site-scale relationships in each sample period. Wildlife managers can use this information and approach to evaluate bat population status and trends locally and regionally for planning appropriate conservation strategies.

Multiple Paternity is Common in Litters of *Lasiurus borealis* Based on Microsatellite Analysis

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Most species of bats give birth to only one pup each year, although Eastern red bats (*Lasiurus borealis*) can produce up to five pups per litter. Offspring in a single litter have been documented to be at different stages of development, suggesting that multiple paternity occurs. We tested the null hypothesis of genetic monogamy in red bats using six autosomal microsatellites and one X-linked microsatellite locus from 31 parent/offspring groups for a total of 128 bats. Average litter size was 3.13 pups. We sampled both pregnant females and mothers with pups that were obtained from bats submitted to both Oklahoma State Department of Health and Texas Department of State Health Services for rabies testing. Multiple paternity was assessed using maximum-likelihood methods and X-linked locus exclusion. The mean polymorphic information content of our markers was high (0.8819) and non-exclusion probability was low (0.00027). Results from the maximum-likelihood approach showed that 22 out of 31 (71%) parent/offspring groups consisted of half siblings, and X-linked locus exclusion suggested multiple paternity in at least 10 parent/offspring groups, rejecting our hypothesis of genetic monogamy. This frequency of multiple paternity is the highest reported thus far for any bat species. High levels of multiple paternity have the potential to impact interpretations of population genetic studies and estimates of effective population size in this species. Further, multiple paternity might be a mechanism for increased genetic variation, which could be an important adaptive strategy in this species.

Winter Community Assemblage and Activity Patterns of Bats in the Southeastern United States
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Despite the spread of white-nose syndrome (WNS; *Pseudogymnoascus destructans*) into central North America, the southeastern United States remains free of the disease, likely due to a warmer climate and the absence of caves. In this region, typical cave-wintering eastern bat species such as tri-colored bats (*Perimyotis subflavus*) and federally threatened northern long-eared myotis (*Myotis septentrionalis*) occur year-round. The presence of such species, their documented activity during winter, and the absence of WNS offer a unique opportunity to understand how bat communities fluctuate throughout the winter. In this study, we investigated spatial and temporal activity patterns of bats in managed pine forests of eastern Texas and central Louisiana. From late-December 2017 through late-March 2018, we rotated 12 acoustic detectors weekly through 108 sites and manually identified over 26,000 calls collected during this time. Although common southeastern species such as eastern red bats (*Lasiurus borealis*), seminole bats (*Lasiurus seminolus*), and big brown bats (*Eptesicus fuscus*) were most frequently detected, tri-colored bats and northern long-eared myotis calls were identified throughout the winter from 51% and 64% of detectors, respectively. Interestingly, despite speculation of this area being an overwintering site for long-distance migrants, silver-haired bats (*Lasionycteris noctivagans*) and hoary bats (*Lasiurus cinereus*) were detected more frequently towards the end of the study, suggesting a more southern winter origin. Understanding winter activity patterns of each species will aid in developing informed conservation strategies for this unique region.

***Development of Fibroblast Cultures for North American Bat Species – A Novel Method for Studying White-nose Syndrome**
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*** Briana N. Anderson** received the **WNS Award.**

White-nose syndrome (WNS) causes substantial mortality in certain species of hibernating North American bats. The responsible agent is *Pseudogymnoascus destructans (Pd)*, a fungus which causes increased arousals and energy depletion during the hibernation season. Elevated immune responses have been observed in torpid *Pd*-infected bats, but bat immunology remains under-studied. Tri-colored bats (*Perimyotis subflavus*) and northern long-eared bats (*Myotis septentrionalis*) suffer extensive WNS mortality, while gray bats (*Myotis grisescens*) and big brown bats (*Eptesicus fuscus*) are infected, but mortality is rarely observed. It is hypothesized that there is a difference in immune responses and/or hibernation metabolism between these species, resulting in interspecific variation in disease severity. To test this hypothesis, wing tissue biopsies were obtained in the field and utilized to create fibroblast cultures. Fibroblasts were infected with *Pd*, and RNA-sequencing was used to assess differences between the above four species. Susceptible species' infected fibroblasts over-expressed several immune and metabolic genes compared to uninfected, while resistant species' fibroblasts did not respond to *Pd*. This study has the potential to explain interspecific differences in WNS disease severity, which could assist in establishing treatment and conservation strategies for North American bats. In addition, we have pioneered a cell culture method to address WNS-questions without using live bats; this will allow researchers to address a myriad of questions, such as which western bat species might be most susceptible to WNS as it spreads westward.

Bat Activity in California Redwood Forests Investigated Across a Summer Fog-climate Gradient
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Fog provides critical hydrologic inputs to coastal ecosystems and may mitigate the impacts of higher temperatures and drought associated with climate change. However, little is known about how fog patterns affect terrestrial fauna species distribution and behavior. We investigated bat species distribution in northern California coast redwood forests at 15 independent sites, surveying across high and low summer fog habitat conditions. Two Wildlife Acoustics SM2BAT detectors were deployed for a minimum of 4 consecutive nights at each site in early and again in late summer 2018, with one detector set in the riparian corridor and the second in nearby forest cover. Temperature and humidity were recorded every 10 minutes to relate bat activity to microclimate conditions. Mist netting was done to augment acoustic detection data and to obtain samples for stable isotope analysis of bat body water. Preliminary results show that bat species detected at a study site ranged between 3 to at least 10, and climate

and forest disturbance history may help to explain significant differences in species diversity. Furthermore, significant differences in species presence and detection rates were observed in same-site early and late summer comparisons emphasizing the need for longer term monitoring with multiple detectors to accurately survey species presence and understand summer activity patterns. This ongoing research will ultimately address the value of coast redwood forests as climate refugia, as well as shed light on how climate variables interact with forest management practices to produce habitat conditions that are more or less favorable to different species.

The Chiropteran Wealth of Nations: Higher Taxon Diversity of the Countries of the World

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Geographic patterns of species richness have been thoroughly examined, allowing an understanding of the processes that generate and maintain biological diversity. Richness of higher taxa have received much less attention, despite its importance in deciphering evolutionary processes in deeper time. We present here a global analysis of bat diversity by countries, introducing a method to partition species richness into components of supraspecific taxa (genera and families), allowing the analysis of diversity at different phylogenetic scales. For comparative purposes, we also present data for non-volant mammals. We found that (1) area, the continent in which the country is located, and latitude are the main predictors of a country's taxon richness; (2) species richness is higher in countries with location in the intertropical zone, but bat species richness is less dependent on area than richness of non-volant mammals; (3) in the New World, genus richness is the main contributor to overall diversity; (4) in the Old World, the chief component of overall bat diversity is species richness, whereas the number of orders contribute the highest to non-volant mammal diversity; (5) Old World countries have higher taxonomic diversity of bats than their New World counterparts, but the difference is weaker than for non-volant mammals. In the Old World tropics, bat diversity is associated with relatively few but very speciose genera; in the neotropics, diversity is generated by a high number of genera, each with relatively few species. This dissimilarity is the result of different diversification histories occurring at different time scales.

A Field Test for Interspecific Comparisons of Behavioral Responses in Novel Environments

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Inter-specific differences in habitat use in bats have been explained in relation to morphology and echolocation. Diversity in other behavioral characteristics, in particular exploratory behavior and responses to novel environments, may also contribute to variation in several aspects of bats' behavioral ecology, including differences in roosting habits and habitat use during commuting and foraging. Furthermore, these behavioral responses may influence species' vulnerability to environmental changes. In this study, we investigated the efficacy of field assays for examining behavioral differences in novel environments in an interspecific context. Our goal was to provide conditions that elicit behavioral responses, including exploration, with the simplest possible design. The test cage, sufficiently large for flight, contained a single object that could also be used as a shelter. Six-minute trials were started in the dark, and a light stimulus was introduced mid-trial. We video-recorded and analyzed the behavior of six species of neotropical bats (N = 54 bats) from two families, differing in roosting and foraging habits. Significant differences in activity levels, modes of locomotion, and interactions with the object were detected among species, demonstrating the effectiveness of this field test. Further investigations of the extent of inter-specific behavioral differences in novel environments using this test will allow us to study correlations between species' inherent levels of activity and their use of their environment, such that we can incorporate this behavioral dimension in an ecological context.

***Good Genes or Good Luck? Little Brown Bats Show Signs of Evolutionary Adaptation to White-nose Syndrome**

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*** Giorgia G. Auteri** received the **Luis F. Bacardi Bat Conservation Award.**

Due to white-nose syndrome (WNS), many species of bats are experiencing tremendous population declines. Whether populations are evolving in response to the disease and to what extent they have experienced a genetic bottleneck are of great conservation interest. We collected tissue from little brown bats (*Myotis lucifugus*) in Michigan, USA that had been found dead from WNS and adults that had apparently survived hibernation in a WNS-positive area. A shotgun sequencing approach was used to look broadly across the genome. Genetic drift was estimated using *F* statistic. An F_{ST} outlier approach was used to identify sites under selection. We identified a total of 19,797 SNPs among 29 mortalities and 9 survivors. The survivors showed signs of a severe genetic bottleneck, with genetic drift an order of magnitude greater compared to mortalities (mean $F = 0.04$ versus 0.006). However, we also found nine single-nucleotide polymorphisms apparently under positive selection. Three of these are within coding mRNA coding sequences. The most extreme outlier, *FOXP2*, is involved in echolocation and sensorimotor function, potentially indicating diet (prey type or hunting ability) during summer is important for contributing to survival. Another of the genes is involved in histamine reception, which likely has a downstream influence on the immune response to WNS. Our findings suggest that this species is capable of adapting to WNS but is also sensitive due to greatly reduced genetic diversity within the population. that it is important to protect populations in both their summer and winter ranges.

Effect of Capture Handling on Vocalizations of *Molossus rufus*

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Individual microchiropteran bats use vocalizations not only to detect food and objects in the surrounding space, but also to share information with conspecifics. Individual bats that are under perceived attack of potential predators or are subjected to potential dangers may produce distress calls and may suffer physiological stress. Both responses may be exhibited by bats when humans manipulate them even if they do it gently. Therefore, vocalizations recorded immediately after manipulation could be influenced by previous states of stress. In this study, we performed simple experiments in an urban open setting to evaluate the influence of manipulation by bat researchers on time and frequency parameters of vocalizations of *Molossus rufus* recorded at 10 and 50 m away from release point. Most bats did not produce vocalizations when subjected to stressful situations such as entering the mist net or staying in the cloth bag, but they did vocalize when were removed from the net or handled to obtain standard data. Vocalizations recorded at 10 m from release point had significantly higher frequency, wider amplitude, shorter duration, and shorter interpulse interval. Because distress calls were not always observed, we suggest that differences in call parameters recorded from the same individuals at different distances were caused by proximity to obstacles or altered physiological states rather than by distress-call inertia. Our results suggest that reference calls recorded at short distances from the microphone should be taken cautiously at least for species with high vocal plasticity such as *M. rufus*.

Seasonal Intake Responses Could Reflect Digestive Plasticity in the Nectar-feeding Bat *Anoura geoffroyi*

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Many studies have used intake response as a tool for understanding digestive capacities of bats to process nectar. Nevertheless, most of them have been done in one season, assuming that this response does not change over the year. One study performed with *Glossophaga soricina* found different intake response over seasons, but these changes are unknown for other bat species; especially those inhabiting cold climates. We measured changes in volumetric intake of *Anoura geoffroyi* (which can be found in places above 2, 500 m a.s.l.) feeding on sucrose concentrations (from 5 to 35% wt./vol.) in spring and compared the results with those published for winter. Because of differences in ambient temperature and nectar availability in the places they inhabit, we predicted different intake

responses among seasons. Contrary to winter, when bats obtained a constant energy intake and body mass gain of 101.07 ± 5.4 kJ, and 1.31 ± 0.1 g, respectively; bats obtained from 23 to 37 % less energy and reduced their capacity to gain body weight from 56 to 74 % when fed on sugar concentrations <15 in spring. Seasonal differences in intake responses could explain digestive plasticity, which may have important ecological implications for bats. Species able to change their digestive traits would have the capacity to change their food intake depending on the energy demands imposed by their environment, while those with low plasticity should change their behavioral and energy-saving strategies when confronting changes in the abundance or the nutritional quality of the nectar they consume.

Landscape Features Associated with Fatalities of *Lasiurus cinereus* at Wind Energy Facilities

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Currently, fatalities at wind energy facilities are the greatest known sources of mortality for migratory tree-roosting bats. Between 840,000 and 1.7 million bats were killed by wind turbines in the U.S. and Canada from 2000-2011, ~80% of which were of three species of migratory tree-roosting bats (*Lasiurus cinereus, L. borealis,* and *Lasionycteris noctivagans*). Recent studies suggest that fatalities are negatively affecting populations of these species. To reduce the impacts of wind energy on bat populations, developers and operators can locate projects in areas of low fatality risk, but this is challenging because habitat use by migratory tree-roosting species of bat is not well-understood. Intuitively, high-risk areas are within spaces that concentrate migrating bats (e.g. riparian corridors or ridgelines), but these spaces are not well-defined. However, recent modelling based on fatality data from wind energy facilities in Ontario, Canada suggest that fatality risk is correlated with landscape features, such as distance to forest and proportion of water and cropland. The data also suggest that fatality rates are correlated more with habitat surrounding a facility (i.e. within a 25 km radius) than within a facility (i.e. within a 1 km or 5 km radius). This knowledge can be used in siting future developments.

The Influence of Artificial Lights on the Foraging Efficiency and Diet of Insect Eating Bats

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Artificial lights may be altering the interactions between bats and moth prey. Unable to make use of bat evasion strategies around lights, eared moths are susceptible to exploitation by syntonic bats (using echolocation frequencies between 20–50 kHz within the hearing range of eared moths). We evaluated the foraging success of syntonic bats and rarer allotonic bats (using echolocation frequencies outside the hearing range of eared moths), in areas with artificial lights and in naturally dark areas, using a handheld plasma metabolite analyzer (STAT-Site M β-HB; Stanbio Laboratory, USA). We used microcrope diet analysis to determine whether bats were consuming more or fewer moths in respective areas. *Pipistrellus hesperidus* individuals trapped around artificial light sources showed variation in plasma metabolite (B-OH) levels, alluding to foraging responses of individual syntonic bats to artificial lighting. Our data emphasizes the need for a better mechanistic understanding of the influence of artificial lighting on the foraging success of bat species. Bat-moth interactions may be influenced by other factors apart from the common assumption that increased refueling rates will occur in syntonic species foraging on moths around artificial lights. Syntonic bats increased selection for moth prey under lit conditions, owing to a reduction in tympanate moth defenses. Eared moths may increase in the diets of generalist syntonic bats foraging around artificial light sources, as opposed to syntonic species with a slightly more specialized diet. The foraging success and diets of allotonic bats, *Rhinolophus capensis*, appear to be negligibly impacted by artificial lighting on a small scale.

Using Structured Decision Making to Identify Management Actions for Combating White-nose Syndrome
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Decisions regarding the conservation of species impacted by emerging infectious diseases are challenging. Wildlife managers must balance trade-offs between mitigating the effects of disease and the implications their actions have for other management objectives. The fungal disease white-nose syndrome (WNS) has decimated bat populations throughout eastern North America and continues to move west. With 33 migratory bat species in Texas, the likelihood that many of these species will be exposed to and spread *Pseudogymnoascus destructans* to uncontaminated sites is high. Thus, we held a structured decision making workshop to assist Texas Parks and Wildlife Department to explicitly incorporate multiple objectives, uncertainty, and risk in their decision process. The decision problem focused on *Perimyotis subflavus*, a species known to be highly susceptible to WNS across its range. The number of potential trade-offs for this decision were minimized by considering alternatives for colonies that hibernate in culverts in East Texas rather than in natural caves. Alternatives included individual actions that may act against *P. destructans* and benefit bats, as well as a no action option, and combinations of actions. We also considered mitigation measures for natural caves to assess transferability of the decision model. The optimal, or best, decision differed for culverts and caves, indicating that a single treatment for WNS applicable for all scenarios is likely not feasible. However, we did identify several alternatives that were viable for implementation in Texas culverts that may yield persistent colonies of *P. subflavus* into the future.

On Roosting Ecology and the Evolution of Bat Landing Maneuvers
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The roosting habits of bats are critical aspects of their ecology. Diverse roost types protect bats from weather and predators while facilitating thermoregulation, maternal care, access to mates and food, and information transfer through social interactions. We hypothesize that the physical properties of roosts also have influenced the evolution of bat landing maneuvers. We tested this by documenting 471 landings from 34 species (21 genera, nine families) in the lab and at field sites in Belize, Bulgaria, China, and Costa Rica. We trained bats to land on a ceiling-mounted force plate and recorded landing impact forces and kinematics using high speed videography. We observed three landing styles: two-, three-, and four-point landings. In two-point landings, bats grasped attachment sites using both feet and employed complex body rotations to invert their bodies before contact, enacting low-impact landings. Bats using three- and four-point landings made additional contact with one or both thumb claws and performed simpler body rotations, resulting in higher impact forces. All individuals within a species used the same style, except in two cases. Phylogenetic character mapping suggests that two-point landings evolved convergently in Phyllostomidae and Rhinolophidae, and appear correlated with roosting on stiff surfaces, such as cave ceilings, where low-impact landings could reduce injury. Three-point landings evolved in tent-making phyllostomids. Ancestral state reconstruction estimates that four-point landings are basal. Our results suggest that bat ancestors landed using all four limbs, similar to maneuvers executed by gliding mammals, and that complex landing styles evolved to accommodate novel roost types.

Changes in Intra-hibernacula Use by the Endangered Indiana Bat in Response to White-nose Syndrome
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Numerous researchers have identified potential mechanisms by which the fungus *Pseudogymnoascus destructans*, causative agent of white-nose syndrome (WNS), has devastated populations of bats that hibernate in caves (and mines) in North America. The unifying theme is disruption of hibernation with observations that bats now hibernate in different locations within the hibernaculum, typically closer to the entrance and at colder temperatures, than

before WNS. Unfortunately, locations and temperatures used over time pre-WNS are often poorly documented and post-WNS documentation is often anecdotal. This study documents location and temperature (microclimate) use patterns pre- and post-WNS, and changes in those patterns, by the endangered Indiana Bat (*Myotis sodalis*) in Priority I hibernacula (historic populations of 10,000 individuals) in Indiana and Ohio. Data were obtained from winter intra-hibernacula surveys from up to 30 years before the advent of WNS and typically for 4 to 6 years following arrival of WNS. Pre-WNS, bats used a wide variety of temperatures and locations and as numbers of individuals using a hibernaculum increased so too did diversity of use, indicating there is no single microclimate that meets the breadth of individual needs for hibernation. Post-WNS, populations of Indiana bats continue to use a variety of microclimates, even as populations change in numbers and sometimes shift among hibernacula. At some hibernacula, post-WNS microclimate use matches Pre-WNS use. These data highlight the danger in managing for a single "best" post-WNS microclimate.

Use of Thermal Videography for Monitoring Colonial Bats

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Knowledge of population trends for threatened, endangered, and at-risk species (TER-S) is important for efficient conservation efforts. Some species form large colonies that open up the possibility of improved monitoring efforts. We developed a monitoring system using thermal videography and custom-built analysis software to automate the monitoring of colonial roost sites. The objective of this project is to demonstrate and validate use of thermal videography and automated analysis for censusing bats as they emerge from their roost sites. This system was deployed at 6 different colony sites over 18 nights of data collection that ranged in population size, roost structure, and background conditions. Thermal cameras were used to record emergence of animals from their roost sites and recorded imagery was analyzed using a digital image processing program developed at the US Army Engineer Research and Development Center. Manual analysis of imagery was compared to results of automated imagery from each site to validate the output from the automated system. Initial results demonstrate the high correlation between manual and automated image analysis. This ability of the automated system to monitor populations of colonial animals will greatly improve monitoring efforts in areas where animals naturally congregate, thereby allowing for improve data on population trends that will assist in future conservation efforts.

Behavioral Strategies for Olfactory Tracking in Bats

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Tracking odors and locating their source is a complex task. Successful tracking requires a suite of adaptations in nasal anatomy and sensory physiology, central nervous system processing, locomotion patterning, and behavioral strategies. The majority of olfactory navigation research has been conducted in invertebrates, with few of these results extended to vertebrate species. Olfaction is a key sense for frugivorous bats, but their behavioral capacities and the mechanisms exploited by bats to detect and follow an odor plume have not been investigated. We used an olfactory behavioral assay to quantify the olfactory search patterns of little yellow-shouldered bats (*Sturnira parvidens),* a Neotropical fruit-eating species. Crawling individuals were first trained to seek out a food reward (banana) and then placed in a test chamber where they were presented with a choice between control and odor-infused solutions of decreasing concentrations to evaluate how olfactory discrimination and tracking behavior change with strength of odor (as a proxy for distance). Bats successfully navigated to the odor source across a 1000 - fold range of odorant concentration. Video analyses were used to quantify the time-course, search trajectories, and movement patterns of the bats localizing odors of different concentrations. The results provide a baseline for building a model of how bats perceive and track odors in their environment and begin to address how bat odor tracking compares to other animals. Understanding the olfactory behavioral strategies bats use to locate resources is important for predicting how environmental conditions influence foraging and decision-making by bats at the landscape scale.

Flies in a Web: Can Community Network Structure Explain Host Specificity of Ectoparasitic Bat Flies?
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Ecological studies on ectoparasites have the potential to clarify patterns of host specificity, coevolution, and network community structure. Obligate ectoparasitic bat flies have been considered highly host specific due to cospeciation with their bat hosts. However, recent studies indicate that cospeciation may not be as common between bat flies and their hosts. Ecological factors such as bat roost-sharing and community dynamics may be more important in explaining patterns of bat fly specificity. We collected bat flies from 493 bats from the Atlantic Forest of Brazil, identified them morphologically, and sequenced the cytochrome oxidase I gene (COI). Of 769 total flies sequenced, 498 yielded high-quality reads that were trimmed, aligned, and used to construct a RAxML parasite tree with 1000 bootstraps in the CIPRES online gateway. To determine incidences of cospeciation across the phylogenies, we paired the topology from this RAxML parasite tree with a pruned host bat tree to create a host-parasite tanglegram. We then used Jane v. 4 to run a cophylogenetic simulation with 300 iterations and default cospeciation parameters. To evaluate the factors that influence host-parasite associations (e.g., host bat phylogeny, host bat roosting ecology, community/environmental factors), we constructed a bipartite network depicting host/parasite associations and used multiple regression on distance matrices (MRM) to measure the influence of various host and parasite traits. We found 9 incidences of cospeciation across the cophylogeny, representing 21.4% of all evolutionary events detected. The MRM and network analyses are still underway and will be completed prior to the commencement of this meeting.

Long-term Banding of California Leaf-nosed Bats Along the Lower Colorado River to Determine Movements and Longevity
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California leaf-nosed bats (*Macrotus californicus*) are residents of the Sonoran Desert in California and Arizona and are active all year. These populations are interesting in part as the northern margin of the largely tropical distribution of a non-hibernating phyllostomid genus. In 1958, a long-term banding study was initiated to examine demography and movements of these bats in the temperate zone along the Lower Colorado River (LCR). The bats were captured principally in the winter in warm mines along the LCR in seven mountain ranges. In 60 years, over 15,000 bats have been banded, and almost 5,000 individuals have been recaptured between one and eight times, for a total of over 8,500 recapture events. Roost fidelity is high, with occasional movements between adjacent mountain ranges between years and seasonally. The longest interval between initial banding and recapture is 16 years, which is an impressive age for a bat of tropical ancestry. At the time of banding, the degree of tooth wear (1–4) was recorded initially and during subsequent recaptures to establish a metric to determine the approximate age of unbanded bats in the population.

Factors Impacting Distribution of *Myotis sodalis* Maternity Colonies in Illinois
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From 2016–2018, the Illinois Bat Conservation Program conducted mist-net and telemetry surveys to expand knowledge of bat distributions in Illinois. Using this data, as well as existing *Myotis sodalis* occurrence data shared by the Illinois Department of Natural Resources and the United States Fish and Wildlife Service, we are creating presence-only Species Distribution Models with MaxEnt to identify factors that may affect the distribution of *M. sodalis* maternity colonies in Illinois. Predictors include: proximity to hibernacula, distance to landscape features, landscape composition, and landscape configuration. We conducted surveys during the 2016–2018 maternity season, concentrating effort in areas with knowledge gaps. We mist-netted for 74 nights at 20 study areas and captured 246 bats of eight species. We captured 17 *M. sodalis* and attached radio transmitters to 11 reproductively active

female *M. sodalis*. We located eight maternity colonies, 21 new maternity roost trees and one roost triangulation. The average distance from roost tree to nearest hibernacula was 63.6 km ± 6.02 (SE). Few maternity records were located in parts of central Illinois where forest cover is fragmented and in areas that are farther from hibernacula. New maternity observations continue to be made where previous records did not exist, expanding our knowledge of *M. sodalis* distributions and landscape-scale habitat requirements. Ultimately, these data and models will aid in improving our understanding of *M. sodalis* maternity colonies and inform forestry management practices in Illinois to support habitat for this federally listed species.

Population Genetics of the Frugivorous Bat *Sturnira parvidens* (Chiroptera: Phyllostomidae)

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Bats of the genus *Sturnira* are an excellent study model to analyze patterns and processes of diversification and endemism in Mesoamerica. *Sturnira parvidens* is a lowland species that occurs from Mexico to Talamanca Mountains in Costa Rica. Phylogenetic analyses show that this species represents a monophyletic group, and phylogeographic evidence defines two lineages within it: one haplogroup on the Mexican Pacific Slope and another one along the Gulf of Mexico-Central America Slope, with the boundary between both units in the Balsas River Basin. Here, we analyze recent genetic information to generate a complete reconstruction of its evolutionary history. We used data from 10 microsatellite *loci* of 136 individuals from different localities throughout the species' geographical distribution, obtained from scientific collections. We recovered and recognize the existence of two lineages within *S. parvidens*, as was previously reported using mitochondrial genes. Nevertheless, with nuclear *loci* we found the boundary between both groups in the Mexican state of Oaxaca, along the dry region of Tehuacán-Cuicatlán and Oaxaca Valleys. We suspect there is probably a strong maternal phylopatry and the genes dispersion could mainly rely on the males. Unifying the results from molecular markers with different forms of inheritance and mutation rates can help to identify evolutionary processes that could not be detected or visualized with any of these markers independently. This approach can help us interpret with greater confidence the historical and contemporary events that have affected the diversity and genetic structure of the populations.

Diversity of Bats in Four Archaeological Zones: Chichén Itzá, Dzibilchaltún, Ek'Balam and Uxmal in Yucatán, Mexico

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The archaeological zones (AZ) of the Yucatan peninsula in Mexico are invaluable for their historical and cultural importance. However, little is known about the biodiversity they maintain and only a few studies have focused on the wildlife living in them. We identified and compared the diversity of bats in four AZ in Yucatan: Chichén Itzá, Dzibilchaltún, Ek'Balam, and Uxmal. We surveyed in wet and dry seasons, six days and nights per site. With mist nets and active roost search we found 23 species of bats representing six of the seven families described for the state, of which two are listed as threatened in Mexico. We recorded 52 roosts, most of which were inside archaeological structures. We found no differences in species richness among AZs nor between seasons. The species turnover showed that the communities of the four AZ were similar (1.61 equivalent communities I.C. = 1.49–1.74). We suggest that the diversity of bats is related with the complexity and structure of the surrounding vegetation and the presence of cenotes. Our results highlight the role of the AZ for the maintenance of bats and the ecosystem services they provide as they afford artificial roosts that offer protection against weather and predators. Furthermore, the richness founded in each AZ was equal or greater than some natural protected areas in the region. Our results emphasize the need to secure, recognize, and include AZ in conservation plans given their role as reservoirs of important bat populations and species.

Morphological and Ecological Differentiation in *Glossophaga soricina*

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Glossophaga soricina is a broadly distributed tropical bat species, which has been classified in five subspecies determined by the geographic regions they occupy. Despite the apparent morphological similarity between

subspecies, studies have found high levels of intraspecific molecular variation, especially between populations separated by The Andes, which could suggest the existence of cryptic species. However, no taxonomic conclusions have been made regarding this matter. In this study, we used geometric morphometric methods to explore the patterns of morphological differentiation between subspecies aiming to detect differences unnoticed by traditional morphometric methods, and we tested ecological niche similarity to infer the possible mechanisms underlying the differentiation. Significant differences in skull and jaw shapes were found between all subspecies and between sexes, along with high levels of ecological niche overlap (D = 0.835) between populations at one side and the other of The Andes. This might indicate that, despite the generalist character of this species, the ecological barrier imposed by The Andes uplift created a sub-optimal region that stopped gene flow between this populations with similar ecological niche requirements, between which allopatric speciation could be occurring. Using multidisciplinary approaches has proven useful for understanding the evolutionary processes involved in the diversification of Neotropical biota and its taxonomic implications. We suggest the inclusion of genetic evidence in this study to test our findings and to shed light on the knowledge of the evolutionary history of this species.

Species Limits and Phylogenetic Relationships Within *Anoura* Gray 1838

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Classical and geometric morphometrics have determined that the Neotropical nectarivorous bat genus *Anoura* Gray 1838 has 10 currently species; these taxonomic revisions have not included all closely related species. The study of their phylogenetic relationships has focused on the position of *Anoura* within the Glossophaginae and on the broader understanding of the evolution of Noctilionoidea. But if we want to understand the species limits within the genus it is necessary to include both morphometric and genetic approaches. We conducted a clustering analysis using Normal Mixture Models to find gaps in the normal distributions of 12 cranial and 11 external morphological measurements commonly used in the description and diagnosis of *Anoura* species and we quantified the shape of the last upper premolar (P4) using Elliptical Fourier Descriptors. To complement our analysis, the molecular phylogeny uses Ultra Conserved Elements and mitochondrial loci. The morphometric analyses using Normal Mixture Models do not support a clear separation within large or small *Anoura* species. We find that the morphospace generated by the shape of the P4 separates *A. geoffroyi* from *A. latidens*, with the type specimen of *A. carishina* nested well within the morphospace of *A. latidens*. However, both species shared part of the morphospace. We propose to treat *A. carishina* as a junior synonym of *A. latidens*, and provide new localities for this species in South America and so expanding its range to Northern Bolivia. Finally, we present an updated phylogeny including all recognized species in the genus.

Development of New Cooperative Relationships in Vampire Bats

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Some animals form enduring cooperative relationships that greatly bolster their fitness. But how does such a relationship develop between complete strangers? One important but untested theory is that individuals develop new cooperative relationships by ‘raising the stakes’ or ‘testing the waters’. They use gradually increasing low-cost investments, such as allogrooming, to decide on whether to make higher-cost investments. This behavior has been demonstrated in human strangers playing cooperative games but not in cooperative behavior within a nonhuman animal. To test this hypothesis, we tracked the formation and dynamics of cooperative relationships between previously unfamiliar wild-caught vampire bats. Using controlled introductions and captive fasting trials, we created opportunities for new food-sharing relationships to either form or not. We generated 38 new food-sharing links between adult past strangers (16% of possible cases) and 73 new sharing links (9% of possible cases) between wild-caught adults and the 14 captive-born bats. We sampled the complete history of grooming between past strangers to see what patterns predicted the success or failure of a new food-sharing relationship. New relationships formed faster between strangers housed in isolated pairs. Bat A’s propensity to groom bat B predicted the probability that B later fed A before the first donation occurred. The A-to-B grooming rate increased asymptotically only up until B fed A. Grooming rates also became more symmetrical over time, but only in new dyads that later shared food. Taken together, confirmation of these four key predictions suggest that vampire bats do form food-sharing bonds by ‘raising the stakes’.

The Energetics of Social Signaling During Roost Location in Spix's Disc-winged Bats
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Long-term social aggregations are maintained by multiple mechanisms including the use of acoustic signals, which may nonetheless entail significant energetic costs. To date, however, no studies have gauged whether there are significant energetic costs to social call production in bats, which heavily rely on acoustic communication for a diversity of social tasks. We measure energetic expenditure during acoustic signaling in Spix's disc-winged bats (*Thyroptera tricolor*), a species that commonly uses social calls to locate the ephemeral furled leaves that they use for roosting. To facilitate this task, *T. tricolor* uses 'inquiry' and 'response' calls; the former is used to maintain contact with group members during flight, whereas the latter are used to signal roost location. This exchange of acoustic signals results in group members rapidly locating and entering the occupied tubular leaf. To determine the cost of sound production in roosting bats, we measured oxygen consumption using open-flow respirometry methods, with and without social signaling. The social signaling trial involved the emission of inquiry calls during a 10-min period during which we recorded the number of response calls produced. The non-social signaling trials used the same method except no inquiry calls were broadcast. Our results suggest that the emission of acoustic signals, including response and echolocation calls, increase oxygen consumption, and that even a few response calls may demand a significant energetic investment; this may explain the presence of different vocal roles in this species.

Exploring the Indirect Mutualism Between Fruit-eating Bats and Endophytic Fungi
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Indirect interactions in ecological networks, i.e. those that occur when the association between two species is modified by a third one, are ubiquitous and critical for shaping the bonds among species, yet are still poorly understood. We explored the hypothesis of an indirect mutualistic relationship within a plant-animal seed dispersal network, specifically focusing on the endophytic fungi that grow within the tissues of fruits that bats eat. Bats are important long-distance dispersers of many tropical plants, yet, by consuming fruits they may disperse not only the plant's seeds, but also the fungi that are contained in those fruits. We characterized fungal communities in fruits of the tropical fig tree (*Ficus colubrinae*) and in feces of the Honduran white bat (*Ectophylla alba*) using targeted amplicon metagenomics (or metabarcoding) to determine if passage through the digestive tract of the bats affected total mycobiome species composition and abundance. Among the most significant results, we show a reduction of >70% in abundance of fungal species known to be plant pathogenic after passage through the gut, while abundance of species known to have antifungal and antibacterial properties significantly increased. These findings suggest that the role of frugivores in plant-animal mutualistic networks may extend beyond seed dispersal: they also promote the dispersal of potentially beneficial microbial symbionts while hindering those that can cause plant disease. This study is a first step towards identifying an interaction that may have consequences for the preservation of healthy tropical ecosystems and provides additional reasons for the conservation of near-threatened animal species, such as *Ectophylla alba*.

Testing Predictions of Optimal Migration Theory in a System of Migratory Bats
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Optimal migration theory has been used for over 25 years as a theoretical framework to evaluate tradeoffs in migratory strategies. The strategies most frequently considered by migration theory are time minimizing, whereby migration is completed as quickly as possible, and energy minimizing, whereby migration is completed as energetically efficiently as possible. Despite an extensive amount of literature dedicated to generating analytical predictions about differences in migratory strategies, identifying appropriate study systems to empirically test predictions is difficult. Due to the qualitative nature of migration theory predictions that compare migratory strategies, empirical tests require that both time-minimizers and energy-minimizers are present in the same

population. We investigated a system of spring migratory silver-haired bats and hoary bats where males and females exhibit different migratory strategies depending on their life history traits. We tested migration theory predictions related to fuel loads and show that, as predicted, time-minimizers have an increased fuel load relative to energy-minimizers. We then use two methodologically novel approaches to investigate if increased fuel loads were achieved by a decrease in energy expenditure, an increase in digestive efficiency, or an increase in foraging effort. We find that time-minimizers have increased fuel load relative to energy-minimizers in accordance to migration theory predictions, but likely achieve increased fuel loads via carry-over effects. This research is the first to validate a migration theory prediction in a system of both time and energy minimizers and uses novel methodological approaches to uncover underlying mechanisms of migratory stopover use.

Tropical Bats as Potential Reservoirs of Lyme Disease in Mexico

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Borrelia burgdorferi sensu lato (s.l.) complex is a group of spirochaetal bacteria that comprises the etiological agents of Lyme disease [LD]. The enzootic life cycle of these pathogens are complex networks that group several hard tick species, primarily from *Ixodes* genus. These genus species feed on a broad spectrum of competent wild vertebrate hosts including bats. In Mexico, scattered information about LD agents is available, however, studies are centered in north and southern Mexico. The aim of this study was to identify the presence and prevalence of *Borrelia* in several neotropical bat species from Veracruz, Mexico. For this, 43 individual bats were collected in the region of "Los Tuxtlas" in Veracruz. Necropsy was performed and a portion of spleen was fixed in 90% ethanol. DNA extraction was performed using Cheelex-100 resin, and amplification of *flagelin* gene was used to calculate *Borrelia* prevalence. A total of six individuals were positive to *Borrelia* DNA which represent a 13.9% prevalence. This is the first study in evaluating the potential role of Mexican populations of neotropical bats as reservoirs of *B. burgdorferi* sensu lato. The findings of this study suggest the possibility of an enzootic focus of *B. burgdorferi* sensu lato in this tropical region, also, ecotourism activities are practiced in this area, raising the risk of contact of human populations and tick populations. These results highlight the need to establish acarological surveillance to detect possible vectors.

Molecular Determinants of Bone Health Across the Lifespan of Long-lived Big Brown Bats

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With age, most mammals experience declines in signaling within the *TGF-β1* pathway, leading to bone degeneration. Big brown bats (*Eptesicus fuscus*) live up to 20 years, which is over 3 times longer than similar sized terrestrial taxa. To test whether big brown bats undergo age-related declines in signaling within the *TGF-β1* pathway, we utilized a known-aged colony and compared data to age-matched C57BL/6 mice. We undertook comparative RT-qPCR assays of the humerus, radius, and metacarpals of mice and bats throughout the lifespan, as well as culture assays of osteoprogenitor cells harvested from the same bones. An RNASeq assay was also performed on the radii of young and elderly bats and mice. Whole bone *in vivo* assays showed elderly bats displayed uniquely elevated levels of *P38* and collagen (*COL1A1*) and sustained levels of *TGF-β1*. Mice showed diminished expression of both genes with age in whole bones, and fewer fibers in culture. Similarly, our RNASeq analyses showed elderly bats, not elderly mice, display greater transcripts of *FBN-1* and *MFAP5*, which act to enhance extracellular microfibril function in regulating the bioavailability of *TGF-β1* and overall bone homeostasis. Data suggest that *in vivo* and *in vitro* bone cells fail to undergo age-related declines in *TGF-β1* signaling that are hallmarks of skeletal aging in mice.

Bat Acoustic Activity During Fall at Wind Turbines in South Texas

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Tadarida brasiliensis, primarily a cave and structure roosting species, is documented to incur high fatalities at wind turbines within their range. Despite their high abundance in Texas, the largest producer of wind energy in the US, there is little knowledge on their activity patterns and behavior at wind turbines. Such knowledge is important for designing species-specific impact reduction strategies. The objective of our study was to identify patterns in *T.*

brasliensis behavior and activity at wind turbines to identify high risk behaviors and periods for informing impact reduction strategies. From 7 August to 28 October 2017, we monitored bat activity at three wind turbines at a wind energy facility in Starr County, Texas. At each turbine we deployed an acoustic detector on the nacelle, and conducted weekly fatality searches within established search plots. Here we present preliminary acoustic detector and fatality results. We recorded 65,423 total bat passes, with the highest activity occurring on 4 September (4,030 total bat passes). Of the total recorded bat passes, 99% were classified as low frequency and possible *T. brasliensis*. We also documented differences in activity among turbines. Nightly bat activity was unimodal, primarily occurring from 10pm to 3am. In addition, bat acoustic activity reflected patterns of fatality at the site. Although preliminary, these results provide information on bat behavior at wind turbines in a region with little publicly available data.

Phylogeography of *Artibeus fraterculus* (Chiroptera: Phyllostomidae) in South America

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Artibeus fraterculus is endemic to Ecuador and Peru. Most of its distribution is restricted to the West side of the Andes especifically throughout the Tumbesian ecoregion. Its habitat is mainly xeric forest and scrub and distributed from 0 to 1600 along the elevational gradient. Very little is known on the population genetics structure of *Artibeus fraterculus* and the effect of the Andes on its distribution and as a potential barrier for its populations. Using UCEs (Ultra Conserved Elements) patterns of genetic divergence among populations of *A. fraterculus* from different locations along Ecuador and Peru were analyzed. A total of 1406 UCE loci were obtained in which all the individuals analyzed were represented. All of the UCEs were concatenated and a phylogenetic analysis from this data set was carried out using RaxML. In addition, to investigate population structure, the program Structure 2.3.4 was used. A phylogenetic tree was recovered, that showed two distinct clades, corresponding to the location of the populations at each side of the Andes. This result is part of an ongoing research and is showing that apparently there is an effect of The Andes as a barrier to gene flow for this two populations of *A. fraterculus.*

Seed Preference and Dispersal by Bats in the Botanical Garden Xoyoquila, in Puebla, Mexico.

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Bats play an important role in seed dispersal, this is the result of the strategies that plants use for regeneration, which depends on the ability of the plant to disperse their propagules and colonize the area. The objective of this work is to evaluate the diversity of the species propagated by bats in the Botanical Garden Xoyoquila with which we may be able to determine the importance of bats in seed dispersal in this garden. We captured 78 bats of nine species during March 2015 to march 2016 in the Botanical garden from Xoyoquitla, Puebla, Mexico. One hundred seed samples were collected from bats, 25 plants species were registered. The plant species that were dispersed by a greater number of bats (5) were *Piper aduncum*, *P. hispidum* and *Saurauia scabrida*. While bat species that disperse a great number of plants were *Sturnia parvidens* (16), *Glossophaga soricina* (11) and *Artibeus jamaicensis* (7). Of the total seed samples 21% belong to *P. hispidum*, 14% belong to *P. aduncum* and 13% to *Saurauia scabrida*. In all the species that were part of the sample, with the exception of *Platyrrhinus helleri* and *Pteronotus parnellii*, they tend to have at least one of the species of Piper spp. In bats' diet, this species represents 49.49% of the total of samples, cataloging it as a species of great importance in the diet of the bats of the botanical garden Xoyoquila, besides representing an ecological importance for the dispersion of seeds and used in reforestations programs.

Variation in Summer Habitat Use in Three Sympatric Species of Forest Bats in the Central Appalachians

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Morphological differences among sympatric forest bat species should predict ecological differences. Smaller bats are able to navigate cluttered forests, but likely stay near water and roost sites, while larger species require less-cluttered areas but may be able to fly farther. We contrasted the foraging and roosting ecology of three morphologically-different forest bat species: *Myotis leibii* (MYLE), *Perimyotis subflavus* (PESU), and *Eptesicus fuscus* (EPFU) in Cumberland Gap National Historical Park in the Central Appalachian Mountains. We combined

acoustic detections from 45 trail sites and mistnet captures from 15 trail, stream, and cave sites (surveyed 15 May–7 August 2018) to generate unique presence points by species (30 EPFU/23 MYLE/9 PESU). We used MaxEnt to create distribution models by species. We tracked 2 EPFU, 5 MYLE, and 4 PESU to roosts (n=6, 5, and 14, respectively) and foraging points (n=140, 158, and 165, respectively), which included live trees, buildings, and rocky slopes. Foraging home ranges were largest for EPFU (4.51 km^2), followed by PESU (2.55 km^2) and MYLE (1.84 km^2). Roost mean distance-to-stream was shortest for PESU (375 m), followed by MYLE (531 m) and EPFU (770 m). EPFU used live-damaged trees during the day and foraged on both ridges and in lowlands at night. PESU live tree roosts and foraging areas were closely associated with streams. MYLE foraging ranges were closely associated with their roosts in historic cabins and shale rock. These sympatric but morphologically-distinct bat species varied in habitat associations and space use in this montane landscape.

Blastocystis Search in a Bat Community from Mexico City

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Blastocystis is a common intestinal protozoan associated with human irritable bowel syndrome, it is worldwide distributed and water-borne transmitted. And in order to know its roll as zoonotic pathogen, this parasite has been searched and identified in feces from several mammals as non-human primates, artiodactyls, perissodactyls, proboscideans, rodents and marsupials, however, has not been looked in order Chiroptera. The aim of the present was to search *Blastocystis* in scats of three bat species from Mexico City that live in close proximity to humans and polluted water sources. For a whole year 366 bats were captured (267 *Tadarida brasiliensis*, 86 *Myotis velifer* and 13 *Nyctinomops macrotis*), from them 213 feces (162 *T. brasiliensis*, 49 *M. velifer* and 2 *N. macrotis*) were obtained and evaluated by PCR using 3 different molecular markers (Barcoding, santin 18S and ITS). In this study, there was no evidence of *Blastocystis* in the assessed urban bat community. Since, diagnostic method employed is highly sensitive, it is likely that this bat species are not suitable hosts for the parasite. But it is also feasible that other factors associated to its behavior, a probable natural resistance, or features related to their environment, may help prevent infection. Because *Blastocystis* is a highly common parasite and the majority of studies realized found it in all groups of mammals evaluated, chiropteran case needs to be further studied.

Using Genetics to Explain Acoustic Divergence in the _Pteronotus parnellii_ Species Complex

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Acoustic traits are critical in echolocating mammals for foraging and communication, and for this reason their variation is generally thought to reflect adaptation. However, the seldom-tested null hypothesis to explain trait divergence is genetic drift. To discover the evolutionary processes responsible for trait divergence, we examined the echolocation frequency and populations genetics of *Pteronotus pusillus* and *P. portoricensis*, two recently split populations in the *Pteronotus parnellii* species complex. By deriving F_{ST} values from multi-locus coalescent isolation-with-migration models, and coupling them with estimates of quantitative trait divergence, or P_{ST}, we tested for drift in these island populations. Compared to traditional comparisons of P_{ST} to F_{ST}, the migration-based estimates of F_{ST} are unidirectional instead of bidirectional, simultaneously integrate variation among loci and individuals, and posterior densities of P_{ST} and F_{ST} can be compared directly. We found the evolution of higher call frequencies is inconsistent with genetic drift for the Hispaniolan population, despite many generations of isolation from its Puerto Rican counterpart. While the Hispaniolan population displays sexual dimorphism in call frequencies, the higher frequency in females is incompatible with sexual selection. Instead, cultural drift toward higher

frequencies among Hispaniolan females might explain the divergence. By integrating Bayesian coalescent and trait analyses, this study demonstrates a powerful approach to testing genetic drift as the default evolutionary mechanism of trait differentiation between populations.

Prescribed Fire Effects on Habitat Use of Tri-colored and Northern Long-eared Bats in the Cumberland Plateau

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Forests of the Cumberland Plateau and Appalachian Mountains of Tennessee and Kentucky are frequently managed with prescribed fire. Several declining bat species such as the federally protected Indiana bat (*Myotis sodalis*) and northern long-eared bat (*Myotis septentrionalis*), as well as the little brown bat (*Myotis lucifugus*) and tri-colored bat (*Perimyotis subflavus*) use habitat within these forests. While many studies suggest that prescribed fire improves bat foraging habitat, more information is needed regarding effects of time since last burn and fire severity on the summer ecology of these bats. Our objective was to determine how summer occupancy of tri-colored bats and northern long-eared bats in Big South Fork National River and Recreation Area is affected by time since last burn and fire severity. From May–August 2018 we collected acoustic data using Anabat SD2 detectors in 36 prescribed fire sites for 3 nights each with varying combinations of time since last burn (0–2, 3–4, 5–7, and >8 years), and burn severity (high, medium or low). Northern long-eared bats were only recorded at 4 sites: one in each time since last burn category and in 3 low severity burn sites. Tri-colored bats occupied 50% of sites burned 0–2 years prior, 25% of sites burned 3–4 years and 5–7 years prior, and 16% of sites burned >8 years ago. Tri-colored bats used low, medium and high severity burn sites in similar proportions. Preliminary results indicate that prescribed burns conducted at frequent intervals may provide good foraging habitat for tri-colored bats in this area.

Investigation of the Phylogeographic Structure of the Subspecies of Northern Yellow Bats by Molecular Analysis

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Northern yellow bats, *Dasypterus intermedius*, occur in North and Central America. Two subspecies are currently recognized based on morphological differences such as size and relative pelage color intensity: *D. intermedius intermedius*, found from Honduras to south Texas, and *D. intermedius floridanus*, which ranges from southern Texas eastward to Florida and South Carolina. In this phylogeographic study, we amplified and sequenced an 836 base pair region of the cytochrome b gene from 33 individuals. Samples were chosen from across the known geographic range, with particular attention paid to samples from south Texas, where the two subspecies' ranges were thought to meet in order to test the hypothesis that molecular data will correspond geographically with the morphologically defined subspecies. Sequences from the Southern yellow bat, *D. ega,* and the Cuban yellow bat, *D. insularis,* were included in the analysis. A maximum likelihood phylogenetic analysis and a median joining haplotype network analysis recovered two well-supported lineages of *D. intermedius* that roughly correspond to the geographic distribution of the subspecies, but with a large region of overlap in southern Texas. A distance value of 0.119 between the two lineages of *D. intermedius*, as well as the relationship to the endemic Cuban species, *D. insularis*, suggest that the taxonomy be re-evaluated according to the genetic species concept to reflect the level of divergence found. Our results from the mitochondrial markers are consistent with recognition of these lineages as full species instead of subspecies. Molecular data from the nuclear genome are needed to corroborate our findings.

Bat Diversity in an Abandoned Mine in the State of Sonora

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Information related to subterranean environments in Sonora, as well as the fauna that lives in them, is very limited. Particularly, studies related to the use of abandoned mines as a roost are scarce. Because of the lack of information about mines as roosts, this work describes the use of an abandoned mine for migrating bats and other species, in La Colorada, Sonora. In order to accomplish the objective, we visited Mina 'El Rubí' during six months (July–

December 2017) and placed three sensors along it to analyze temperature fluctuations. Another sensor was placed outside the mine to compare the outdoor temperature with the inside temperature. Species were captured and identified by different methods such as camera trap, bait traps and direct collection. Topographic measures were also taken to create two maps of the mine. Mina 'El Rubí' has a horizontal extension of 16.9 m and no vertical extension was found. The climate of the mine through the six months had a mean temperature of 26.57°C while the outdoor mean was 27.13°C. Temperature range on a single day in the outside reached 25°C, while the range between temperatures inside the mine was barely 3°C. Recorded fauna represented 15 orders, 26 families, 30 genera and 30 species, identifying two Phyllostomidae bats (*Choernoycteris mexicana*/ *Macrotus californicus*) and one Vespertilionidae bat (*Myotis velifer*). The mine is used as a temporary and permanent refuge for species that seek protection and for those that migrate to USA looking for food.

Geographic Variation in Echolocation Calls of *Balantiopteryx plicata* in Mexico

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The acoustic signals emitted by animals generally vary with geography. Geographic comparisons are valuable in determining the factors that influence divergence of acoustic signals. Insectivorous bats depend mainly on echolocation pulses to locate prey, navigate, and communicate. The identification of search phase echolocation calls of bats is useful in the field identification of different species. However, identification is hampered by intraspecific variation in calls, the extent of which is poorly documented for most species. The calls of some species are known to vary by sex/age, habitat, and geographic region. We studied the variation in search-phase of echolocation calls in the sac winged bat (*Balantiopteryx plicata*) by analyzing the most common call characteristics such as frequency, duration pulse, bandwidth and number of harmonics elements. We analyzed individuals from six different localities of central species distribution in Mexico, from 49 individuals (28 males and 21 females), sites varied in terms of vegetation and elevation. Results showed tree harmonics with the most energy concentrated in the second one, except in one location which also was the lowest elevation (30 meters above sea level). Using a Kruskal-Wallis test and a principal component analysis, substantial variation among localities was found, this variation was associated with geographical distance between sites. Our results provide evidence that geographic variation in echolocation calls may evolve as a consequence of local adaptation to climate and elevation conditions. Several of ecological factors (such as vegetation, climate, and topography factors) affected the structure of echolocation calls of this bat species.

***Are *Eptesicus fuscus* resistant to, or tolerant of, *Pseudogymnoascus destructans*?**

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White-nose syndrome (WNS), caused by *Pseudogymnoascus destructans* (Pd), continues to drive rapid declines of North American bats. Two of nine WNS-impacted species (i.e., *Myotis lucifugus* and *Eptesicus fuscus*) both hibernate in conditions favoring Pd growth. However, little brown bats have faced significantly steeper declines.

Two competing hypotheses could explain this difference in impacts. Big brown bats could be: (i) resistant to *Pd* (i.e., maintain low pathogen loads) or (ii) tolerant of *P. destructans* (i.e., exhibit limited disease and morbidity despite high pathogen loads). The resistance hypothesis predicts that big brown bats should maintain lower fungal loads than little brown bats when hibernating in identical conditions that favour growth of Pd ,while the tolerance hypothesis predicts that big brown bats will exhibit high fungal loads without evidence of disease. We tested these hypotheses using a replicated inoculation-challenge experiment. We housed Pd-inoculated and sham-inoculated groups of both species in separate cages within two identical incubators both maintaining 8°C and 98% relative humidity. Consistent with the tolerance, but not the resistance hypothesis, inoculated big brown bats in both incubators had significantly higher prevalence and intensity of infection based on qPCR after 60 days. Although big brown bats appear tolerant of high Pd loads, management actions that reduce loads for this species could be important for conservation by reducing potential inter-species transmission within and between hibernacula.

Investigations of New Aroma Technologies for the Early Detection and Control of White-nose Syndrome

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White-nose syndrome (WNS) disease-suppression strategies are much more effective when the disease can be detected early, long before symptoms and signs development. Early detection of WNS allows for controls to be applied much earlier before the disease becomes well-established in cave hibernacula. Electronic-nose (e-nose) devices, instruments that utilize sensor arrays capable of detecting volatile organic compounds (VOCs) in air samples by aroma signature patterns, are now commonly used for disease detection in the biomedical field. E-nose instruments detect the unique aroma mixtures of VOCs produced by different pathogens and associated diseases, allowing their detection and identification. Our objective is to expand the use of e-noses to monitor wildlife diseases, initially for early detection of WNS to facilitate earlier applications of disease-control measures. To establish a reliable aroma library, initial research is needed to determine if bat species have distinct aroma signatures. We first collected and analyzed air samples from healthy (uninfected) individuals of eight bat species, caught during summer, to establish species-specific aroma signature patterns in defined databases for both portable and Heracles II e-noses. Results from discriminant factor analyses suggest that all eight bat species have a distinguishable and unique aroma profile. Successful outcome of this research will provide a new monitoring tool useful for identifying species that are difficult to differentiate visually and for determining the effective location, timing and implementation of WNS disease-suppression activities.

The Effect of Prescribed Burns on Bat Activity and Species Composition in Upland and Riparian Habitats

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A prescribed burn is planned fire used as a forest management method to reduce the risk of wildfires and to promote ecological diversity by enhancing habitat for native species. However, while this method benefits forests in many ways, it also may lead to unintended consequences on wildlife, including bats. Given the decline of forest dwelling bat populations due to white-nose syndrome, the impact of wind farms, and habitat degradation, the effects of prescribed fire on these species deserves more study. In this multi-year study conducted in Siloam Springs State Park, Illinois, we examined bat activity acoustically using Pettersson D500 recorders placed in forested upland and riparian habitats in areas that were burned in the calendar year of data collection or burned the previous year, and areas that have never been burned. After two weeks, recordings were collected and analyzed, and the recorders were moved to new sites in each burn category, with a total of 17 sites monitored over the course of two field seasons. Our results indicate that bat activity was highest in sites that were burned in the year of recording and overall activity was highest in the areas that were burned as opposed to the areas that were unburned. This suggests that prescribed burning may have a positive influence on bat activity with potential benefits including opened flight corridors, increased prey density, and additional tree roosting habitat. Future directions will include classifying echolocation recordings to determine if species composition is affected by prescribed burning.

Disruption of Cutaneous Respiration Plays a Role in WNS Pathophysiology

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We have a basic understanding of the effects of *Pseudogymnoascus destructans* (Pd), and white-nose syndrome, on bats but a fundamental question about WNS pathophysiology remain: Why does a simple skin infection lead to dramatic changes in hibernation behaviour and energetics? We hypothesized that disruption of gas exchange across a bat's wings (cutaneous respiration) plays a role in WNS pathophysiology. Using sophisticated respirometry techniques we separated cutaneous from pulmonary respiration and water loss of bats to address four predictions: 1) WNS-susceptible bats (*Myotis lucifugus*) rely on cutaneous respiration more than WNS-tolerant/resistant bats (*Eptesicus fuscus*); 2) Cutaneous respiration decreases with increasing WNS severity; 3) Reduced cutaneous respiration increases pulmonary respiration; and 4) Increased pulmonary respiration increases energetic costs and water loss. We found that *M. lucifugus* relies on cutaneous respiration more than *E. fuscus* (P <0.05*),* with cutaneous respiration contributing more than 15% of total respiration in *M. lucifugus*. We did not find an effect of Pd-infection on cutaneous respiration in torpid or normothermic *E. fuscus,* or torpid *M. lucifugus*. However, at normothermic body temperature, Pd-infected *M. lucifugus* reduced cutaneous respiration by 85% compared to control bats, and cutaneous respiration declined with increasing WNS severity (R^2 = 0.86). Consequently, disruption of cutaneous respiration is associated with enormous increases in pulmonary respiration (R^2 = 0.97), energetic costs (R^2 = 0.98), and water loss (R^2 = 0.80). Taken together, our findings highlight the extraordinary physiology of bat wings and suggest that efforts to treat WNS should consider implications of topical anti-Pd agents for wing physiology and cutaneous respiration.

Population Biology of *Diphylla ecaudata* in Guanajuato, Mexico

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Diphylla ecaudata is a very rare vampire bat species whose largest populations recorded have 70 individuals. They inhabit tropical environments from Tamaulipas, Mexico through Central America to Brazil and the structure of their populations has been scarcely investigated. Therefore, we expect that a population of *Diphylla ecaudata* in Sierra Gorda Biosphere Reserve, Guanajuato, Mexico should have similar sex and age classes proportions, and the number of organisms should be around 70, as it is the common situation previously known. We trapped hairy-legged vampire bats at the entrance of the tunnel El Mezquite, in Majada town, with a mist-net of 6 m long set at the entrance of the tunnel, from April 2013, March to August 2014 and May to December 2015. We got standard body measures and marked individually each specimen with a collar with color code beads. We identified their sex reviewing their genitals and assigned juvenile or adult age class by reviewing their phalanges ossification. A total of 36 vampires were captured, 32 were re-captured. Sex ratio was: 19 females (52.8%) and 17 males (47.2%; X^2 = 0.11, 1 d.f., P >0.05); age structure: 11 juveniles (30.6%) and 25 adults (69.4%; X^2 = 6.41; 1 d.f., P <0.05). The population mean size was 74 individuals (min. 26–max 186). Population sex structure is 1:1, there are more adults than juveniles and this is one of the largest populations of *D. ecaudata* recorded in Mexico. These are among the first detailed population structure results of *D. ecaudata* in Mexico.

Molecular Methods for Detection of RNA Virus in *Desmodus rotundus* in Different Populations of Mexico

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Desmodus rotundus is a species of sanitary concern and economic importance by its incidence in cattle, this bat could carrier a great diversity of viral entities that cause significance problems in several sectors of cattle raising.

The purpose of this study is to detect the presence of viral genomes of economic and sanitary importance (Chikungunya, Zika and Dengue viruses) by using molecular methods in *Desmodus rotundus* from different parts of Mexico. We caught a total of 45 individuals, both males and females, adults and juveniles, these were measured and sexed under standard parameters. We collected the brain of each individual and stored in RNA later. Viral RNA extraction was carried out using the trizol method, followed by endpoint RT-PCR that allowed the amplification of the viral products, and finally amplicons were obtained and visualized in an electrophoresis run in agarose gel using a UV light transilluminator, results were documented and analyzed. We obtained an amplicon of 80 base pairs (bp) for Zika virus in two individuals, representing an incidence of 11.1%. An amplicon of 106 bp was verified for Chikungunya in three individuals, which was equivalent to 22.2% of our sampled population. PCR products were sequenced and a haplotype analysis was carried out using the BioEdit program. Presence of Dengue virus was also examined, searching for the expected amplicon of 362 bp, however, no positive individual was detected. We corroborated the presence of viruses from the Flaviviridae and Togaviridae families for the first time in the hematophagous bat *Desmodus rotundus*.

Wing Ecomorphology and Flight Speed in Bats from Inferno Cave, Santiago, N.L., Mexico

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The relationship between morphological design and ecological function is a central theme in the biology of species. Ecomorphology inquire the connections between the design of an organism and its performance, and studies how these connections influence the ability to use the resources in their habitat. It is known that wing morphology of bats influences their flight capacity for lift, speed, and type of foraging, however, flight speed is not known for all bat species and in Mexico, only a few studies have been done in this subject. We explored the relationship between wing morphology and flight speed in eight species from two bat families (Vespertilionidae and Phyllostomidae) captured at Inferno Cave, in the state of Nuevo León, México. We trapped a total of 57 bats using mist nets near the cave entrance, we took morphological measurements and each bat was photographed with the wing extended. ImageJ program was used to measure the wing area and wing span. These data together with other morphological measurements were used to calculate the aspect ratio and wing loading and then each was compared with flight speed. To measure flight speed, a 19-meter long tunnel was built with PVC pipes and a tarp that covered its perimeter. We released each bat and registered flight duration along 4 meters to estimate speed. Our results indicate that flight speed increases with forearm length and wing loading. When comparing the aspect ratio and wing loading, it shows an ecomorphological segregation based on the type of foraging.

Insect Suppression Services by Insectivorous Bats on Walnut Crops of Chihuahua, Mexico

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Mexico has become the second largest worldwide producer of walnut, a very profitable crop with yearly incomes of $350,000 USD. However, walnut plantations also suffer high economic losses of up to 50,000 USD annually due to pest damage. The optimization of pest suppression ecosystem services by bats will favor both human development and environmental health by reducing cost from crop losses and the use of pesticides. However, the efficiency of this bat service is directly related to bats abundance and their ecological role as insect predators. In this project, we use acoustic surveys to determine bat species associated with walnut crops, their activity patterns, and habitat use. Our study site is the municipality of Jiménez, Chihuahua, the main walnut producer in Mexico. We selected three sites from three different treatments: xerophytic scrubland, organic and intensive walnut crops. We started surveys of bats and insect communities in May 2018 and will continue sampling bimonthly for one year at each site. We defined bat´s habitat use and activity using search calls and feeding buzzes. We placed mist-nets to catch bats within the area and obtained guano for diet determination and pest intake through NGS. Partial results from May and July 2018 showed that bat species assemblages are similar across treatments with the dominant species being *Tadarida brasiliensis*, *Myotis velifer,* and *Antrozous pallidus*. Bat activity and insects abundance was less in the rainy season

(July). Further acoustic and diet sampling will reveal seasonal difference of habitat use depending on food availability and walnut phenology.

Improving Bat House Designs to be Efficiently Used as a Conservation Tool

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Bat houses are frequently used as a conservation measure to increase bat roost habitat, often in cases where citizens have excluded bats from their dwellings and more and more as a potential tool to combat white-nose syndrome (WNS). However, very few bat houses are colonized by reproductive females in temperate and northern regions. Many studies reported thermal properties and location as key factors for roost choice by female bats. We proposed to test pre-existing and newly designed bat houses based on a review of the preferences and requirements of the bats most impacted by WNS: little brown and Northern long-eared bats. The newly designed bat houses were based on passive heating and included insulation, greenhouse zones and/or phase changing material panels. We also evaluated the best orientation and mounting type. Internal temperatures of bat houses were compared on seven sites of Québec, Canada, using iButtons. Newly designed bat houses significantly increased the amount of time within the optimal temperature range of reproductive *Myotis* females (22–40°C) compared to standard bat houses, with an increase of more than three degrees in average during the night. Easterly orientations warmed up the bat house sooner compared to southerly or westerly orientations. Installation on buildings increased the amount of time within the optimal temperature range by a better retention and diffusion of heat during the night compared to pole mountings. A good orientation, mounting and passive heating design could improve bat houses efficiency as a conservation tool while remaining affordable and handy for citizens.

Seasonal Ecology of the Lesser Long-nosed Bat at the Edge of its Range

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The lesser long-nosed bat (*Leptonycteris yerbabuenae*) is a migratory pollinating bat that was removed from the Endangered Species List in the United States in 2018 and from threatened status in Mexico in 2013. The seasonal ecology and conservation status of the species is well-understood in the core part of its range on mainland Mexico and in the southwestern United States, but relatively little is known about the species on the Baja California peninsula in northwestern Mexico, a part of its range separated by the Gulf of California. We studied the seasonal ecology of lesser long-nosed bats on the Baja peninsula at 8 focal roosts along a 450-km north-to-south transect to test hypotheses about migratory or residential status of the species on the Baja peninsula. We provide evidence of an extensive population of lesser long-nosed bats on the Baja peninsula that is primarily seasonally migratory and includes 2 mating roosts with males on the southern part of the peninsula. Seasonal ecology of lesser long-nosed bats was closely associated with the flowering and fruiting season of the cardón (*Pachycereus pringlei*), the dominant columnar cactus on the peninsula. However, we discovered that some female lesser long-nosed bats arrive and give birth at southern roosts in mid-February, about 2 months earlier than other migratory populations in more northern Sonoran desert habitats. We documented the loss of nearly a third of the known maternity roosts during the study, demonstrating that action to protect key roosts remains a high priority.

Interspecific Variations in Hibernation Physiology and Implications for White-nose Syndrome in Western Bats

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As white nose syndrome (WNS) continues to spread there is great interest in predicting which bat species are under increasing threat. To understand how diseases impact new regions, each component of the epidemiological triad, including host, pathogen, and environment must be considered. Recent works have pointed to the importance of host traits in the development and severity of WNS, including torpid metabolic rate (TMR) and evaporative water loss (EWL). Among western bats, there is little information available about the influence of environmental conditions on hibernation physiology and behavior. We predicted there would be interspecific variation in hibernation physiology, such as accumulated fat stores, TMR, EWL, and preferred microclimate. To test these predictions, we used dataloggers to record hibernaculum microclimate, quantitative magnetic resonance to measure body composition, respirometry to measure TMR and EWL, and passive acoustic monitoring to measure flight activity outside hibernacula. We studied eight species in seven locations across the western United States. Contrary to expectations, we observed little variation in TMR among species and among temperatures typical of hibernacula. Bats often chose hibernacula with highly variable environments that would be associated with high water vapor deficit and do not correspond to minimum TMR. Interestingly, we found interspecific variation in EWL, which lends further support to recent studies suggesting EWL plays a large role in WNS susceptibility. Interspecific comparisons of hibernation physiology provide insight into the physiological diversity of hibernation and will contribute to efforts to mitigate the effects of WNS in currently unaffected regions.

Gut Microbiome Analysis of Three Native Minnesota Bat Species

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Microorganisms associated with the vertebrate gut can influence the behavior, immunity, and development of their hosts. The Chiropteran gut microbiome is poorly understood relative to other large mammalian orders; here we establish the baseline of taxonomic variation in the fecal microbiome of three common sympatric species. We sequenced the 16S rRNA gene using the Illumina MiSeq platform of the fecal pellet microbiome as a minimally invasive way of profiling the gut community of three North American bats, *Myotis lucifugus*, *M. septentrionalis*, and *Eptesicus fuscus*. Pellets were collected as part of a mist-net survey over three summers from 2015–2017 broadly encompassing the forested landscapes of Minnesota. In our analysis of 310 fecal samples, we investigated the influence of age class, species, sex, geographic location, and reproductive state on the diversity and taxonomic composition of the microbiome. The majority of identifiable bacteria present in all species were members of the Proteobacteria, Actinobacteria, and Firmicutes phyla, though seven other phyla also contributed greater than 2% of the relative abundance in some samples. Gammaproteobacteria and Alphaproteobacteria together made up on average more than 60% of the Proteobacteria present in all samples. The microbiomes of the *Myotis* spp. showed similar levels of alpha diversity, both lower than that of *E. fuscus*. Reproductively active female bats were host to more diverse fecal microbiomes than non-reproductive females, perhaps in part due to the higher energetic demand of lactation and gestation, as well as changes in the immune system associated with pregnancy.

Microbiota Composition of the Sebaceous Patch of Reproductive Males of *Leptonycteris yerbabuenae*

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The adult males of the lesser long-nosed agave pollinator bat *Leptonycteris yerbabuenae* (*Phyllostomidae:*

Glossophaginae) develop an interscapular glandular complex (dorsal or sebaceous patch) during the mating season. For this study, a total of 17 bat males, 12 adults and 5 young, were sampled in the cave of San Juan Noxchitlan, Oaxaca, Mexico. Interescapular sebaceous patch samples (N = 11) were used for DNA extraction, amplification and sequencing of the V4 region of the 16S rRNA gene to characterize their microbial diversity. Sequences were clustered into Operational Taxonomic Units (OTUs) to a 97% sequence identity and taxonomically assigned. The results showed that the sebaceous patch bacterial diversity is mainly composed by Firmicutes (48%) and Proteobacteria (36%), with smaller contributions of other groups, including Actinobacteria (3.6%), Fusobacteria (2.8%), Cyanobacteria (2.4%), Tenericutes (0.5%), Bacteroidetes (0.4%), Verrumicrobia (0.03%), and 6.2 % of unassigned bacteria. There are 26 shared OTUs in the sebaceous patch that represent 30 to 75% of bacteria abundance found in the samples. The distribution of these 26 shared OTUs is homogeneous among samples, where 16 correspond to anaerobic and fermenting bacteria. The population of fermenting bacteria in the sebaceous patch is more than 65%, suggesting they have a preponderant role in the reproductive behavior of *L. yerbabuenae*. These results show strong evidence to support the fermentation hypothesis, an inclusive model that recognizes that the production of short-chain fatty acids by fermentative anaerobic bacteria hosted in the scent glands of mammals, is a symbiotic relationship important in mammalian chemical recognition and reproductive behavior.

Genotoxicity Assessment in Insectivorous and Nectarivorous Bats at Agricultural and Urban Areas of Nuevo Leon, Mexico

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Bats can act as indicators of environmental pollution because they cover different trophic guilds and they are susceptible to bioaccumulate metals and other toxic substances due to their high metabolic rate and high food intake in relation to their body mass. We studied genotoxicity in 4 insectivorous (*Tadarida brisiliensis*, *Nycticeius humeralis, Myotis auriculus* and *Antrozous pallidus*) and 2 nectarivorous (*Leptonycteris nivalis* and *Choeronycteris mexicana*) bats at agricultural and urban areas in the state of Nuevo Leon, Mexico. We took blood samples of these bats during July and August 2018 and prepared 2 smears per individual bat. Subsequently, we used the Hemacolor Rapid Staining Kit in the laboratory to fix and stain the smears. The frequency of micronuclei (MNE) in 2,000 peripheral erythrocytes per individual was quantified using a microscope. Our results indicate no genetic damage in any of the samples, however we suggest doing more tests to standardize the staining method and compare with other protocols for genotoxicity assessment.

Genetic Variation and Genetic Structure Between Two Species of the Genus *Sturnira* (Phyllostomidae: Stenodermatinae) in Mesoamerica

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Mesoamerica has a complex geological history and a variety of environments, which in turn have generated a high biodiversity at several taxonomic levels. Diversification processes in multiple vertebrate species in the region have been studied, however, there are not analyses that contrast levels of genetic variation and structuration between mountain and lowland environments. *Sturnira parvidens*, a bat with tropical distribution, and *Sturnira hondurensis,* from temperate mountain zones, are an excellent model to compare how the environment could influence genetic information of the species. We assessed levels of genetic variation and genetic structure using DNA sequences of mitochondrial (*ND2*) and nuclear (*RAG2*) loci (156 *S. parvidens;* 141 *S. hondurensis*). High mitochondrial genetic variation (*Hd* = 0.974 and 0.983, respectively) and low nuclear variation (*Hd* = 0.632 and 0.9) are consistent with the recent evolutionary processes and mutation rates reported for these species and molecular markers. We found two haplogroups within *S. parvidens* characterized by a West-East division. Regarding *S. hondurensis,* there is not a clear evidence of geographic structure, however, we detected a differentiated lineage that inhabits the Pacific Slope and western Trans-Mexican Volcanic Belt. This result is consistent with the distribution of the subspecies *Sturnira hondurensis occidentalis*, therefore, we suggest that the recognized geographic range of this taxa must be expanded towards central Mexico. While both species have similar historical processes, the biology of each organism is determinant by its evolution.

Ecological Niches Reflect the Diversification Patterns of *Pteronotus* Bats

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Bats of the genus *Pteronotus* are widely distributed through the Neotropical regions. This group has been subject to recent taxonomic changes proposing two main monophyletic groups and new species. These changes had significantly expanded the evolutionary history knowledge of this genus, but the information about the role of the environment over its lineages diversification is still not understood. Niche modelling is a useful and versatile approach to explore ecological use, geographic distribution, and niche divergence between species, which can allow us to further explore how environment can promote the speciation. We explored the influence of abiotic variables such as temperature and precipitation on the diversification patterns of the *Pteronotus* bats. We constructed a database containing all the available species distribution records and extracted the environmental values from the current bioclimatic envelopes of WorldClim. This allowed us to perform an n-dimensional hypervolume approach in order to characterize and quantify the environmental niche and the overlap between lineages, in order to analyze possible signals of ecological diversification. Additionally, we modeled the potential geographic distribution of eight of the *Pteronotus* lineages, searching for patterns of habitat use between them. Our results provide insights of the most significant abiotic variables for these bats. The most notorious difference between clades were between *P. personatus* and *P. mexicanus* species. We also identified two sister species that are sensitive to different environmental variables: temperature for *P. mesoamericanus* and precipitation for *P. mexicanus*. We conclude that the recent diversification of *Pteronotus* bats is related to climate fluctuations.

Molecular Assessment of Dietary Breadth for *Nycticeius humeralis* in the Midwestern United States

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The evening bat (*Nycticeius humeralis*) is a small, forest-dwelling bat, widespread in eastern North America, but understudied. We have few specific data on its diet and variation across the species' range. Our goal was to use next-generation sequencing (NGS) to compare diets of evening bats in Indiana and Missouri. We collected guano samples from bats captured in west-southwest Missouri in Summer 2016 (22 bats) and central Indiana in summers 2015 and 2016 (14 bats, 3 sampled twice). We extracted DNA and sequenced the arthropod minibarcode region of the CO1 gene on an Illumina MiSeq. Using custom scripts in Qiime and R, we clustered sequences into molecular OTUs, compared common OTUs to sequences in the BOLD database, and filtered results by similarity (≥ 98%) and geography to identify prey taxa. We detected 8–48 unique OTUs per bat in Indiana and 10–32 OTUs per bat in Missouri. Evening bats consumed insects from 12 orders, mainly Coleoptera, Diptera, and Lepidoptera. We found substantial overlap across areas at the order and family level, with less overlap at the genus and species level. Of note is that in each area >10 bats consumed *Stenolophus ochropezus* (Coleoptera: Carabidae) and *Lygus lineolaris* (Hemiptera: Miridae). We detected wood roaches (Blattodea: Ectobiidae), Braconid wasps (Hymenoptera: Braconidae), and stout barklice (Psocodea: Peripsocidae) only for bats from Indiana, and root-maggot flies (Diptera: Anthomyiidae) and phantom midges (Diptera: Chaoboridae) only for bats from Missouri. Using a standardized approach to analyzing high-resolution NGS data yielded valuable information on dietary breadth and overlap across the evening bat's range.

***Foraging Strategy of the Nectar Feeding Lesser Long-nosed Bat**

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Every spring tens of thousands of female lesser long-nosed bats (*Leptonycteris yerbabuenae*) arrive pregnant to a maternal cave in the Sonoran Desert of Mexico after a long migration of more than 1000 km from central Mexico. During the lactation period, they rely on the nectar, pollen, and fruit of the Saguaro cacti (*Carnegiea gigantea*) as their main food source, while the Saguaro relies on these bats as its main pollinator. In order to reveal the foraging strategy of the lesser long-nosed bats, we used miniature GPS devices with an ultrasonic microphone to track bats' movement and behavior. We used a drone to create a 3D model of the visited cacti fields, characterized the cacti distribution and the number of open flowers. Analyzing bat movements in relation to their food distribution allowed us to identify visits to a specific cactus. We found that lesser long-nosed bats conduct long commutes every night, flying up to 103 km each way from the cave to the foraging site. They concentrate their feeding in a specific area inside the cacti field, visiting specific cacti very often thus maintaining a foraging territory along a night and during consecutive nights. Social interactions including social calls, chasing and expelling another bat while feeding, were recorded near the cacti. These findings suggest a highly developed navigation ability and spatial memory that allow the bats to revisit the same cacti every night.

Diet of Two Frugivorous Bats in Restored Patches

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Diets potentially play a central role in determining the dynamics of competition among species. Ecological restoration aims to accelerate the process of natural succession. Restoration plantings represent maximum restoration intervention whereas exclusion of disturbance is considered minimal restoration intervention. The objective of this work is to evaluate the effect of the level of restoration intervention in the diet of *Carollia sowelli* and *Sturnira parvidens.* The experiment was established in 2006 in Los Tuxtlas, Veracruz, Mexico in 24 30 X 30 m plots: 16 plots were planted with animal or wind dispersed tree species and the remaining eight plots were excluded from the disturbance. We use 18 plots to sample bats; two mist nets of 12 m were in the 18 plots during 2 nights per plot. Preliminary results in two field trips raised an effort of capture of 6,912 mt / hrs / net. The most abundant species were *Carollia sowelli* and *Sturnira parvidens.* The plots with plantings had the highest number of excreta samples for both *Carollia sowelli* and *Sturnira, parvidens* while in the plots under minimal intervention, these species were not recorded. For *Carollia sowelli* we registered a total of 608 seeds of two tree species *Cecropia obstusifolia* and *Conostegia sp. For Sturnira,* we resgistered a total of 305 seed of five species: *Cecropia obtusifolia*, *Conostegia xalapensis*, *Ficus pertusa*, *Solanum schlechtendalianum* and *Sommera arborescens*. Our results suggest that these two frugivorous bats are using only the plots under maximal intervention.

Potential Distribution of the Pollinating Bat *Choeronycteris mexicana* at the Northern Edge of Its Range

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Choeronycteris mexicana (Phyllostomidae: Glossophaginae) is distributed from the southern US to Mexico, Guatemala, Honduras, and El Salvador in a wide variety of vegetation types from arid thorn scrub to tropical deciduous forest and mixed oak-conifer forest. The altitudinal range documented is from 300 to 2400 msnm. This bat is considered near threatened by global criteria (International Union for Conservation of Nature) and threatened by Mexico's endangered species list due to a significant decline rate. Little is known about the species habitat requirements, particularly at the northern edge of its range. In order to help guide field surveys to identify roosts and

foraging areas, we studied the potential distribution of the species using presence-only data and ecological niche modelling algorithms. We created 1-km resolution models for the northern edge of the bat's range. We analyzed the species representation within federal, state and private protected areas and prioritized areas in need for research and conservation based on information gaps and land use change trends for northern Mexico.

Marked Phylogeographic Structure of *Pteronotus psilotis* (Chiroptera: Mormoopidae) Reveals a Diversification Process in Mexico

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The Wagner's mustached, *Pteronotus psilotis* Wagner 1843, is a bat restricted to tropical regions of the new world. Recently, based on a multilocus analysis and geometric morphology, was suggested to elevate the subspecies (*P. personatus personatus* and *P. personatus psilotis*) at the species level (Pavan y Marroig, 2017). On the other hand, Zárate-Martínez *et al*. (2018) with mitochondrial sequences suggested the presence of two lineages in Mexico. The objective of this work was to determine the historical processes that led to the genetic differentiation and geographical distribution of the two lineages of *Pteronotus psilotis* in Mexico. We analyze mtDNA (HVII and COI) and 5 introns of 140 *P. psilotis* bats from 14 locations in Mexico. The concatenated phylogenetic analysis and the haplotypic networks resolved two main haplogroups that correspond to the Gulf of Mexico-Mexican Pacific (GPM), and Southeastern of Mexico (SM), with a genetic distance of 3.4% for COI and with a separation time of 1.2. Ma [0.872, 1.702 Ma, 95% HPD], that support the presence of two lineages in Mexico. The nucleotide diversity decreased with the increase of the latitude in the slopes of the GPM suggesting the presence of Pleistocene refuges around the Isthmus of Tehuantepec with a later diversification. Our data suggest that the demographic expansion in GPM was about 10 kya, but that in the SM was presented demographic stability. Historical isolation, local adaptations and a life history of the species favored the phylogeographic patterns found in this study.

Whole-genome Sequencing Reveals Signatures of Dietary Specialization on New World Leaf-nosed Bats

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The shift and specialization into a new food habit is considered one of the most important events in the natural history evolution. Where the species will start to explore different ecological opportunities, new demands on their nutrient acquisition strategies and this can lead to an adaptive radiation. The family Phyllostomidae, exhibit a diverse and a high dietary spectrum of feeding habits. Each of these food habits is accompanied by strong ecological, behavioral, morphological, and physiological traits. However, there have been few studies about those genes related with the dietary specialization. To analyze which are those genes and the genomics signals related with the diet specialization, we obtained the genomic information of five species: the nectar-feeders *Leptonycteris yerbabuenae*, *Leptonycteris nivalis,* and *Musonycteris harrisonii*; the frugivory *Artibeus jamaicensis*; and the insectivory *Macrotus waterhousii*. We incorporated the genomic information deposited on database of the blood-feeder *Desmodus rotundus*. We generated a genomic comparative approach to identify those genes and genetic changes associated with a different diet. Additionally, we performed a coalescent analysis in order to understand the changes of their effective size in their natural history. We obtained the whole-genome assembly of the Lesser long-nosed bat and it was used as reference genome to identify *Single Nucleotide Polymorphism* (SNP). We identified more than 29 million of SNPs unique for each bat. More than 3 million of SNPs are shared in all the leaf-nosed bats with a different distribution of SNP frequency. Each specie shows a particular trajectory on its effective population size.

Bats Are Not Squirrels: Revisiting the Cost of Cooling in Hibernating Mammals

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Many species use stored energy to hibernate through periods of resource limitation. Hibernation, a physiological state characterized by depressed metabolism and body temperature, is critical to winter survival and reproduction, and therefore has been extensively quantified and modeled. Hibernation consists of alternating phases of extended periods of torpor (low body temperature, low metabolic rate) and energetically costly periodic arousals to normal body temperature. Arousals consist of warming, euthermia, and cooling phases. Warming and euthermic costs are regularly included in energetic models, but although cooling to torpid body temperatures is an important phase of the torpor-arousal cycle, it is often overlooked. When included, cooling cost is assumed to be 67% of warming cost, as measured in a single ground squirrel species, regardless of body size or ambient environment. We derived a model of cooling cost from first principles and validated the model with empirical energetic measurements. We compared the assumed 67% proportional cooling cost with our model-predicted cooling cost for 53 hibernating mammals, including 17 bat species. Our results indicate that using 67% of warming cost only adequately represents cooling cost in ground squirrels. In smaller species such as bats, this proportion overestimates cooling cost. Our model allows for the generalization of energetic costs for multiple species using species-specific physiological and morphometric parameters. Our model also allows for predictions over variable environmental conditions, which is imperative in understanding the bioenergetic effects of white-nose syndrome.

Restoring Forests for Bats: A Case Study from the Osa Peninsula, Costa Rica

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Traditional methods of tropical reforestation, notably natural regeneration and active tree planting, are employed to mitigate species loss in deforested areas. However, these methods are poor at re-establishing several community interactions, as many animal species are slow to return. We are using neotropical bat diversity as a case study for informing innovative restoration techniques, specifically 'rewilding' as a method for accelerating successional processes, as part of a large-scale restoration experiment conducted by Osa Conservation. The outcome of rewilding in deforested areas may be affected by the state of the source animal populations. Thus, in this study, we are using bat capture by mist-netting as one method to characterize the state of the bat fauna within remnant forest circa 2 km from the restored area. We will compare the species composition and richness of phyllostomid bats sampled at 24 forest sites to that of the deforested area, sampled in 30 experimental plots in the initial stage of restoration. We will present this information as a case study of how to inform which restoration techniques to employ in order to attract missing or underrepresented taxa in the area. Such techniques may include the construction of artificial bat roosts, as well as planting species which will support bats in the form of natural roosts and food sources. This case study can be scaled up to inform restoration efforts throughout the Neotropics in order to increase the efficiency and success of restoration efforts.

How Is Relative Sensory Organ Volume Related to Diet in Phyllostomids?

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Phyllostomids are emerging as a prime example of adaptive radiation in mammals. They employ more feeding strategies than any other bat family and almost all bat feeding strategies are represented within the family. Previous work demonstrated that dietary innovation, particularly the move from insectivory toward frugivory, is associated

with much higher rates of diversification relative to other bat families. Specifically, the evolution of a short, wide palate served as a key innovation which triggered the adaptive radiation into new dietary niches. Here we hypothesize that along with the changes in dietary niche and skull shape there must also be a corresponding shift in relative size of sensory organs that reflect the differing feeding strategies employed by frugivores, nectarivores, animalivores, and sanguivores. Our prediction was that higher rates of frugivory and nectarivory would be associated with larger orbits and olfactory bulbs. Using iodine stained specimens representing 47 species of both phyllostomids and their immediate outgroups, we gathered micro-CT scans of skulls and brains from phyllostomid subfamilies and dietary classes and quantified the relative sizes of orbits, olfactory bulbs, and cochlea. Interestingly, we found that while there is no strong tie between diet and the size of orbits or diet and the size of olfactory bulbs, there is a strong tie between diet and total size of the orbits and olfactory bulbs, with the largest in frugivores and nectarivores. This indicates that there might be multiple avenues of sensory specialization among frugivorous and nectarivorous lineages.

Maternity Roost Dynamics of *Myotis lucifugus* in a Post White-nose Syndrome World

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We have studied maternity roost population size and dynamics in central New York since about 1988 with data focused on 8 locations (out of about 35 roosts studied over the last 30 years). Roosts were in barns or other "out-buildings" or, in several cases, in bat boxes. In 2018, I utilized visual observations, video recordings with low-light/infrared lighting formats, bat detectors (Petterson D-1000), and (in the last year) a Wildlife Acoustics Echo Meter Pro. Population sizes of adult female *Myotis lucifugus* have remained low, approaching 97% reduction in population size compared to pre-white-nose syndrome (WNS) sizes. Big brown bat (*Eptesicus fuscus*) populations have appeared stable, in fact showing an increase based on their moving into roost sites formerly occupied by little brown bats. Consistent small numbers of Northern long-eared bats (*Myotis septentrionalis*) have been present in one location. Our story is one of roosts that come and go. For example, one roost, the most populous summer roost of *Myotis* we had seen in New York, was razed and lost. Two other roosts have been taken over by *Eptesicus* females. Three of the traditional *Myotis* maternity roosts have had zero (or several) bats present during the birthing and lactating seasons compared to prior numbers that were in the hundreds. We reject that *Myotis lucifugus* is rebounding from WNS, but, we acknowledge that several roosts appear to have had few but stable numbers of the bats during the past 3 years.

Density of *Leptonycteris nivalis*' Foraging Resources Near a Maternity Roost at Cumbres de Monterrey National Park

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Leptonycteris nivalis is listed as endangered by the International Union for the Conservation of Nature (IUCN), the United States, and the Mexican endangered species legislation. It is distributed from central Mexico to southern United States. Each spring mainly pregnant females migrate north following the flowering events of *Agave*, which are its main food source in the north. During their journey *L. nivalis* pollinates agaves allowing greater genetic diversity in these plants of ecological and economic importance. Cumbres de Monterrey National Park is relevant for populations of *L. nivalis* because it contains a maternity cave called "El Infierno". Within the park the paniculate Agave species documented are: *A. americana, A. asperrima, A. gentryi, A. salmiana, A. montana, A. ovatifolia,* and *A. parryi.* There is temporal variation in the flowering onset for each agave species, even different populations of the same species may differ. In this study we designed a stratified random sampling considering the vegetation and land use for estimating wild agave populations' ecological parameters during the months of June, July, and August 2018. We used central point quadrants to characterize vegetation, measure density of agaves and their relative-importance value in each vegetation community. We recorded the phenological status of each agave species at each sampling site. We found differences in density of agave by vegetation type and identified areas in need of restoration efforts. Our study provides fundamental information for bat habitat management decisions.

Cranial Morphological Variation in *Sturnira hondurensis* (Phyllostomidae: Stenodermatinae)

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Geometric morphometry techniques have been useful in intraspecific studies because they allow us to detect small changes in the shape of organisms, or some of their structures. We used that technique to analyze the skull of three genetic groups previously and recently described within *Sturnira hondurensis*: western, center, and eastern lineages. This species is distributed in montane and temperate forests, from southern Sonora and Tamaulipas in Mexico to northern Nicaragua. Our goal was to provide information on the degree of morphological variation within the species. We analyzed 193 specimens of *S. hondurensis*, using 5 cranial modules: dorsal view, braincase lateral view, rostrum lateral view, glenoid fossa, and posterior edge of palatine. Additionally, we analyzed length and width of the skull. The western group showed a tendency to have a taller and rounded skull and a more curved posterior edge on the palatine than the other groups; additionally, this group was the smallest and the only one where females were larger than males. Center and eastern groups showed similar shapes and were larger than the western group. We also found a correlation between the degree of morphological and genetic variation, which suggests a possible relation between the morphological differentiation and the short divergence time between lineages. We suspect there could be a speciation process indicated by subtle genetic and morphometric differences, possibly caused by environmental and ecological factors that promote the differentiation of the west group.

Analysis of Genetic Diversity of *Sturnira hondurensis* Populations Along Its Distribution Range Using Microsatellites

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Populations represent functional units in the ecosystems they occur, they significantly impact them, and are the main target of management and conservation politics. Population genetics offers an insight into the evolutionary processes that determine the genetic state and interactions of the populations. *Sturnira hondurensis*, a common Mesoamerican fruit-eating bat species, plays an important role in forest regeneration, however, no study has been made yet on its population genetics. The subject of this study was to assess the genetic diversity, level of differentiation and population structure of *S. hondurensis* along its distribution range. We obtained genotypes for 8 microsatellite loci of 114 individuals from 11 different localities in Mexico, Honduras, and El Salvador. Allelic and genotypic richness (average = 15 alleles per locus; 114 genotypes) and diversity (average = 0.72; average = 1) were high in all localities, genetic distances among individuals (Bruvo distances ranged from 0.09 to 0.38), G'_{ST} differentiation among localities (between 0 to 0.5114), Analysis of Molecular Variance among individuals (0.0986, $p = 0.001$), localities (0.061, $p = 0.001$) and geographical regions (0.0838, $p = 0.001$), and Bayesian analysis of Structure supported big differentiation between two big groups. The most and least diverse and rich localities are allocated in eastern Mexico, and western Mexico, respectively, and the biggest differentiation occurs among western Mexico and central America localities. There are two clearly differentiated groups: an isolated one from western Mexico, and a bigger one composed by eastern Mexico and central America. Our results are congruent with the information about the historical dispersion and colonization movements proposed by previous works.

Glucocorticoids and Their Relation to Immunocompetence and Oxidative Stress in an Endemic Insular Bat

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One of the most common tools used in conservation physiology is the assessment of environmental stress by measuring glucocorticoids (GGs). Use of fecal samples has become widely used in the field, but interpretation of fecal GCs can be mis-interpreted if metabolic and hormone metabolite excretion rates are unknown. Thus, GCs have

to rely on other physiological biomarkers to assess stress response more accurately. Immunocompetence is often related to GCs levels, and production of reactive oxygen species is an associated cost of both. Therefore, we evaluated the relationship between fecal cortisol metabolites (FCM) with different antioxidant enzymes (SOD, CAT and GPx), and immune parameters (humoral and inflammatory) in the fish-eating bat (*Myotis vives*i). We induced a) acute stress by movement restriction, and b) strong rise in GCs levels after injection of adrenocorticotropic hormone (ACTH) and/or phytomehagglutinin (PHA). Inflammatory response was lower with higher basal FCM levels, but it had increased after acute stress. Humoral response increased with higher FCM levels in both baseline and acute stress conditions. When organisms were simultaneously injected with ACTH and PHA, their FCM concentration decreased. Antioxidants were positively related to basal levels of FCM. There was a general positive relationship between biomarkers and FCM levels but more studies on the short and mid-term effects of GCs on different physiological parameters are needed to further understand its implication for animal fitness.

Validating an Aerial Bat Detection Technology: Acoustic Detection from Above

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Throughout the United States, millions of acres of undeveloped land maintained by the Department of Defense for readiness, provides habitat for significant populations of endangered, threatened, and at-risk bat species. Natural resource managers charged with the stewardship of these lands and the monitoring of such species under the Endangered Species Act, Sikes Act, and National Environmental Policy Act, are unable to access large areas due to personnel hazards from the testing of certain weapons platforms and the potential for unexploded ordinance (UXO). Building off the fundamental ideas of the Autonomous Aerial Acoustic Recording System, an aerial bird monitoring technology developed and field-tested under the US Army Corps of Engineers Environmental Laboratory (Dr. Richard Fischer) and the University of Tennessee (Dr. David A. Buehler, Dr. Stacy Worley, and Dr. John B. Wilkerson), we have developed an Aerial Bat Detection Technology (ABDT) to supplement ground-based ultrasonic acoustic sampling in accessible areas, as well as providing access to previously inaccessible areas within these DOD installations. The ABDT has been designed to acoustically detect bats along transects at virtually any altitude above the ground and improve our understanding of bat ecology, demographics, and occupancy across various ecosystems. The ABDT is comprised of a remote-controlled weather balloon and payload that incorporates an ultrasonic microphone array and redesigned data logger, engineered at the University of Tennessee. We will present the results of the initial validation testing from this microphone array and incorporated data logger.

Creation and Validation of the R-package Countcolor for Quantifying the Fluorescence Emitted by *Pseudogymnoascus destructans*

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Pseudogymnoascus destructans colonizes the wing membrane of hibernating bats in dense fungal hyphae aggregates, forming cupping erosions. These fungal cupping erosions emit a characteristic fluorescent yellow-orange color when the wing membrane is transillumnated with 360 nm UV light. The purpose of this study was to create and validate the R package "countcolors" for quantifying the distinct orange–yellow UV fluorescence in bat-wing membranes caused by *P. destructans*. Validation of the R-package was completed by first quantifying the percent area of twenty, one-million pixel images. These generated pixel images were of two known pixel colors ranging from zero to one-hundred percent of the pixels. The R-package positively perfectly correlated with the generated pixel images of known pixel colors. Subsequently, 40, 2.5 centimeter square UV transillumnated photographs of *Myotis lucifugus* bat wings were given to a single evaluator. The area of fluorescence was both manually measured and calculated using ImageJ and quantified with the countcolor R-package. There was good agreement between the two methods (Pearson's correlation = 0.915), however the manual analysis showed a consistent negative bias. Using the R-package countcolor is less time intensive than manually measuring the fluorescence and our results show countcolor can improve the accuracy when quantifying the area of *P. destructans* infection in bat wing-membranes.

Born to Be Piled: Staying Close to Your Relatives Gives You a Better Chance of Survival

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Tequila bats (*Leptonycteris yerbabuenae*) use hot caves during their nursing period not only for protection but also to reduce the energetic costs and speed-up development of their pups, therefore reducing the time-period of mother dependence. As a migratory species, faster development is beneficial since resource availability is limited to a short period of time and the young have to be fit to endure the migration to south-central Mexico in the autumn. In the Sonoran Desert thousands of female tequila bats gather together in the early spring to give birth to their young. We studied the dynamics of infant grouping (clusters) formations, the mother-pup recognition, and abiotic factors of the cave that could be contributing to such behavior. We recorded the activity of 10 clusters. We also measured the temperature pattern of two cluster at three sites (center, periphery and 40 centimeters from the cluster). Almost every cluster was made in open and flat area of the cave's ceiling and ceased once the females took the pups. These sites had a mean temperature of 28°C (± 2°C), but due to the aggregation of bats the temperature in the center could reach up to 36°C and 33.5°C in the periphery. The results showed that there's a significant positive relationship between the temperature difference and the number of pups. Even though females of this species use hot caves during their nursing period, it seems they carefully group their pups during the night to further facilitate the advantage of thermoregulation from the group huddling.

***Frugivory in Phyllostomids is Associated with Microbiome Functional Specialization**

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While frugivory is a common dietary guild in the Phyllostomidae, it remains unclear how fruit-eating bats are able to cope with a diet that is low in key nutrients such as proteins and lipids. A standing explanation is that fruit bats must engage in facultative insectivory to meet their nutritional requirements, but new evidence suggests that mammalian gut microbiomes, the community of symbiotic bacteria inhabiting the gut, are functionally specialized to provision their hosts with nutrients missing from the diet. Because neither of these hypotheses has been explicitly tested in bats using molecular techniques, it is unclear which of these forces may have been more important in facilitating the evolution of frugivory in this clade. Using an ecologically diverse assemblage of Neotropical bats, we tested these hypotheses using 16S rRNA microbiome sequencing, functional annotation by ontology, and diet metabarcoding of fecal samples from frugivorous and insectivorous host species from Belize. We found limited evidence of insectivory in the feces of fruit-eating bats, including the presence of insect orders Trichoptera, Hymenoptera, and Lepidoptera. We also found that the microbiomes of frugivorous bats were enriched for functions related to peptide biosynthesis, carbohydrate and fatty acid metabolism, and vitamin B6 metabolism compared to insectivorous bats, supporting the hypothesis that the microbiome provisions hosts with nutrients lacking in fruit. This evidence suggests that both incidental consumption of insects and selection on microbiome functions may have been useful adaptations to a frugivorous lifestyle in phyllostomids.

Winter Activity of Four Species of Cavernicolous Bats in Tennessee

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For bats captured outside of caves in the southeastern US during the winter hibernation season there is significant variation in *Pseudogymnoascus destructans* (*Pd*) loads and prevalence within and among species. Our previous research suggests that these variations in Pd susceptibility may be due to differences in activity during this season. To understand differences in winter activity among species we deployed Passive Integrated Transponder (PIT) tags

and associated data-logging detection systems at 3 Tennessee hibernacula. We used these systems to monitor the winter activity of four target bat species (*Myotis grisescens, M. leibii, M. sodalis,* and *Perimyotis subflavus*) with varying susceptibility to Pd. Prior to the hibernation seasons of 2016–2018, we deployed 1,271 PIT tags across our 4 target species. Passive integrated transponder detections indicated *Myotis leibii* were more active during the hibernation season (November–February) than other target species, with an average of 42.35% of tagged individuals detected at cave entrances per month (range = 6.06%–72.7%; P <0.001). Of the 111 PIT-tagged bats active during winter, only 29.7% (n = 33), the majority of which were *M. leibii* (69.6%, n = 22), were detected at a cave entrance more than once per night. The length of time between detections in the same night ranged from 11.5 minutes to 399 minutes (6.65 hours). Our initial results suggest species specific differences in hibernation activity at sites impacted by white-nose syndrome (WNS), which may influence susceptibility to Pd.

Glow in the Dark: Tracking Movements of Bats on an Island Systems

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Bats (order Chiroptera) are the most diverse group of mammals on Caribbean islands where they can occupy a wide variety of niches. Recent studies have shown that the advent of humans on these island systems has drastically changed the landscape and altered the distribution of numerous vertebrate species, including bats. Understanding how species distribute themselves on the islands can help demonstrate the adverse effects of climate change and anthropogenic impacts. The island of Eleuthera which spans a distance of 457.4 km^2 on the Great Bahama Bank was chosen as a study site. Fluorescent powder was used to mark bats in three caves located in the northern, central, and southern parts of the island. Each cave was tagged with a specific fluorescent dye and checked nightly. Initial results indicate that the bats do not move between the caves. This study highlights the use of inert dyes in understanding the movement of bats in The Bahamas. Future directions include rechecking the caves for the presence of the dyes.

Scent Dog Fatality Searches at a California Wind Farm Suggest Spatial Clumping of Bats

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Despite many studies of bat fatalities at wind energy sites across North America and Europe, few studies have shown spatial differences among fatalities at turbines. However, fatality studies using human searchers may not provide a high enough percentage of fatalities to detect spatial relationships. We hypothesized that a better searcher efficiency rate might lead to a better understanding of fatality patterns such as the clustering of fatalities. We used scent dogs to increase our ability to detect fatalities at a project with 48 turbines at Altamont Pass in California where most previous studies suggest few bat fatalities. We used a Hot Spot analysis in ArcGIS 10.4.1 (ESRI, Inc., Redlands, CA) to quantify the degree to which fatalities were spatially clustered among turbines. The first year we found 229 bats including 133 (58%) *Tadarida brasiliensis*, 84 (37%) *Lasiurus cinereus*, and seven (3%) *Lasiurus blossevillii*. The hot spot analysis identified one turbine on the southeast edge of the facility with 17 fatalities as a strong hot spot (P <0.01) and another turbine on the outer north-central edge with 12 fatalities as a moderate hot spot (P <0.03). Additionally, five of seven western red bat fatalities were distributed within a narrow (~ 213 meters) east-west band occurring between latitudes 37.711743° and 37.708948°. Few other projects in North America or Europe have reported spatial differences in fatality rates among turbines or within projects, but such information could be useful for developing mitigation strategies for new projects.

The Earliest Asian Bats and their Significance for Understanding Character Evolution in Stem Chiropteran Families

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Early Eocene bats are known from Africa, Australia, Europe, North and South America, and India. The oldest species date to ~55 million years and are known only from isolated teeth and jaw fragments. Slightly younger fossils from the early and middle Eocene include preserved postcrania of at least six stem families. The absence of early

Eocene bats from Asia is unusual given Asia's likely role in the evolution of many orders of extant mammals. Here we describe two upper molars from the earliest Eocene of the Junggar Basin, northwest China. We assign these teeth to Chiroptera based on a suite of characters consistently present in primitive bats, including dilambdodonty with strongly lingually shifted paracones and metacones, absence of mesostyles, long primary cristae, hooked parastyles, and exaggerated fovea. The M^3 is most similar to an unnamed taxon from the middle Eocene of Pakistan, while the M^2 shows affinities with *Icaronycteris menui* from the early Eocene of Europe. The unique combination of plesiomorphic characters preserved in these teeth has implications for understanding the evolution and potential monophyly of several stem bat families. These specimens lack both a talon heel and lingual cingulum, suggesting that these are derived within Chiroptera. The Junggar Basin bats also retain rudimentary conules, as expected from comparisons to potential outgroups including primitive eulipotyphlans and stem eutherians. These teeth shed light on the mosaic evolution of chiropteran dental characters and suggest that such families as Icaronycteridae and Archaeonycteridae may represent grades of chiropteran evolution rather than monophyletic groups.

Conservation Actions Are Needed for Both Acute and Chronic Threats to North American Bats

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Acute threats to biodiversity attract attention and are prioritized for conservation actions when compared to chronic threats. However, it is not clear how acute vs chronic threats impact biodiversity in the long term, or how they interact. We investigated how the acute outbreak of white-nose syndrome (WNS) and chronic land cover change in eastern North America would impact bats over time. We identified land cover preference for two WNS-impacted species, the tri-colored (*Perimyotis subflavus*) and northern long-eared (*Myotis septentrionalis*) bat and modelled how future land cover change and spread of WNS would affect their distributions. We hypothesized that both land cover and WNS affect current bat distribution and that WNS would have the same effects on future bat distribution as land cover change. We collected bat distribution data at 161 sites using the North American Bat Monitoring Program from 2015 to 2017 in North Carolina, USA. We used the National Land Cover Database, and current WNS occurrence data, as covariates for dynamic occupancy modeling. We found land cover was important in explaining occupancy, colonization, and extinction probability. However, WNS only impacted extinction probability. We predicted future bat distribution in 2035 using projected land cover and WNS occurrence. We found land cover change would cause decreases in both species' occupancy. Northern long-eared bat extinction probability would increase due to land cover change, regardless of WNS spread. Even though WNS has an acute impact on bats, the management of WNS must go hand in hand with protecting critical habitats.

Roost Selection of Southeastern Myotis in an Old-growth Bottomland Hardwood Forest

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Little is known about the roosting habits of southeastern myotis, *Myotis austroriparius*, in Coastal Plain forests. Our objective was to quantify characteristics of roosts selected by southeastern myotis in Congaree National Park, an old-growth bottomland hardwood forest in the Upper Coastal Plain of South Carolina during winter (November–March) 2015–16 and 2016–17 and summer (May–August) 2015 and 2016. We located roosts through opportunistic cavity searches and tracking radio-tagged bats to roosts. We quantified tree characteristics, the herbaceous layer in front of the cavity opening, habitat type, canopy closure, and cavity opening size of roost and random trees. We ran logistic regression models to test which characteristics were the most important for distinguishing all roosts versus random trees, winter versus summer roosts, summer roosts versus random trees, and winter roosts versus random trees. Although we located many canopy roosts during the study, our analyses were conducted only on roosts with basal cavity openings. There were no significant differences between winter and summer roosts or between winter roosts and random trees. Roosts had significantly smaller cavity openings than random trees ($P = 0.006$), significantly larger diameter at breast height ($P = 0.016$), and smoother cavity interior texture ($P = 0.062$). Cavity opening area and diameter at breast height also differed significantly between summer roost and random trees ($P = 0.024$ and $P = 0.039$, respectively). This suggests that roosts are selected for their cavity properties rather than for their surrounding habitat, perhaps to decrease risk of predation, improve thermoregulation, and provide larger spaces for maternity aggregations.

Drivers of Human Behaviors: The Theory of Planned Behavior and Flying Fox Hunting in Southeast Asia
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Although many threats to bat populations derive from the degradation and loss of foraging and roosting resources, direct mortality from hunting and/or persecution threatens 10% of bat species globally and more than a third of Old World fruit bats (Pteropodidae) (IUCN 2018). Sensitization and outreach campaigns that vaunt the importance of bats may change values over generations, but effective real-time interventions need detailed insight into behavioral drivers of the action of concern. The Theory of Planned Behavior (TPB) provides a conceptual framework to interrogate the motivations of human behavior that has been used in psychology for more than 30 years. The TPB posits that human behavior is guided by beliefs about: the likely consequences of the behavior (behavioral beliefs); social pressure to perform or not perform the behavior (normative beliefs); and whether people feel they have the resources, opportunities, or abilities to perform the relevant behavior (control beliefs). More recently, the TBP has been applied to environmental and conservation behaviors that range from littering to illegal hunting of tigers. Here we introduce the TPB and detail its use as a conceptual framework to understand the diverse drivers of flying fox hunting across Southeast Asia. We illustrate questionnaire development with a case study from Sulawesi, and close with consideration of other human-bat interactions and conflicts that could benefit from application of the TPB framework.

After the Invasion: White-nose Syndrome and Bats in Michigan
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Pseudogymnoascus destructans was first detected in Michigan in spring 2014. During winter 2016–2017 and 2017–2018, we visited 47 mines, 2 caves, and 1 tunnel, counted overwintering bats, and determined species composition, to make comparisons pre- and post-white-nose syndrome. Statewide, the total population fell 83%; 24 sites registered population declines greater than 90%, including multiple hibernacula that formerly sheltered more than 10,000 animals each. Overall, little brown bats (*Myotis lucifugus*) decreased by 78%; northern long-eared bats (*M. septentrionalis*), by 96%; and eastern pipistrelles (*Perimyotis subflavus*), by 94%. These species disappeared from 10, 75, and 75%, respectively, of the underground locations from which they were known before the disease. Big brown bats (*Eptesicus fuscus*), in contrast, exhibited no substantial change in numbers or distribution. A preliminary analysis suggested that size of the initial population had no effect on the extent of the decline at each hibernaculum, although sites with a maximum ambient temperature greater than 7 °C and those with water vapor pressure deficits less than 0.5 kPa were consistently devastated.

Key Ecological and Social Considerations for Implementing Agave Restoration for Nectar-feeding Bats in Northeast Mexico
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Endangered Mexican long-nosed bats (*Leptonycteris nivalis*) migrate every year between central Mexico and the US Southwest. During migration, they feed on the nectar of agaves (*Agave spp.*). However, agaves are also harvested for many uses throughout Mexico. Efforts are underway to establish agave restoration programs that will enhance forage resources for *L. nivalis*. However, little is known about how to implement these programs in ways that are both ecologically and socially appropriate. In this study, we addressed two questions: 1) What agave characteristics provide high-quality food resources for bats? and 2) What social factors should be considered when implementing agave restoration with local communities? We worked in northeast Mexico around two important roosting caves for the species. To address the first question, we monitored bat feeding activity at flowering agaves with infrared cameras for 58 nights (summers 2016–2018). To address the second question, we conducted 45 semi-structured

interviews with agave harvesters from 14 communities, focusing on current agave management and potential motivations or barriers to agave restoration. Preliminary results from the foraging study indicate that bats prefer clumped agaves, suggesting that agaves should be planted in groups during restoration projects. Analysis of interviews revealed several key considerations for working with local communities. Considerations include understanding trade-offs and identifying when incentives are needed, listening to local knowledge, investing in long-term monitoring, and understanding local variability in agave growth and reproduction. These findings provide valuable information for organizations seeking to implement agave restoration programs for the Mexican long-nosed bat.

The Genome-wide Selective Pressure of Bat White-nose Syndrome on Affected Populations of *Myotis lucifugus*

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Novel pathogens can cause massive declines in population sizes, but seldom lead to extirpation of host species. Rather, disease acts act as a selective pressure on survivors, driving the evolution of tolerance/resistance. Bat white-nose syndrome (WNS) is a rapidly spreading wildlife disease in North America. The fungus causing the disease, *Pseudogymnoascus destructans,* invades skin tissues of hibernating bats, resulting in disruption of hibernation behavior, premature energy depletion, and subsequent death. We use whole-genome sequencing to investigate changes in allele frequencies within (temporal variation) and across (geographical variation) genomes of three populations (PA, NY, and MI) of *Myotis lucifugus*, to scan for signs of genetic resistance to WNS. Our results show a very minor decrease in heterozygosity within the populations across time, i.e. prior to WNS (pre-WNS) compared to populations that have survived WNS (post-WNS). We also see low F_{ST} -values between pre-WNS populations, except for a sharp increase in values on scaffold GL429776 between PA and MI. These values are even higher in comparisons between post-WNS PA and MI populations and NY and PA populations. Thus, our results suggest WNS has not subjected *M. lucifugus* populations to selective pressure, but may have allowed the rise of a local adaptation in PA through weakening connectedness of populations. Of the genes in the high F_{ST} -value region, KITLG, stands out due to its involvement in thermoregulation, and should be subjected to closer inspection. The existence of remnant populations is thus likely due to other factors in bat life history besides genetic adaption.

Community Ecology and Phylogeography of Bats in the Guianan Savannas of Northern South America

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The Guiana Shield of South America contains one of the largest contiguous expanses of pristine tropical rainforest remaining in the world. Smaller tracts of savannas are also present, but its biodiversity is less known and studied. In lowland Neotropical areas, bats typically comprise the most species-rich group of mammals. We compare the bat faunal community and phylogeography in the savanna habitats of the Llanos in Venezuela, Rupununi in Guyana, and Sipaliwini in Suriname. Measures of species diversity and relative abundance from standardized field survey methodology enable comparison among these 3 grassland regions. Genetic variation is summarized by DNA barcoding to examine biogeographic patterns across larger forest-savanna landscapes. A total of 76 species of bats are documented, of which 18 species are reported from all 3 savannas and 30 species are reported from only one of the savannas. Endemism is low with 3 taxa restricted primarily to dry open habitats. However, 8 species have divergent phylogeographic lineages associated with savanna populations. Although bat species are usually distributed over wide regions of the Neotropics, the habitat mosaics of the Guiana Shield have different faunal assemblages. Going back into the Miocene, the contractions and expansions of forest-savanna paleoenvironments over time have contributed to speciation and the current high levels of biodiversity in South America.

A Tale of Two Strategies: Winter Torpor Patterns of Two Southeastern Tree-roosting Bat Species
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Determining whether a population of bats is susceptible to white-nose syndrome (WNS) requires knowledge of its torpor patterns, particularly the amount of time that skin temperature (Tsk) is below the upper growth limit of *Pseudogymnoascus destructans* (19.5°C), the fungus that causes WNS. Southeastern myotis (*Myotis austroriparius*) and tri-colored bats (*Perimyotis subflavus*) are susceptible to WNS when they hibernate in caves and mines. In parts of their range they overwinter in trees and other structures such as bridges but, it is not known whether they are susceptible to WNS when roosting in these structures. Our objective was to determine the torpor patterns of southeastern myotis and tri-colored bats that use trees and other structures during winter at two sites in South Carolina, with special emphasis on the amount of time Tsk was below 19.5°C (i.e., Pd-zone). We placed temperature sensitive radio-transmitters on southeastern myotis during winter 2015–16 and 2016–17, and on tri-colored bats during winter 2017–18, tracked them to their roosts, and recorded Tsk using Lotek dataloggers. Southeastern myotis rarely went into extended torpor but instead exhibited daily torpor. Mean Pd-zone bout time was 8.1 hr and only 4 of 22 bats stayed in the Pd-zone for >1 day. In contrast, tri-colored bats often exhibited extended torpor bouts; mean Pd-zone bout time was 19.8 hr with a maximum of 9 days. Our data suggest that winter torpor patterns of tree-roosting southeastern myotis may allow them to survive WNS infections whereas tree-roosting tri-colored bats may be more susceptible.

Tochmatzintla Bats, Sierra del Tentzo, Puebla, Mexico.
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Bats are the most diverse mammals in Mexico, and they are considered key in ecological processes, such as pollinization, seed dispersal, and regenerators of disturbed environments. This work documents the richness, abundance, and diversity of bats from the Communal Goods of Tochmatzintla, Hutlatlauca, Puebla. The sampling was done in dry season during 2015 and 2016. We use mist nets to capture bats, conventional data was taken. The presence of 12 species was confirmed, from 8 genera and three families, representing 6.96% of the state registers. All species are considered of least concern by the IUCN and none are in CITES. The capture effort was 1295 meters of net; *Rhogessa alleni* was the species with highest abundance. The species richness index was Dmg = 2.611. Shannon's diversity index was H´ = 2.177. The similarity index changed between sites and there is an allometric relationship between weight and length of the forearm, according to their feeding habits. The communal goods of Tochmatzintla offer a wide array of natural habitats, therefore it is recommendable to make species inventories, in order to establish habitat conservation programs for environmental education, generating citizen awareness, and wildlife management policies.

Dermatomycosis in *Tadarida brasiliensis* from Mexico City
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Since the appearance of white-nose syndrome (WNS) in 2007, concerns regarding diseases that produce mortalities in bats have risen. Besides *Pseudogymnoascus destructans*, very few information exist about pathogenic fungus in bats. The present is the first report of dermatomycosis in a bat from Mexico City, which happened in the spring of 2016 when an adult male *Tadarida brasiliensis* was found prostrate, weak, and dehydrated. The wings show grossly skin clinical signs of multifocal coalescent lesions with brown circular appearance, on both dorsal and ventral surfaces. Eighteen hours later, the animal died. Necropsy reveals generalized lack of adipose tissue and severe multifocal pneumonia as a probable cause of death. Histopathological analysis corroborates an interstitial pneumonia, but also reveals lymphoid depletion of the spleen, which suggests an immunosuppression process, of indeterminate cause. Pathologic changes in skin include parakeratosis, and moderate, multifocal to coalescing hyperkeratosis. Spores were adhered to stratum corneum and hair follicles. The findings of this report are relevant

since reveals for the first time that *T. brasiliensis*, a mollosid that commonly shares refugees with vespertillionid bats, is susceptible to fungal secondary pathology due to immunosuppression process. This fungal-immunosuppression process occurs also in US vespertillionid bats, which acquire the WNS disease due a suspected immunosuppression. The cause of immunosuppression and the fungus characterization need to be further studied, in order to increase knowledge and improve the understanding of fungal diseases in bats, to develop preventive measures and implement treatments.

Developing an Open Source Neotropical Bat Call Fact Sheet with a Costa Rican Focus

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Vocal signatures allow for the identification of a wide range of bats and represents a non-invasive, cost-effective survey method to measure diversity, temporal activity, and distributions of rarely captured species. Despite the simplicity of this type of data collection, it takes years of experience to identify bats by their vocal signatures, particularly without a complete and comprehensive public access dataset. This is particularly true for the Neotropics where high diversity, large species ranges, and other environmental factors affecting bats may contribute to call variations. As species are shared across borders and geographical ranges, call summaries can be used for species identifications across species distributions. This project compiled acoustic data from the Neotropical bat call database (>1,8700,000 records), recorded by Bruce Miller from Mexico to Bolivia and Cuba with numerous international collaborators. Fact Sheets and Interactive ID keys by country are being made freely available to provide key call parameters for users to identify bat calls. Data recorded in the Osa Peninsula, Costa Rica, by Beatriz Lopez Gutierrez, has been used to enhance the database and create identification Fact Sheets for Costa Rica. With the aid of these free tools, researchers, conservation managers, and keen citizen scientists recording bats will be able to identify their own data, vet "black box classifiers" and become proficient in identifying future recordings.

Ecological Adaptation or Phylogenetic Constraint in Evolution of Echolocation Call and Morphology in *Molossus*?

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In this study we explored the evolution of several parameters of echolocation calls and morphological characters in the broadly distributed Neotropical bat *Molossus*. *Molossus* are morphologically conservative and the level of genetic divergence, even among well characterized species, is low, which has made the genus a taxonomic challenge. Therefore, better phylogenetic resolution and understanding of the patterns of diversification of echolocation calls and variance in morphological characters could help to discern the underlying speciation processes. We obtained tissues from 190 specimens, including all the recognized species of *Molossus* and two outgroups. The genotyping by sequencing approach was performed and single nucleotide polymorphisms were filtered and aligned with the genome of *Myotis brandtii* as reference and *De Novo*. We generated Maximum Likelihood and SVDquartet trees that resulted in well resolved phylogenies with fourteen distinct clades. A total of 10 echolocation call parameters and six morphological characters were mapped onto the phylogeny and independent contrasts analyses were performed among variables of these two datasets. Based on our results only a few characters, in either datasets, have strong phylogenetic signal, but quantitative echolocation call parameters seem to be highly correlated with size. Our study indicates that both echolocation and morphology often evolved in *Molossus* as a mosaic of primarily ecological adaptations and phylogenetic constraints.

***Phylogenetic Signal in Skull Shapes of Stenodermatine Bats**

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*** Sara C. Lucero-Verdugo** received the **Avinet Award.**

The Stenodermatinae subfamily is considered the most diverse in species and morphologies within phyllostomid bats. Its origin has been related to the change and specialization to a frugivorous diet and the evolution of a robust skull. That is why the great skull variation present in stenodermatines could has a phylogenetic or ecological

component. Our goal was to describe the variation in the skull shape of 10 genera along all subfamily, and to analyze if this variation has a phylogenetic component. We quantified the shape variation of mandibles and cranium using geometric morphometrics and modularity methods. We used the phylomorphospace and the phylogenetic signal estimation to compare morphologies with the most recent and complete phylogeny of Noctilionoids bats. In all analyzed shapes we found significant differences among all genera. The phylomorphospace allowed us to observe that some species are close in their morphology but distant in the phylogenetic relationships, mainly in the mandibular modules where greater variation and absence of phylogenetic signal was obtained. This may be due to a high plasticity in response to ecological factors, so that the mandibular characters could be useful in ecomorphological studies. In contrast, in the cranial modules we found significant phylogenetic signal, indicating a phylogenetic congruency. This suggests that the cranial characters provide information in phylogenetic studies of stenodermatine bats.

Acoustic Library of Mexican Insectivorous Bats: SONOZOTZ-AMMAC-CONABIO

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Mexican bat researchers, members of the Mexican Society of Mammalogy (AMMAC), along with mathematicians and computational scientists, integrated the first reference acoustic library of Mexican insectivorous bats and developed the first online open-source platform to share acoustic data of bats worldwide. We developed a standardized sampling and recording protocol and held three training workshops. Sixty individuals attended, including researchers, students, independent professionals, and representatives of NGOs and federal agencies. In 2016 and 2017, we sampled bats in 183 localities of eight Mexican ecoregions that ranged from sea level up to 3600 m in elevation. A total of 173 people from 30 academic institutions participated in the sampling collections. We recorded 2,302 echolocation calls from 1,604 individuals belonging to 7 families and 67 species, representing 63.3% of the insectivorous bat species of Mexico. *Myotis velifer* was the most recorded species (n = 308), followed by *Tadarida brasiliensis* (n = 221), and *Pteronotus parnellii* (n = 203); in contrast, six species were recorded one single time. The platform was developed in a wxpython framework and contains taxonomic, morphometric, photographs and sonograms for all recordings. The platform along with all the hosted data will be freely accessible and it can be strengthened to increase and extend the calls of representative species from any country.

Indirect Effects of the Landscape on Fruit Production in Baobab Trees of Kenya

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Baobab trees (*Adansonia digitata*) span mainland Africa and observations and exclusion experiments suggest that fruit bats are the primary pollinators. Bats' nightly movements are motivated by the availability of resources in the landscape, such as water, flowers, and fruits. The distribution of water and food in the landscape is therefore predicted to indirectly influence the number pollinating visits to baobab trees, and as a consequence the number of fruit produced by baobab trees. To test the indirect effects of the landscape on fruit production, we counted the number of fruit on baobab trees in an approximately 4.0 km by 3.0 km plot near Nuu, Kitui County, Kenya. In

addition, we recorded all possible fruiting trees (i.e., mangoes, bananas, pawpaw, and figs). We predicted that more fruit per baobab tree would occur where: i) there is a greater density of mango trees, fig trees, and baobab trees within a 500m buffer around the focal tree; ii) the closer the focal baobab is to its nearest neighbor (e.g., baobab, mango, or fig tree); and iii) the closer the focal baobab is to a water source. The number of baobab fruit per tree is influenced by density and proximity of other baobab and fig trees, but also by the number of introduced fruiting trees, such as mangoes. The findings suggest an intricate relationship between the configuration of the landscape, its components, and its influence on pollinators such as fruit bats.

Population Genetic Demography of the Tri-colored Bat and Implications for the Impact of White-nose Syndrome

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The recent emergence of threats to North American bat conservation has prompted an increase in population genetic research on high-risk species. The tri-colored bat is affected by both white-nose syndrome and wind turbine mortality. However, little work has been done regarding the population structure and effective population size of this species. Using mitochondrial sequence and nuclear microsatellite data, we analyzed male and female structure across the sample range of *Perimyotis subflavus* and estimated the effective population size of their populations. Pairwise F_{ST} values indicate that there is one panmictic population based on microsatellite data, while mitochondrial data support two populations within the sampled range. AMOVA results suggest that females are making short distance movements. These data yield contrasting results for effective population size and size change over time. Mitochondrial data suggest an increase in female effective size for both Appalachian and western populations since the last glacial maximum, while microsatellite data suggest a recent bottleneck. The persistence of the tri-colored bat is dependent upon the maintenance of genetic diversity, and calls for the conservation of genetically distinct populations as well as the preservation of hibernacula and swarming locations.

Interspecific Interactions Between Sympatric Nectarivorous Bats (*Leptonycteris*) and Corroboration of Historical Roosting Sites in Central Mexico

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Leptonycteris nivalis and *L. yerbabuenae* are physically and ecologically very similar nectarivorous bats, so they are expected to have different feeding habits when their distributions overlap to avoid competition. In addition, *L. nivalis* was reported in different caves more than 10 years ago, but these caves were never visited again. The objectives of this work are: to determine the use of food resources by *L. nivalis* and *L. yerbabuenae* when their distributions overlap in Central Mexico; and to determine the presence of *L. nivalis* in caves reported as historical roosting sites. We sampled the diet, foraging activity, and resource availability in the periods autumn–winter and spring–summer. Also, caves were visited and the presence or absence of *L. nivalis* was corroborated. The results showed that these bats share more than half of the plant species in their diets in both periods. In autumn–winter the genus *Ipomoea* dominates their diet, while in spring–summer their diet is dominated by the genus *Agave*. The above, added to the high availability of food resources identified indicates that there is no competition for food between these bats when their distributions overlap in Central Mexico. On the other hand, *L. nivalis* was found in a single cave of those historical records that were visited again. This colony in the state of Michoacán represent a breeding colony for the species, which is a great contribution in its conservation.

Assessment of Bat Guilds for Automatic Acoustic Classification

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Automatic acoustic classification of bat signals is often focused on species level, deriving all the associated ecological information from an output label reference that can be unreliable. However, it is possible to produce direct ecological audio tagging without the need of species names, provided that a set of meaningful label categories exists. Bats' sonar has allowed them to exploit a wide range of niches and it has evolved to reflect species sensory requirements. There have been different proposals to categorize bats into guilds but to date there are no assessments on their effectiveness in automatic time explicit event detection and classification. Here, we used deep learning methods and four guild categorizations to determine performance on raw audio input labelling with constant overall architecture except for the number of output classes. We used a total of 1385 files comprising 26361 pulses from 66 species and 8 families distributed in Mexico to generate a 6:2:2 partition for training, testing, and validation sets. Results showed a tendency of Schnitzler and Kalko's 2001 guild definition to outperform other classification schemes at detection tasks with 80% mean precision and 70% mean recall. The analysis here probes the robustness for the use of guild levels to classify bat echolocation calls. Bat acoustic monitoring programs based on their functional roles can be useful to identify key or redundant species, to develop ecological studies and to implement conservation and management plans.

The Value of Working with First Nations Communities to Discover and Monitor Endangered Bats in Ontario

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First Nations peoples in Ontario have a strong cultural link to the natural world and possess Traditional Ecological Knowledge (TEK) stemming from generations of observation and interaction with wildlife. Conservation researchers in Ontario have begun to incorporate TEK into conservation efforts for wildlife such as moose and turtles. Many First Nations communities in Ontario are located in areas with suitable habitat for bats, and many are located in the central and northern parts of the province where species affected by white-nose syndrome (WNS) are still present in larger numbers than the south. We are working with five First Nations communities across Ontario to gather historic and contemporary knowledge of bats. We provided equipment and training to community members to conduct acoustic monitoring for bats, and to monitor roosts through exit counts. In 2018, we recorded acoustic activity of endangered bats at four communities. We located little brown myotis (*Myotis lucifugus*) roosts at two communities, with a combined total of 405 individuals counted. We have found strong community interest in bats and their conservation, and have trained or engaged a total of 75 community members. We found there to be strong value in gathering TEK and working closely and respectfully with First Nations communities as a method to conserve endangered bats. We hope to continue collaboration with communities, and encourage others to consider this two-way exchange of information.

Consumption of Spiders by Bats

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Myotis lucifugus, an aerial insectivorous bat, consumes spiders in low temperatures at the start and end of the summer in the Northwest Territories, possibly due to a shortage of flying insect prey. However, in Alaska, this species consumes spiders even during high aerial insect abundance in mid-summer. This suggests that abundance of aerial insects may not be the factor favouring spider consumption. Instead, less competition from gleaning bats may allow *M. lucifugus* to consume spiders all season. To examine this hypothesis further, my study investigates the consumption of spiders in Alberta in two species of bats: a gleaner (*Myotis evotis*), and an aerial insectivore (*M. lucifugus)*. To better understand why bats may choose to consume spiders in certain conditions, I am examining whether there are seasonal changes in spider consumption by these species, how they forage for spiders, and whether these differ between the species. When handfed spiders, most *M. evotis* and *M. lucifugus* bats readily consumed them. However, under observation in a fight cage, both species have not been observed hunting and consuming

spiders on their own when given the opportunity. I collected fecal samples and will analyze them to determine the frequency of spider consumption by these two species, if there is seasonality in spider consumptions, as well as the species of spiders that are most readily consumed. Further results will be presented.

Deciphering the Bat Signal: Evaluation of Mobile Acoustic Transect Surveys on Prince Edward Island
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The North American Bat Monitoring Program (NABat) developed a protocol to standardise bat monitoring in North America due to the impacts of white-nose syndrome (WNS) on native bat populations. The protocol includes stationary point surveys and mobile transects, and while mobile transects have been used for bat monitoring in a range of jurisdictions, their effectiveness has varied depending on the landscape. A study was designed to test the effectiveness of mobile transects on Prince Edward Island (PEI), a heavily developed, agricultural province in Canada. It was hypothesised that mobile transects and stationary point surveys have differing effectiveness at monitoring bat populations on PEI, and that the effectiveness of mobile transects could be altered by changing the timing and type of equipment used in these surveys. Mobile transects testing omnidirectional and directional microphones were conducted over 9 nights at 3 sites, totalling 396 km of surveys. The results showed that there was no significant difference between the number of bat passes recorded by the stationary and mobile acoustic recorders, however, there was a significantly higher number of bat passes recorded by the omnidirectional microphone. Additionally, the results indicated that the number of bat passes recorded per mobile transect during the time intervals of 22:00–23:00 and 23:00–0:00 were significantly higher than those recorded during the time interval of 21:00–22:00. This study demonstrated that testing various aspects of roadside sampling methodology is crucial for determining the best techniques for monitoring mobile at-risk species in variable habitats.

Seasonal Patterns of Insect Migration Linked to Impacts of Bats with Wind Turbines
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Nocturnal insect migrations are ubiquitous and involve kilotons of biomass that are prey to bats that fly to the altitudes of the insects. In temperate zone regions, insect migrations occur in spring and autumn, but these seasonal movements of insects differ in altitude and the meteorological factors that determine winds that support insect movements. None-the-less, these seasonal patterns are broadly predictable, strongly determined by weather patterns, and of important concern for conservation, including impacts of bats with wind turbines. Because many migratory insects are important agricultural pests, insect migrations in spring have received considerable attention from agricultural researchers seeking to protect crops by predicting pest infestations. These spring migrations are characterized by altitudinal layering of fluxes of migratory insects at altitudes of 100's to 1000's of meters above ground level, which are typically above the rotor sweep (<150 m) of contemporary industrial wind turbines. In contrast, in autumn, return migrations of insects are driven by the southward advance of cold fronts, with migratory movements of insects often occurring as "walls" rather than layers of insects that are moving from ground level through the lower altitudes where winds (as well as bats and birds) are harvested by wind turbines. We argue that these seasonal differences can explain why wind turbine fatalities to vulnerable bat species are highly seasonal, with ~75% of fatalities in North America occurring in August through October, during the period of fall insect migration.

Migratory Wanderings: Bat Migration at the Regional Scale
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Migration syndromes vary across taxa but typically are comprised of common characteristics, including (1) persistent movement over longer distances and times compared to station-keeping behaviors, (2) straightened movements in a seasonally appropriate direction, and (3) suppression of responses to resources or stimuli to which the organism would normally respond. Mark-recapture studies of small-bodied organisms that are rarely recaptured often lead to the impression of to-and-fro migration patterns, based on the assumption that animals migrate

according to the typical characteristics of migration. With the recent rapid expansion of the Motus Wildlife Tracking System (motus.org) I have tracked migrating silver-haired bats (*Lasionycteris noctivagans*) and eastern red bats (*Lasiurus borealis*) at regional scales. The Motus automated telemetry network provides more detail about individual movement patterns within a migration season. In many cases, migrating bats travelled widely over many hundreds of kilometers, including flights in seasonally inappropriate directions. Migration for these individuals does not follow a simple to-and-fro pattern, but rather involves 'wandering' movements over large regions. Explanations for these deviations from stereotypical migration patterns may involve thermoregulatory strategy or social/mating system. Variation in migration patterns is interesting from the perspective of the fundamental drivers of migration systems, and also contributes important information for assessing conservation and management plans of migratory species.

Status of *Leptonycteris yerbabuenae* in Arizona

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The lesser long-nosed bat (*Leptonycteris yerbabuenae*) was ruled to be an endangered species throughout its range in the southwestern United States and Mexico by the US Fish and Wildlife Service in 1988. *Leptonycteris yerbabuenae* is a colonial roosting, nectar-feeding species that occurs in Arizona in a limited number of roost locations seasonally from May to September. Concern over reported long-term population declines and absence of the species from known roosts, decline in the pollination of agaves, and fears of the "death of an ecosystem" were among the reasons cited for listing the species. In the twenty years following the completion of the Recovery Plan there has been a tremendous effort to obtain population estimates and trend information, improve monitoring techniques, and understand migratory movements within Arizona and beyond. These efforts have resulted in a better understanding of the temporal and seasonal ecology of the bat and led to its removal, in May 2018, from the federal list of endangered and threatened species.

What We Know About Migration of *Leptonycteris*: Stories from the Past, Gossip, and Current Paradigms

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The lesser long-nosed bat, *Leptonycteris yerbabuenae*, is among the best-known species of Phyllostomid bats. Despite the initial confusion about its taxonomic identity and nomenclature, today it is well understood. The original idea was that these bats would migrate from central and southern Mexico where they spent the winter, to northern Mexico and southwestern United States where they spent the summer. One theory suggested that *L. yerbabuenae* would have two genetically independent migratory routes in which some bats would fly north in the spring along the Pacific coast of Mexico, spend the summer in the Sonoran desert, and fly south along the Pacific coast again, while other bats would fly north in the spring along the Sierra Madre Occidental, spend the summer in the Sonoran desert, and fly south in the fall along the Sierra Madre as well. This theory was later debunked. Then evidence surfaced that not all bats migrated but that mating occurred only in central and southern Mexico, with two clear-cut birth peaks, one in the north in the summer, and one in the south in the winter. As more research was conducted in the 2000s and the 2010s, it became clear that the species is much more plastic than previously thought, and it can behave opportunistically, pushing the limits of its geographical and ecological distribution in every which way whenever a new door is opened.

Culvert Use of Over-wintering Tri-colored Bats in Texas

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The tri-colored bat (*Perimyotis subflavus*) is under review for listing under the Endangered Species Act by the United State Fish and Wildlife Service and is listed as a species of greatest conservation need by the Texas Parks and Wildlife Department due to population declines caused by white-nose syndrome. Previous studies have documented colonies of over-wintering tri-colored bats using box culverts in Texas. Our objective was to understand and quantify which structural and environmental factors best explain culvert use of over-wintering tri-colored bats in

Texas. We surveyed 208 culverts in Texas for tri-colored bats during the winter of 2016–2018 and recorded environmental and structural features at each site. Of the 208 culverts, we documented 42 occupied by tri-colored bats. We used mixed models to identify which culvert features best explained utilization of winter-roosting tri-colored bats. Variable selection indicated drivers for abundance and presence were not identical. However, we determined that maximum length (m) was the strongest positive correlate for tri-colored bat presence and abundance. We present important structural and environmental characteristics that influence tri-colored bat presence and abundance. With the recent petition to list the tri-colored bat on the threatened or endangered species list, there is a need to further investigate the potential susceptibility to WNS of culvert-roosting bats at more southern latitudes for local and regional planning efforts.

***From Morphology to Genes: Adaptations to Migration in Tequila Bats**

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*** Angelica Menchaca** received the ***Bat Research News*** **Award.**

Across a range of organisms, related species or even populations exhibit strikingly different scales and patterns of movement. Animal migration requires adaptations in morphological, physiological, and behavioural traits. Wing shape is an informative predictor of flight performance and can be used to infer ecological traits such as habitat use and migratory ability. A significant proportion of phenotypic variance in migratory traits is genetic but the genes involved in shaping these phenotypes are still unknown. The tequila bat (*Leptonycteris yerbabuenae*) exhibits partial migration within its northern and southern populations. Here I used traditional morphometrics of 13 linear measurements and geometric morphometrics of 15 landmarks to reveal significant variation in wing traits across three populations with different migratory strategies. The data unveiled signatures of sexual dimorphism and geographical variability in wing size and shape related to migratory behaviour and foraging strategies. Next, I used next-generation sequencing to compare brain and blood transcriptomes of migratory and non-migratory bats and identified differentially expressed genes (DEGs) that contribute to the migratory phenotype. Enrichment analysis of brain revealed well represented pathways implicated in cognition, learning or memory, as well as locomotory exploration behaviour in migratory bats. Blood analysis revealed pathways associated to immune response-activating signals and T-cell differentiation, regulation of pathogen processes, as well as amino-sugar metabolism. This is the first study to show wing-shape variation at the population level and to characterise genes associated to behaviour as a result of different environmental pressures due to migration in a mammal.

Phylogenetic Relationships and Genetic Introgression between *Pteronotus fulvus* and *Pteronotus gymnonotus* (Chiroptera: Mormoopidae)

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Pteronotus fulvus and *P. gymnonotus* are Neotropical insectivorous bats of the family Mormoopidae, part of distribution is sympatric and distinguish between them mainly for the length of the forearm. Recently, in the south of Mexico, bats have been observed that present intermediate morphological characteristic between *P. fulvus* and *P. gymnonotus*, which could indicate hybridization between these two species. From these observation, a possible genetic introgression between the two study species were evaluated. Amplifying a fragment of mitochondrial DNA, three nuclear fragments and including GenBank sequences (Total = 17 *P. fulvus* and 32 of *P. gymnonotus*), with these sequences phylogenetic analyzes and haplotype networks were performed. Also six microsatellite loci of 137 *P. fulvus* and 39 *P. gymnonotus* were amplified, where with analyzes of Bayesian assignment were done. The nuclear phylogenetic analyzes separated both species. However, the phylogeny and the mitochondrial haplotype network showed a mitochondrial capture of *P. fulvus* in all individuals of *P. gymnonotus* from Mexico, Guatemala, and part of Panama. According to the different Bayesian assignment methods used with microsatellites, two well-differentiated groups were found K = 2 and 10 to 42 hybrids were identified corresponding to 5.7–23.9% of the

samples analyzed. The results of sequences and microsatellites indicate an asymmetric introgression resulting from repeated reproduction events during the colonization of *P. gymnonotus* into Central America and Mexico.

Effect of Land Use Change on Bat Communities of Mexico: Implications for their Viral Richness
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In the last 50 years, land use change has increased globally at an alarming rate, modifying the composition and structure of host communities. This has led to increased contact rates between humans, domestic animals, and wildlife, favoring outbreaks of infectious diseases. We hypothesized land use change would alter the composition of bat communities, which would be reflected through changes in alpha and beta diversity indexes, and its viral richness associated. Bat species were classified according to their tolerance to the type of land use (dependent, vulnerable, and adaptable), so fitted a model of loss species through three-time periods (1993, 2002, and 2011). Bats and viral richness were determined by the total number of species in quadrants, conformed by a grid of 500 km^2 across Mexico. The loss of bat species and viruses over time was quantified by the nested component of taxonomic and phylogenetic beta diversity. A general linear model was performed to explore the correlation between beta diversity of bats and the change of their viral communities. The results showed that land use change altered the composition of bat communities, decreasing the number of species particularly in the southeast of Mexico. However, no significant changes were observed in viral communities. The beta diversity of the viral communities was not explained by the taxonomic ($P = 0.758$), or phylogenetic beta diversity of the bats ($P = 0.770$). This result could be associated with low sampling efforts on the detection of viruses from rare bat species.

Where the Bats Rest: Determinants of Hibernacula Suitability for Widespread North American Bats
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Censuses of bats are typically carried out on known roost locations over multiple years. Long-term records indicate that caves known to be used by hibernating bats may become abandoned and recolonized over time. This study elucidates the environmental factors influencing hibernacula habitation by three North American bat species (*Myotis lucifugus, Eptesicus fuscus,* and *Myotis sodalis*) across their ranges in the continental United States. Known hibernacula sites of these species are used alongside a suite of high-resolution environmental layers to construct suitability maps attuned to wintering sites. A composite model approach using geographically-partitioned occurrence records is used to highlight areas of variability in model results. The inclusion of environmental layers incorporating geologic and hydrologic properties is shown to be critical for supporting suitability models through comparisons of model construction methods. The landscape suitability maps, alongside an understanding of sources of model uncertainty, allow for the identification of caves and structures most likely to host the focal bat species. This work is intended to complement broader population models and provide a tool for surveying potential hibernacula sites.

Using Guano as a Noninvasive Method to Analyze Stress Levels in Free-ranging Big Brown Bats
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Prolonged circulation of stress hormones can be detrimental for individual health and reproductive success; therefore, monitoring stress levels in wild animal populations is important for conservation. Conventional methods of measuring stress hormones in wild populations includes taking blood samples from captured individuals, which can cause stress and undue harm. Recently, studies have shifted to a noninvasive method by extracting hormone metabolites from fecal samples. While this method is established in larger mammals, it has not been tested extensively in bats. The goal of this study was to examine corticosterone metabolites from guano collected from reproductive, female big brown bats (*Eptesicus fuscus*) and validate the effectiveness of this method by comparing our results to previous studies where corticosterone levels were measured via traditional methods. Bats were captured using mist nets placed outside a maternity roost at Siloam Springs State Park, Illinois at three specific time periods: when bats were pregnant, lactating, and post lactating. Guano samples were stored in 1.5 mL microcentrifuge tubes with 95% ethanol in a -80°C freezer until extraction. Corticosterone metabolites were

extracted, and an enzyme immunoassay kit was used to estimate hormone metabolite concentrations. Results indicate hormone levels changing at different points in the reproductive season with the highest concentrations found during lactation, followed next by pregnancy, then post lactation. This supports the hypothesis that increased maternal investment has a positive correlation with increased baseline stress levels, as previous studies have shown, and thus offers validity to the method of assessing baseline stress hormones from guano.

Conservation of a Colony of *Nyctinomops laticaudatus* in Uxmal, Yucatan, through Socio-environmental Perceptions

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There is a colony of *Nyctinomops laticaudatus* inside the Mayan Ruins of Uxmal, it is believed that these organisms damage the structure with feces depositions, so it has been thought that their exclusion, this idea based on the bad perception of bats and unknowledge of the environmental services they provide. The socio-environmental perceptions help us to understand the way in which people perceive the environment, this is important to start the resignification of the importance of the bats, so the objective of this research was to assess the socio-environmental perceptions of the visitors to the zone about these bats. We proposed guidelines for establishment of an environmental education program. Mixed opinion surveys were applied to a sample of domestic and foreign visitors. The obtained responses were categorized and analyzed using the Ordinary Least Squares Test of Gretl (Gnu Regression, Econometrics and Time-series Library) program. An informative flyer on the importance of these bats and its potential conservation was elaborated and provided to visitors. We obtained 323 surveys, most visitors believed that bats are important in the area, so they should be preserve, besides considering interesting and enjoyable its presence. Statistical analysis indicated that conservation will be determined by the following function: Conservation = $\beta 0 + \beta 1$ Age + $\beta 2$ Knowledge + $\beta 3$ Feeding + $\beta 4$ Diseases + $\beta 5$ Anthropogenesis + $\beta 6$ Extinction + $\beta 7$ Information + ε. The socio-environmental perceptions were positive, so it is feasible the acceptance and participation of visitors of Uxmal in a future environmental education program.

"Stress" Compromises the Normally Benign Virus-bat Relationship Leading to Increased Viral Replication

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In recent years several viruses that cause no obvious ill effects in their natural bat hosts have spilled over into other animals, including man, causing serious and often fatal disease. While much is known about these viruses, most of the information is from their interaction with the spillover hosts or with surrogate laboratory animals. Little is known about bat-virus relations that may have evolved over millennia. We have examined the relationships of North American brown bats with herpes and corona viruses that we have isolated or detected in them. We have explored the hypotheses that *bat viruses in their natural hosts cause long-term, low grade persistent or latent infections and that a variety of stressors upset the delicate virus-bat relationship leading to increased virus shedding.* Our methodology involves preliminary molecular characterization of virus-host interactions in cultured bat cells followed by validation of our findings in wild-caught (and non-invasively sampled) or experimentally-infected animals. We have found that in contrast to their infection of human cells, coronaviruses are unable to suppress innate anti-viral responses in bat cells leading to low levels of replication and long-term persistence. Knocking down innate responses in these cells leads to enhanced viral replication and cell death. We have also found that many, if not all, bats are persistently infected with corona and gamma herpesviruses. Suppression of innate responses due to secondary infections, or the stress of emerging from hibernation, suppresses innate responses leading to reactivation of increased viral replication.

Eastern Red Bat Habitat Selection in Areas with Different Land Use Histories in Southeast Ohio
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The eastern red bat is experiencing population declines prompting concern from wildlife stewards and managers. To provide these groups with recommendations for improving habitat for this species on its summer range, we investigated capture rates and day-roost habitat at two locations in southeastern Ohio with different land use histories. We mist-netted 65 nights and tracked 46 adult eastern red bats (male = 22, female = 24) to their day roosts on a state dedicated nature preserve and a recently reforested coal mining property during the summers of 2016–2018. Capture rates differed between sites, with 1.14 male and 0.6 female bats/night captured at the nature preserve, and 0.8 male and 0.2 female bats/night captured at the reforested mine. Model rankings varied between sites but differed only slightly between sexes. A model using diameter, difference between roost tree and canopy height, and tree species as explanatory variables was the top model of roost tree selection for both sexes at the nature preserve. At the previously mined site, where forest stands were typified by smaller, more numerous stems, the top model only used basal area of trees >25 cm in diameter as an explanatory variable. Female selection was not modeled at this site due to small sample size. These results show that habitat use in red bats is similar between males and females during the summer months, but local habitat conditions can drive differences in selection, even within a small geographic area. Further data collection is underway and additional analyses will be conducted.

Temporal and Diet Segregation in Bats Emerging from Santa Catalina Cavern, Matanzas, Cuba
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Santa Catalina Cavern is a 19 km long system which contains elaborate formations and supports approximately 3 million bats from 12 species. All these bats roost within a 2 km strip located in the warmest section of the cave. Given the cavern has just five exits, we examined whether different species showed a preference to which exit they used, and investigated how these species avoid 'traffic jams' at emergence. Survey work was completed monthly between 2014–2016, and involved placing harp traps for four hour sampling periods (with traps being emptied at 5 minute intervals) at two of the five exits; 'La Rampa' and 'Las Raíces'. At La Rampa a total of 80,722 bats from eight species were caught, with *Mormoops blainvillii*, *Phyllonycteris poeyi,* and *Pteronotus macleayi* being the predominant species here. At Las Raíces a total of 3,441 bats from 10 species were caught, with *Pteronotus macleayi* being the most common. At both exits different feeding guilds had clearly separated emergence periods (Insectivorous 17:00–18:00, Pollen and Frugivorous: 18:00–19:00, and Nectarivorous: 19:00–20:00). Our results indicate that, although emergence periods for different feeding guilds are similar at the two exits sampled, there are marked differences in overall bat 'traffic' between them, as well as well-defined exit preferences for different species. Understanding emergence patterns such as these have strong empirical applications for the conservation and maintenance of bat populations inhabiting extensive cave systems, for example allowing rangers to know which exits are particularly important to safeguard against human activity or prevent being overgrown by vegetation.

Home Range of Reproductive *Myotis sodalis* and *Myotis septentrionalis*: Comparison of Ground-based and Aerial Methods
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Studies designed to gather data on threatened and endangered species in the United States have recently focused on quantifying landscape use of existing populations, rather than the typical presence/absence approach. Landscape use data obtained via statistically verifiable methods inform and facilitate targeted management decisions. Accordingly, our objective was to quantify home ranges of adult female reproductive Indiana bats (MYSO) and northern long-eared bats (MYSE) at Camp Atterbury Joint Maneuver Training Center in Bartholomew County, Indiana, using both ground-based telemetry and aerial data collection methods. Five MYSE and 23 MYSO were radio-tagged, and both tracking methods were implemented. Bats tracked using either method, with ≥15 independent locations, were subject to individual analysis of home range (95% of locations) and core-foraging area (50% of locations) using a uniform density analysis with least square cross validation. Aerial methods resulted in a subset of 14 MYSO with ≥15 locations, with a mean home range of 1,249.6 ha (SE = 159.7 ha). Four MYSE, tracked aerially, had a mean

home range of 1,136.5 ha (SE = 356.7 ha). Ground-based methods resulted in a subset of four MYSO with a mean home range of 771.33 ha (SE = 258 ha). Two MYSE, tracked via ground-based methods, had a mean home range of 873.7 ha (SE = 364.69). Home ranges of MYSO tracked via ground-based methods are likely underestimated due to detection range capabilities of ground-based VHF equipment. Conversely, MYSE home ranges are likely overestimated using aerial methods. Field methods in home range studies may vary in effectiveness based on resources and subject species.

Activity Patterns of the Western Red Bat, *Lasiurus blossevillii,* in Northern California

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Lasiurus blossevillii is a tree-roosting bat found throughout the western United States. In California, the species is known to be present year-round in the Central Valley. However, the local seasonal migratory patterns in the state are not well understood. The aim of this study is to examine the activity patterns of *L. blossevillii* in Northern California. Using acoustic data, we acquired the activity patterns from three different habitat types: an agricultural area in the valley at 60 m asl, canyon and ridge oak woodland at 600 m, and a pine-juniper forest at 1554 m. Long-term acoustic monitoring equipment was placed at each site to record nightly echolocation calls of bats and the recordings were analyzed to identify species using SonoBat software. *Lasiurus blossevillii* had the highest levels of activity during the months of June and July across all three sites, with the higher elevation pine-juniper forest having the greatest activity. Both lower elevation sites retained low levels of activity throughout the winter suggesting temperatures warm enough for occasional foraging. The agricultural site in the valley showed a late-year increase in activity during October and November, possibly indicative of migratory activity.

Phylogenomic and Trait Evolution Analyses Explain the Radiation of the Most Speciose Genus of Bats, *Myotis*

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Convergent evolution, the independent development of the same trait in different taxa, is a common process in nature that raises questions regarding the processes driving repeated adaptations. Here we study from phylogenetic and biogeographic perspectives questions related with the parallel evolution of phenotypic traits, using as a model system the genus *Myotis,* the most numerous group of bats, found worldwide, in which three ecomorphs seem to have evolved repeatedly in several biogeographic regions. We analyzed genomic and morphological data of nearly 90% of all living *Myotis* taxa to estimate species relationships and divergence times and identify patterns of trait evolution potentially linked to geological and biogeographic events. Our results based on ultraconserved elements (UCEs) suggest changes in the currently known phylogenetic relationships of the New and Old World clades. Our results imply that the origin of this genus could have taken place at least 13–20 millions of years (My) earlier than previously suggested. Our divergence time estimates suggest an earlier presence and diversification of modern *Myotis* in Palearctic regions with early colonization events to the Americas and at least one re-colonization event from the New to the Old World. We also document the ecological lability of this group by analyzing an extensive dataset of skull characters and found similar features present in all clades. Taken together, our results document the phylogenetic and biogeographic basis of a striking example of adaptive convergence in one of the most successful groups of mammals.

High-throughput RNA Sequencing, *de Novo* Transcriptome Assembly, and Functional Annotation in Five Tropical Bat Species

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High-throughput RNA sequencing is a powerful tool that allows us to perform gene prediction and detection of novel transcripts. In this study we have generated whole transcriptomes from liver tissue in five species of tropical bats classified into five different families: *A. jamaicensis* (F. Phyllostomidae), *Mormoops megalophylla* (F. Mormoopidae), *Myotis keaysi* (F. Vespertilionidae), *Nyctinomops laticaudatus* (F. Molossidae) and *Peropteryx macrotis* (F. Emballonuridae). This is the first report of transcriptome assembly by RNA-seq in these species, except for *A. jamaicensis*. HiSeq 4000 multiplex sequencing generated a total of 403 million paired-end reads of 101 bp length, sequencing depth ranged between 30 to 69 million paired end reads of which 99% were used for de novo assembly. De novo assembly was performed with Trinity protocol, final non-redundant transcripts consisted of 685,849 for *A. jamaicensis*, 469,620 for *M. megalophylla*, 456,572 for *M. keaysi,* 617,036 for *N. laticaudatus* and 634,439 for *P. macrotis*. We were able to recover between 65 and 75% of vertebrates single copy orthologues, suggesting that the assembled transcriptomes have a good level of completeness. Detection of putative orthologues and orthology grouping of proteins assigned 226,373 genes to 20,467 orthogroups, only 78 genes classified in 17 inferred orthogroups were species-specific, whilst 36.4% were shared among the five species. In this qualitative study we ensured by several bioinformatic analyses that the new generated transcriptomes are of good quality and sufficient completeness. In this sense, we are looking forward to contribute with the generation of genomic database in bats, as we consider that transcriptomic data will be of interest for future research in the evolutionary biology of these flying mammals.

A Small-scale Response of Urban Bat Activity to Tree Cover

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Bats in urban areas depend on trees, and bat activity increases with tree cover. To effectively manage bat habitat in cities, it is important to know the distance to which tree cover most strongly influences bats (i.e., the 'scale of effect'). The aim of this study was to estimate the scale of effect of tree cover on bats in Toronto, Canada. To achieve this, we measured bat activity at 52 sampling sites across the city. We then examined the relationships between bat activity and percent tree cover measured within each of 19 landscape scales, 0.025 to 3.5 km in radius, surrounding each sampling site. We found that the scale of effect of percent tree cover on total bat and individual species activity ranged from 0.025 to 0.2 km among species. Our results suggest that adding or removing urban trees influences bats up to 200 m away. Urban tree management decisions should consider the impacts to bats beyond the site of management and within the surrounding landscape of a 200 m-radius scale.

Management of Surviving Bats, People, and White-nose Syndrome at the Caves of the Rockwood Conservation Area

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Bats have been affected by white-nose syndrome (WNS) in North America since 2006, which was identified in hibernacula in Ontario in 2009. Although there has been precipitous decline of some species of bats, many still persist in low numbers at hibernacula. The natural caves of the Rockwood Conservation Area are frequently impacted by human activities at all times of the year and yet at least four species of bats still swarm and hibernate within them. These include the big brown bat (*Eptesicus fuscus*), little brown myotis (*Myotis septentrionalis*), eastern small-footed myotis (*Myotis leibii*) and tri-colored bat (*Perimyotis subflavus*). Internal survey, acoustic monitoring, swarming season capture, and radio-tracking have been conducted at the caves to better understand how and when they are used. Swarming bats have also been swabbed for the presence of WNS. No bat protection, public education, or decontamination is currently conducted at the caves, but a multi-agency meeting will be held to

coordinate what measures (i.e. gates, signage, public education, decontamination material) can be taken to improve the management of this habitat for bats.

Stress-induced Changes in Body Temperature of *Lasionycteris noctivagans*

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Acute stressors such as capture and handling can elicit physiological responses in endothermic animals. One example is an increase in body temperature (T_b) commonly referred to as stress-induced hyperthermia (SIH). For species that employ torpor, an inactive state characterized by reduced T_b and metabolic rate, a rapid increase in T_b could be advantageous, especially in the context of escape from predators. We quantified SIH in silver-haired bats (*Lasionycteris noctivagans*) because they readily enter torpor and roost in exposed places where they could be vulnerable to predators. We tested the hypothesis that handling stress causes SIH in three contexts: a) during the nocturnal, active phase, b) during the inactive, normothermic phase, and c) during pronounced torpor. We used a standardized protocol in which T_b was measured immediately upon handling, and again, after several minutes. We found that SIH occurred for inactive, normothermic bats. Surprisingly, stress caused a reduction in T_b for bats following the active phase and, although in the opposite direction, this rate was indistinguishable from that of normothermic bats. As expected, we observed a large increase in T_b during rewarming from torpor following handling. This warming rate was greater than previously reported for any torpor-using endotherm and could reflect a tendency for silver-haired bats to roost in exposed locations that may be vulnerable to predators. This study provides new information on SIH and illustrates the need to evaluate the hypothesis that SIH and rewarming from torpor are influenced by predation risk and activity state.

Morphological Diversification under High Integration in a Hyperdiverse Mammal Clade

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The demands of flight select for small body size in flying animals, including bats. Sensory systems therefore occupy finite cranial space and thus there are potential trade-offs in size among sensory structures that might evolve in highly integrated fashion within the skull. At the same time, low integration has been linked to increased morphological diversity and speciation rates. Phyllostomid bats occupy the widest range of dietary niches among mammals. If bat skulls are highly integrated, then why are phyllostomids so morphologically diverse? We assessed disparity in the shapes of skulls and integration between the facial skeleton and cranium, and how these parameters may have facilitated dietary diversity and increased speciation within phyllostomids relative to their outgroups, which both have fewer species and are all insectivorous. We analyzed 3D images of micro-CT scanned skulls from 141 bats across 65 species from the families Phyllostomidae, Noctilionidae, Mormoopidae, Mystacinidae, Furipteridae, and Thyropteridae. Phyllostomid skulls were more integrated and less disparate in shape when compared to all outgroups combined. Shape diversity followed the diet-predicted adaptive peaks confirming the well-established link between diet and the diversification of phyllostomids. The changes in skull shape and feeding style within phyllostomids are driven by relatively simple changes in the length and width of the rostrum. The tight link between rostrum shape and diet allows their highly integrated skulls to exhibit such functional diversity. This finding provides one of the best empirical examples of how even highly integrated structures can allow unique morphologies and spur adaptive radiations.

Identifying Immune Response to White-nose Syndrome in a Resistant Bat Species (*Eptesicus fuscus*)
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Since its arrival in 2006, white-nose syndrome (WNS) has had a devastating impact on bat populations in North America. Bats affected by WNS appear to die of starvation, possibly due to the increased metabolic costs, and fat reserve depletion due to immune system activation. During hibernation, mammalian immune systems are generally suppressed; however, once they are exposed to the responsible agent of WNS, *Psuedogymnoascus destructans* (*Pd*), the immune system seemingly produces a partial response. Nonetheless, not all bat species are susceptible to this syndrome. Big brown bats (*Eptesicus fuscus*) have experienced relatively little mortality since the WNS debut, raising the question of how/if their immune system combats this pathogen. To investigate whether infected bats change their use of energy (fat), bats were inoculated with *Pd* and meloxicam (an immune suppressant). Metabolic rates (MR) were measured as O_2 consumption during torpor, and arousals were monitored via temperature-dependent dataloggers. It has been shown that a greater change in mass corresponds to an increased level of arousals and arousal duration during hibernation. Survival rates between treatment groups were also significant. Photos of wing damage were taken via UV, showing extensive deterioration among inoculated individuals. Immune responses were measured by cytokine levels from blood and wing tissue from each bat before, during, and after hibernation using RT-qPCR. Assays for this aspect are currently being designed. With this knowledge, we hope to better understand how *Pd* affects this species of bat and compare the evidence to susceptible species as this disease continues to spread westward.

Susceptibility of Tri-colored Bats Using Alternate Winter Roosts to White-nose Syndrome
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The causative fungal agent of white-nose syndrome (WNS), *Pseudogymnoascus destructans,* can grow at temperatures as low as 2°C and as high as 19.5°C, with maximum growth rates occurring between 12.5°C and 15.8°C. Therefore, to assess a bat populations' susceptibility to WNS, an understanding of winter torpor patterns and roost conditions are needed. Tri-colored bats (*Perimyotis subflavus*) use alternate roosts (e.g., tree cavities, bridges, foliage) during winter in parts of their range, but information regarding torpor patterns and the environmental conditions of these roosts is lacking. From November 2017 to March 2018, we measured skin temperature (Tsk) of tri-colored bats at the Savannah River Site in south-central South Carolina, an area devoid of caves or mines, using temperature-sensitive radio-transmitters. We also measured ambient temperature (Ta) and roost temperature (Tr). In addition to three bridge roosts, we tracked individuals to 18 tree roosts (14 cavity roosts, 4 foliage roosts). Mean Tr was amenable to WNS growth in both bridge (13.1°C) and cavity (11.2°C) roosts although Tr was >19.5°C on numerous occasions. Bats were susceptible to WNS (Tsk <19.5°C) 61%–95% of their total transmittered time. Torpor bout duration varied considerably with a minimum of 21.1 hours to a maximum of 9.6 days. Torpor depth increased as minimum Ta decreased, and foliage roosting bats displayed significantly greater torpor heterothermy than cavity or bridge roosting bats (P <0.001). Preliminary results indicate tri-colored bats utilizing alternate winter roosts experience varying degrees of WNS susceptibility dependent upon roost structure and ambient temperature.

Climate Change and the Impact of Hurricanes on the Survival of Bats on Small Islands
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Climate change has been identified as one of the major challenges for the survival of bats. Few studies address the issue in the Neotropics where tropical hurricanes typically move westward towards the West Indies. An expected outcome of climate change is an increase in hurricanes' strength. This increase in the intensity of tropical cyclones has taken its toll on bat survival. The island of Puerto Rico has received the impact of two catastrophic hurricanes within the last 19 years. The impact of category 3 hurricane Georges in 1998, which resulted in the widespread mortality of phytophagous bats, and the category 4 hurricane Maria in 2017. We performed post-María monitoring at four localities where bats had been studied before the hurricane, including one location studied before and after hurricane Georges. The results revealed high mortality and reduced body mass of phytophagous species. Some

differences are observed with respect to mortality rates after hurricane Georges in terms of the species affected. After Georges, the phyllostomids *Monophyllus redmani* and *Erophylla bombifrons* represented, respectively, 38% and 60% of the fatalities. After Maria, *M. redmani* represented 40%, *E. bombifrons* 6% and *Brachyphylla cavernarum* 53% of the fatalities. Furthermore, hurricane Maria caused floods in some localities resulting in the unusual mortality of the insect-eating species. Bats have slow recovery rates when subjected to hurricanes. The reduction in population size and body mass reported here, have important implications for the survival of species on small islands, especially if the frequency and strength of hurricanes increases.

Fecal Glucocorticoid Metabolite Assays: A Tool for Little Brown *Myotis* Conservation in a White-nose Syndrome World

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The little brown bat, *Myotis lucifugus* (MYLU), is facing regional extinctions from white-nose syndrome (WNS), a deadly fungal infection of cave-dwelling bats. Disease as a stressor can lead to chronically elevated stress hormone (glucocorticoid) levels that in turn may suppress the immune system and negatively affect fertility, metabolism, body condition, and ultimately fitness. Among threatened populations, tracking glucocorticoid levels to identify and mitigate negative stressors may be valuable for conservation. Typically, transient blood glucocorticoid concentrations are assessed via invasive blood sampling. Conversely, fecal glucocorticoid metabolite (FGM) assays are available to provide information on an animal's hormonal status over several hours without the need for invasive procedures. Here, I explain the theory and methodology behind my project to validate FGM analyses for use in MYLU by completing a standard hormonal challenge (ACTH challenge). Data collected on ectoparasites, neutrophil-to-lymphocyte ratios, and other standard measures will also be analyzed for covariance with the FGM assay. The implications of these data for MYLU conservation will also be discussed as the ultimate goal of this research is to provide new tools to protect this vulnerable species. MYLU that survive WNS form the core of recovering populations and must be protected. Since handling of these bats is restricted, validated FGM assays may be valuable for using baseline stress as a proxy for overall health of a given population and for developing effective conservation plans.

Look Before You Leap: Focus Groups Significantly Improve Instruments for Understanding Bat-human Interactions in Southern Nigeria

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To understand the complex human dimensions of bat conservation, social ecologists are faced with the challenge of what and how to ask questions, often developing questionnaires based on observations, preliminary interviews, and existing instruments. This approach though employed in broad socio-ecological contexts, provide limited exploratory value for developing effective survey instruments on complex bat-human interactions issues in areas with intense bat hunting. Focus groups – a diverse group of people gathered to participate in a semi-structured discussion about a topic, is heavily employed as exploratory tools in developing sociological instruments. However, it remains unclear how effective they are in complex socio-ecological settings like bat hunting. Here, we evaluate the effectiveness of focus groups in developing appropriate instruments to understand bat-human interactions in southern Nigeria. We conducted surveys using questionnaires based on literature, observations, and interviews in three localities in southern Nigeria in 2016. A series of exploratory focus group discussions were conducted in the same localities in 2017. More respondent options provide higher resolution data. Therefore, we compared options on questionnaires items developed based on literature, interviews and observations with exploratory focus group-generated options. A t-test showed that focus group-based options of bat perceptions and values significantly improved respondent options. Markedly, although all analyzed questionnaire items had open ended options, there was no similarity between focus group major themes used in improving respondent options and previous questionnaire open-ended-responses. These results underscore the importance of local community-specific exploratory focus group discussions as a critical tool in bat conservation efforts.

Stable Isotope Analysis Reveals Community Structure of a Diverse Neotropical Bat Fauna in Northern Belize
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Using the stable isotope ratios of Carbon ($\delta^{13}C$) and Nitrogen ($\delta^{15}N$) to infer trophic niche breadth, we describe the community structure of a diverse Neotropical bat fauna. Overlapping niches in isotope space infers a shared dietary resource, which may be partitioned spatially, temporally, or are subject to competition. While many of these animals are grouped into broad trophic guilds (*sic* frugivore, insectivore), the details of their diets and the degree to which they overlap with other species remains largely unknown. The purpose of this study is to characterize community structure of a tropical bat community to make inference on the predictions of niche theory and the competitive exclusion principle. We predicted, (1) the diet of bat populations would have more overlap between species within a guild than species within different guilds, (2) no two populations' niches would overlap completely, and (3) larger animals should have a larger niche breadth. Inferring niche breadth using stable isotope analysis, we found that while these guilds are informative, there are several species with niches that overlap with members of other guilds, and many species within guilds which do not overlap with one another. There were also several species which overlapped significantly (<95%) with one another and may compete for resources. Understanding the trophic community structure of animal communities is fundamental to conservation and management of endangered species and ecosystems, evolutionary studies, as well as providing insight into the diet of species which are not well known to science.

Frugivorous Bats in Brazil's Atlantic Forest: Effects of Habitat Fragmentation on Diet
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Brazil's Atlantic Forest has a long history of anthropogenic disturbance and is one of the most highly fragmented landscapes on Earth. These patches of remnant forest are uneven in size and exist in different states of succession and composition; the effects of habitat fragmentation on animal abundance, biology, and species composition are wide ranging. Using stable isotope analysis of Carbon ($\delta^{13}C$) and Nitrogen ($\delta^{15}N$), we hope to elucidate the relationship between habitat fragmentation and dietary niche breadth for three commonly captured species of Neotropical frugivorous bats; *Carollia perspicillata, Artibeus lituratus,* and *Sturnira lilium*. What is known about these species diet is that they are all to some degree omnivorous, with insects found in fecal and stomach content analysis studies. Understanding the relationships between trophic and landscape metrics, we can determine if there are differences in the diet of bat populations captured in habitat fragments of various sizes and composition as compared to those captured in contiguous forest.

Bats and Viruses in Western Asia: A Model for One Health Surveillance Using Research Networks
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Bats are critical components of ecosystems and natural reservoir hosts to zoonotic viruses, e.g. henipaviruses, filoviruses, and SARS-related coronaviruses. However, research on the distribution of bats, diversity of bat-associated viruses, and potential for zoonotic disease emergence is limited. We launched a new collaborative One Health project to leverage regional expertise to fill this gap for Western Asia. Our primary aim is to identify ecological, life-history, and environmental drivers of bat-associated viral diversity across the region. Over the next 5 years, we will collect >20,000 non-lethal samples from bats to screen and characterize coronavirus diversity at regional laboratories. Additionally, we will identify correlates of increased disease risk by combining viral data with host, geographic, and environmental data. Our second aim is to create the Western Asia Bat Research Network (WAB-Net), a regional initiative to bring together bat ecologists and public health representatives from >12 countries to foster scientific collaboration and strengthen regional capacity for zoonotic disease research. The WAB-Net will host annual workshops, in-service training opportunities, and One Health research exchanges to provide field-to-lab training in disease surveillance. Since project inception (Oct 2017), we have identified key personnel in

high-engagement countries (Georgia, Jordan, Turkey, and Pakistan); established standardized protocols for biosafety practices and non-lethal bat sampling; identified field sites; collected viral samples in Turkey and Georgia; and hosted the first annual WAB-Net meeting in Georgia. Our model is both cost-effective and sustainable because it leverages existing, regional expertise in wildlife research and laboratory diagnostics for One Health surveillance.

Building Better Genomes

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Third generation sequencing tools have enabled economical and swift non-model organism genome sequencing. Yet with about a thousand species of bats worldwide, just over a dozen have any meaningful genome assembled - none with chromosome-scale contiguity. We paired a trio of sequencing technologies to produce highly contiguous genomes for two *Mytois* speices impacted by white-nose syndrome, *M. lucifugus* and *M. septentrionalis*. The current pipeline can be completed in a few months for under $8,000 per bat. We highlight a few of the advantages and insights that high quality genomes offer: detailed comparative genomics to highlight species-specific profiles and refined population genetic assessments using extended haplotype homozygosity metrics.

Reconstructing the Genomic Diversity of a Widespread Sub-Saharan Bat Using Archival Museum Collections

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Modern phylogeographic methods have confirmed that species with broad ranges often exhibit fine-scale patterns of genetic variation that are not reflected in their morphology. Recent genetic analyses of the Straw-colored fruit bat (*Eidolon helvum*) deviate from this trend in identifying this species as broadly panmictic. However, the limitations of sampling, along with potential for modern anthropogenic impacts to distort observed patterns suggest that additional work is needed to assess true historical patterns of geographic variation in this species. We used Next Generation Sequencing methods to assess patterns of variation found in historical collections of *E. helvum* and *E. dupreanum* from the American Museum of Natural History. Specimens collected between 1909 and 1983 were compared with published sequence data from more recently collected tissue samples. We identified lineage-specific patterns of temporal and spatial genomic diversity and identified potential barriers to gene flow present across the species' range. Studies utilizing such "archival" DNA from specimens in museum collections have the potential to illuminate patterns of both past and contemporary biodiversity, and to help assess the impacts of habitat loss and climate change on species at the genomic level.

The Ecology and Evolution of Information Acquisition by Predatory Bats

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In the evolutionary chase between predators and their prey, prey often evolve to be as cryptic as they can, while in turn predators hone their sensory strategies to detect prey. Examinations of the sensory strategies implemented by predators to detect their prey, as well as the ecological consequences of these interactions, are at the crux of understanding and predicting predator-prey dynamics. Using bats as a study system, we review the sensory strategies used by predators that attend directly to cues and signals generated by their prey, and those that attend to the signals and behaviors of other predators. We discuss the costs and benefits of using private versus public information, and the association of different predatory strategies with particular features of predator sensory systems. We place bat information-gathering strategies in a phylogenetic framework, and reveal that attending to prey-emitted cues and eavesdropping on prey communication signals are strategies that have evolved independently multiple times in roughly a third of bat families. This pattern suggests that some lineages have traits that make them more likely to evolve such hunting strategies. Elucidating the tradeoffs and evolutionary origins of relying on diverse sources of information to detect prey is necessary to advance our understanding of the sensory ecology of predator-prey interactions. Here we provide an overview of the sensory ecology of hunting in bats and, by identifying current gaps in knowledge, highlight fruitful directions for future research.

Drivers of Bat Occupancy on the Gulf Coast of Texas
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The Texas gulf coast boasts a diverse array of habitat types, but many native habitats on which wildlife are dependent are fragmented and shrinking from human development and climate change. Over the next century, sea levels are predicted to rise 0.6–1.2 m, coinciding with increased precipitation of 10–15% and more extreme weather activity on the gulf coast. Few studies have researched bats in this region and none have examined the drivers of occupancy for high frequency (>35 kHz; HiF) and low frequency (<35 kHz; LowF) bats. San Bernard National Wildlife Refuge (SBNWR) lies on the Texas gulf coast and is dominated by saline prairie, upland prairie, and bottomland hardwood forest. The objective of this study was to identify drivers that influence the occupancy of HiF and LowF bats on the SBNWR. We monitored bats using Pettersson D500x acoustic devices from May to August 2018. We surveyed 18 upland prairie, 21 saline prairie, and 26 bottomland forest sites and collected 514,241 call files. The drivers we examined were salinity, insect abundance and diversity, forest stand size, and vegetation structure. We sampled invertebrates using Townes-style malaise traps, collecting over 10,000 insects with the most abundant orders being Lepidoptera, Hemiptera, and Diptera. We predicted that occupancy would be greatest in bottomland hardwood forest and lowest in saline prairie habitat, with increased salinity levels and low insect diversity being the most influential drivers negatively impacting bat presence. We will continue to monitor bat occupancy on the SBNWR during summer 2019.

Vocalizations of *Molossus rufus* at Emergence in Different Social and Environmental Contexts
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Urban landscapes impose additional challenges to microbats, which strongly rely on vocalizations for orientation, food detection, and communication. To improve their perceptual abilities, bats can adjust vocalizations depending on the task to be performed and the environment. In this work, we determine whether individuals of *Molossus rufus* adjust the attributes of their vocalizations in relation to the social context and some environmental variables which reflect the challenges of the urban environment. We selected 16 roosts in the city of Villahermosa, Tabasco, Mexico, which represent a wide range of environmental conditions. We recorded vocalizations of bats at dusk emergence 10-m away from the roost entrance on three non-consecutive days. We simultaneously counted the number of individuals leaving the roost and recorded air temperature, relative humidity, noise level, light intensity, and number of mobile objects (vehicles and persons) in the roost proximity. We obtained 25 hours of recordings, in which we identified 10,700 call sequences: 6,800 social call sequences and 3,900 echolocation passes (4–5 pulses per pass). We identified 15 types of social vocalizations and 5 types of echolocation vocalizations based on its form in the spectrogram. In general, pulses from sites with more obstacles were dominated by FM components and exhibited shorter interpulse interval and greater amplitude. Higher frequencies allow *M. rufus* to exploit relatively cluttered sites, while lower frequencies allow them to detect objects from longer distances in open spaces. The ability of *M. rufus* to adjust its vocalizations could be a key to understanding its high tolerance to urbanization.

Ono Grinds: Using Genomic Metabarcoding to Explore Hawaiian Hoary Bat Diet
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The Hawaiian hoary bat (*Lasiurus cinereus semotus*), an endangered, endemic island bat, is widely distributed across the main Hawaiian archipelago, yet its ecological needs remain poorly understood. Island populations face many threats including fatal collisions with wind turbines, and proposed mitigation for species recovery aims to build foraging habitat for bats with an emphasis on native plant species. Previous research has focused on distribution using acoustic surveys, home range using radio telemetry, and prey availability using insect trapping. Past attempts at identifying dietary items of this insectivorous bat are limited in scope and breath, examining prey items by observation of physical parts in guano often overlooks soft-bodied prey items. Here we employ a genomic technique to investigate the prey composition and diversity in the Hawaiian hoary bat. A total of 72 fecal pellets

were collected from 27 individuals across 3 islands (Hawaii, Oahu, and Maui). Guano was collected during mist netting and opportunistically under daytime tree roosts. We used an Illumina platform to sequence two different barcode regions of insect DNA from fecal pellets and prey taxonomic units were detected through matching with DNA in public databases. Data were evaluated for dietary composition and diversity, and relationship of sex, island, and season to prey types. We also inspected data for insects known to be native to Hawaii and those which have been introduced. Comprehensive dietary analyses using genomics assists in describing trophic connections between bats and insect prey, and thus benefits functional habitat restoration for this species.

Assessing the Genetic Variability of the Mexican Long-nosed Bat Using Microsatellite Markers

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The Mexican long-nosed bat (*Leptonycteris nivalis*) is an endangered migratory nectarivore that has been suspected of experiencing population declines. It is important to assess the genetic variability of species of conservation concern, because those with lower levels of genetic diversity tend to have decreased adaptive potential. We selected 24 microsatellite markers designed for the lesser long-nosed bat (*L. yerbabuenae*) to test their effectiveness in *L. nivalis*. Ten loci have successfully amplified DNA from individuals of *L. nivalis*, captured at both the northernmost and southernmost extent of the range. Of those ten, six have been genotyped in 111 individuals from both roost sites. Two loci were almost entirely monomorphic and each had a homozygote excess. One locus showed null allele frequencies of 0.1523 and 0.2199 in the northern and southern populations, respectively. Three loci were determined to deviate from Hardy-Weinberg Equilibrium after a sequential Bonferroni correction. No genotypic linkage disequilibrium was detected between any of the loci. Observed heterozygosity ranged from 0.017 to 0.886 across the six different loci. Preliminary analyses using these loci suggest low population differentiation (Fst = 0.008) and a lack of genetic structure, which is supported by previous genetics studies on *L. nivalis*. The contemporary effective population size was estimated from microsatellite linkage disequilibrium to be 3861, with a 95% confidence interval ranging from 264 to infinity. The inclusion of infinity suggests the results from these six markers designed for *L. yerbabuenae* may be unreliable and additional loci should be screened for further analysis.

Body Size and Call Frequency as Predictors of Bat Activity in Harvested Forests

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As the list of endangered bat species grows longer, it becomes apparent that conservationists need to consider the varying effects of habitat management practices on multiple species. For example, selective tree harvest is a management practice that should affect clutter-specialized bats differently than bats that hunt in open areas. Generally, smaller-bodied, higher-call frequency bats tend to forage in more cluttered areas, and therefore may be negatively affected by selective harvest. We conducted a two-year study of the effects of selective harvest on nightly bat activity. The purpose of our study was to determine whether body size or call frequency predicted habitat use for six species: *Eptesicus fuscus*, *Lasionycteris noctivagans*, *Lasiurus borealis*, *Lasiurus cinereus*, *Myotis leibii*, *Myotis septentrionalis*. We conducted the study immediately following selective harvest in spring 2017, then repeated the study in 2018 to determine whether effects persist across years. We used acoustic sampling to compare bat activity in selectively harvested forest plots to adjacent unthinned plots. We recorded for three nights each year at each location and analyzed calls with Sonobat. We included the following predictors in our generalized linear models of bat activity: harvested vs. unthinned, study year, stand basal area, stem count, and distance to water. We used Akaike Information Criterion to select the best model to explain bat activity for each species. Our models indicate that both body size and call frequency usually predict the effects of selective harvest, with the exception of *M. leibii*.

Roost Ecology of *Leptonycteris yerbabuenae* (Phyllostomidae) in El Colorado Bay, Sonora

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The lesser long nosed bat *Leptonycteris yerbabuenae* is a migratory species specialized in the consumption of nectar, pollen and fruits of columnar cactus, agaves, and ceibas. Bats migrate from central Mexico to the Sonoran

Desert. Along the migratory route, these populations congregate and form transient roosts that they use for short periods of time, before arriving at the maternity roosts. Because of the lack of information about *L. yerbabuenae* through the migratory route and because of the importance of roosts during their maternity period, this work describes the use of a roost used by a *L. yerbabuenae* population, in Bahia El Colorado, Sonora. We visited the roost from March to October in 2015 where we took topographic measures to create two maps of the insides of the roost. We put temperature sensors to describe the internal microclimate of the roost, also we estimated the population size of *L. yerbabuenae* and we analyzed the diet of this population, by identifying and counting of seed and pollen grains from their guano. This roost has an extension of 72 meters, and a medium temperature of 29.6 and 27.9 ºC. The biggest number of individuals (1000) was registered in April. This population feeds on organ pipe (*Stenocereus thurberi*) and its nectarivorous diet consists of 86% of pollen from columnar cacti and 7% of pollen from agaves. This is a roost that pregnant *L. yerbabuenae* individuals used on their migratory route before arriving at their maternity roost.

Heavy Metal Concentrations in *Tadarida brasiliensis* from Zones with Different Conditions of Human Intervention, Central Mexico

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Metal pollution has notably increased in the atmosphere, and little is known about its accumulation in bat tissue. Thus, it is important to carry out comparisons of the exposure of bat populations according to different conditions of human intervention. We aimed at determining concentration of vanadium, copper, zinc, cadmium, and lead, in liver tissues of insectivorous bats from two parts of Mexico City, at North and South, and two rural landscapes, called Tequixquiac and Tlalcozotitlán. We hypothesized that there is a pollution gradient, with higher metal concentrations in urban bats than rural ones. We collected 70 bats and their liver samples were analyzed for total content of metals by a Inductively Coupled Plasma-Mass Spectrometry technique. Metal concentrations ranged for vanadium: ≤0.73 ppm; copper: 10.8–41.5 ppm; zinc: 41.6–168.5 ppm; cadmium: 0.08–1.63 ppm; and lead: 0.02–2 ppm. Urban bats had high copper and zinc concentrations, which were associated with motor vehicle traffic. All metal levels on urban bats were similar, indicating that they were exposed to similar metal levels within the city. Tequixquiac's bats had the highest vanadium concentrations, which could be associated to fossil fuel combustion probably from the emissions of Tula industry complex. Tlalcozotitlán's bats had higher cadmium levels, which could come from fertilizers used in agricultural areas. Lead concentrations were similar for all bat populations. Lead was banned decades ago but this finding could be related to this metal still being widely distributed in the environment. Each bat population is affected by different sources, suggesting there's not a single pollution gradient or source.

Multispecies Occupancy to Assess Foraging Habitat of Bats Across Marin County Open Spaces

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Bat species distributions are affected by landscape level and microhabitat features that operate on many scales. Understanding habitat characteristics that drive species richness of bats or restrict habitat suitability for certain species may provide for opportunities to improve habitat management for bats. We conducted a multi-species occupancy study across lands managed by four open-space agencies in Marin County, CA, where 13 bat species potentially occur. During the summer and fall of 2017, we placed acoustic detectors (Pettersson D500x) at 50 randomly selected points across the study area, for at least 7 nights per location, to examine bat occupancy in relation to landscape-level and microhabitat covariates. We recorded all 13 species, with some widespread across all sites and habitat types (e.g., *Myotis californicus* and *Tadarida brasiliensis*) and others very restricted (e.g., *M. evotis*). Detection probabilities and occupancy varied by both species-specific characteristics (e.g., call intensity and frequency) and habitat covariates (e.g., vegetative clutter and broad habitat type). Understanding the distributions of bat species in relation to habitat features can inform habitat management actions to support individual species,

guilds, or overall species richness across the region, and multi-species occupancy analysis provides a powerful tool to examine the relationship between habitat covariates and bat distributions using acoustic monitoring.

The Role of Nectarivorous Bats in the Pollination of *Agave tequilana* in Three Municipalities of Jalisco
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Agaves are very important in arid and semiarid regions because they produce plentiful resources during its flowering, attracting lots of visitors like insects, birds, and bats that feed on their nectar and pollen. *Agave tequilana*, the species used to produce tequila, faces problems because it is propagated only by clonal shoots causing loss of genetic diversity, which in turn makes it vulnerable to diseases. Tequila-producing *Agave tequilana* fields were visited in the municipalities of Tototlan, Arenal, and Arandas in the state of Jalisco. In each field two 6-meter-long mist nets were placed for 5 nights around two inflorescences from 20:00 to 6:00 to capture and identify floral visitors. Also, in each field ten different inflorescences were filmed for 24 hours. Pollen samples were taken from the feces and bats' fur to identify the plant species from which they feed. We performed an interaction network analysis. From the videos, the number of bats visiting per hour was obtained, and Kruskal-Wallis tests were carried out. The activity patterns were also analyzed and compared between the 3 fields. Arenal field had the greatest richness of bat species and the greatest abundance. In the three fields more than 90% of the visits were of insects. However, the visits of bats coincided with the production of nectar and pollen. The activity patterns were significantly different in the 3 fields. We confirm that there is a close relationship between nectarivorous bats and *Agave tequilana*, bats feed on their nectar and pollinate it at the same time.

A New Species of Fossil Bat of the Genus *Icaronycteris* from the Green River Formation (Eocene)
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Although many well-preserved specimens of fossil bats have been collected from the early Eocene of the Green River Formation of Wyoming over the past 70 years, only two nominal bat species have been described from this horizon: *Icaronycteris index* (Jepsen, 1966) and *Onychonycteris finneyi* (Simmons et al., 2008). A new fossil species of the genus *Icaronycteris* shows a higher bat diversity during the early Eocene than previously presumed. This new species, recently recovered from the Sandwich Beds of the South Dempsey Quarry in southwest Wyoming, stands out by its smaller size, but also differs from other Eocene bat species in an array of anatomical details. Wing anatomy shows this new bat was capable of powered flight, but wing shape and limb proportions indicate a more fluttering flight style than displayed by *I. index*. The phylogenetic relationship of this new bat is estimated based on phylogenetic analyses with an inclusion of fossil taxa, based on 699 characters. Comparative analyses of linked evolutionary and functional characters of this new bat support the hypothesis of a rapid radiation of bats during the early Eocene.

What do Restored Patches Offer to Bats?
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Ecological restoration aims to accelerate the process of natural succession. Restoration plantings represent maximum restoration intervention whereas exclusion of disturbance is considered minimal restoration intervention. The general objective of this work is to evaluate the effect of the level of intervention on the availability of food or refuge for bats. The experiment was established in 2006 in Los Tuxtlas, Veracruz, Mexico in 24 30 X 30 m plots: eight plots were planted with animal dispersed tree species, eight plots were planted with wind dispersed species and the remaining eight plots were excluded from the disturbance. The availability of food for bats was measured in 18 plots only. To sample bats, two mist nets of 12 m were set in the 18 plots during 2 nights per plot in the periods when trees are producing flowers of fruits. Results revealed that all levels of intervention have a similar composition of trees, which offer food for bats. After a first year of sampling, with a capture effort of 16,800 m/h/net, 290

individuals of 16 bat species were captured. The planting of animal dispersed trees has the highest number of bat captures (154 bats) whereas the lowest abundance was recorded at the minimum intervention (60 bats). Therefore, it seems that the maximum intervention level is attracting more bats by offering not only food but also refuge.

Bats in the City: An Environmental Education Project

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Environmental education is an essential multidisciplinary component in conservation efforts, especially for taxa facing negative human perceptions such as bats. In the industrial city of Monterrey, Mexico the bats are usually forgotten. Mexico lacks environmental education and citizen science programs, especially in big cities like Monterrey, to raise awareness on the importance of biodiversity. To increase awareness and sensitize the human population on the importance of bats and their ecological services, we created the project "Bats in the City". We installed 10 bat houses and gave conferences to governmental institutions, elementary and high schools, and visitors of protected areas. Two bat houses have been permanently dwelled and three temporarily. We also organized a "Bat Night" at the Ecological Park La Huasteca, where, with a thermal camera and bat detectors, people were taught about bats. Interviews, videos, and talks on the radio are constantly broadcast in media throughout the state. In order to bout the gap in environmental knowledge is important to begin with kids. We applied 3 semi-structured questionnaires to 30 kids between 6–12 years old, before and after our intervention to assess the impact of our activities on their bat´s perception. A qualitative data analysis in ATLAS.TI 7.5 showed that awareness was increased in 85%. The activities have reached a total of 200 people directly. Our efforts like the first bat environmental group in the northeast of Mexico will continue installing bat houses, communicating and teaching the importance of bats, and make alliances with decision makers.

Identification and Description of Echolocation Calls of the Mexican Long-nosed Bat

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The high demand and uncontrolled use of agave plants, as a raw material for the preparation of beverages such as tequila and mescal, are one of the main causes of the decline in the population of the Mexican long-nosed bat (*Leptonycteris nivalis,* Phyllostomidae). However, information on the biology, distribution, abundance, and habitat of this species is limited. Passive acoustic sensing has emerged as a powerful tool for quantifying anthropogenic impacts on biodiversity, especially for echolocating bat species (Aodha et al., 2018). The aim of this study is to identify and describe the echolocation calls of the species *L. nivalis* to provide a method of passive monitoring for the species without the need to interfere with its normal foraging and roosting activities. We recorded echolocation calls from individuals of *L. nivalis* in the northeastern region of Mexico. The recordings were made using three main methods, release calls, wild calls (search flight during the foraging period), and calls inside the tunnel (during search flight inside a 20m × 1m x 1.5m tunnel). Based on the following echolocation parameters: frequency of the start of the call (StartF), frequency of the end of the call (EndF), duration of the call (Dur), and total frequency spread of the call (BWdth), we identify and describe the calls of echolocation for the species and we observe the differences between the three acoustic monitoring methods used. This study will aid in developing a passive acoustic monitoring method that will increase the ability to identify key conservation sites.

Spring Migration of *Myotis sodalis* Tracked via Aerial Telemetry

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Migration behavior is poorly understood in the life history of many bat species. The US federally endangered Indiana bat (*Myotis sodalis*) hibernates in winter and travels after spring emergence to summer maternity sites, but information on migration behavior in this species remains limited. We tracked individual migrating female Indiana bats using aerial telemetry resulting in the location of 17 previously unknown maternity colonies and identifying connections among 8 hibernacula and 20 maternity colonies across 8 different states. Maternity colonies were

164.6 ± 26.2 (± SE) km from hibernacula and bats were on the landscape for an average of 7.3 ± 1.4 calendar nights. Nightly migration rate was 9.9 ± 0.8 km/hour and bats were active on the landscape for an average of 6.1 ± 0.4 hours/night. Ambient air temperature at night influenced bat activity where 87% of temperature data points were of inactive bats when air temperature was <9.8°C. Data points on active bats during temperatures <9.8°C represented a normothermic state within a roost. Although there was no difference in tree size (i.e., diameter at breast height) during staging, migration, or arrival at the maternity grounds ($F_{4,129} = 0.6301$, $P = 0.6419$; overall mean = 44.3 ± 1.2 cm), 61% of staging trees were live, and arrival trees were either snags (77%) or live-damaged (10%). The migration landscape was largely forested, but in agricultural areas, bats preferred forested corridors. Understanding bat behavior during migration helps fill a life history gap for the species, as well as provides information for land managers to better conserve travel, foraging, and roosting habitat.

Bat Ectoparasite Richness at El Infierno Cave, Santiago, Nuevo León, Mexico

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We studied ectoparasites in a community of bats in the cave El Infierno in Santiago, Nuevo León. We collected data between June and August 2018 through capture and review of 29 individuals of 6 bat species (*Leptonycteris nivalis, Desmodus rotundus, Nycticeius humeralis, Choeronycteris mexicana, Myotis auriculus, Antrozous pallidus*). We identified two genera of batflies (Diptera: Streblidae) *Trichobius* and *Basilia* and ectoparasites in the order Ixodida and Acari. Our study is the first of its kind at El Infierno cave and informs about ectoparasites richness, range and their host diversity.

Population Genetic Structure in *Glossophaga soricina* Inhabiting the Human-dominated Landscape of El Salvador

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Habitat reductions affect the distribution and dispersal of species, potentially promoting genetic differentiation as gene flow among separating populations becomes limited. Deforestation has proceeded further in El Salvador than in any other country in Central America, with only 14% forest cover now remaining. The capacity of a species to face such loss of habitat depends on habitat specificity but also other factors. Ultimately, size of habitat patches may increase or reduce levels of genetic diversity. This work focuses on seven remnant patches of forest in El Salvador (Cerro El Tigre, El Imposible, Los Volcanes, El Refugio, Finca Lutecia, Gotera, and Río Sapo). The genetic diversity and structure of the populations of Pallas´s long-tongued bat *Glossophaga soricina* ($n = 68$) was assessed by reference to 10 nuclear microsatellites. Genetic diversity based on the heterozygosity index found to be moderate compared with that obtained for other bat species (Ho = 0.456 ± 0.031, He = 0.603 ± 0.028). No significant correlation between size of forest fragments and levels of genetic diversity was found; with genetic structure assuming values close to zero suggesting a total lack of genetic differentiation among sites ($Fst = 0.004$, $P = 0.999$). In contrast, a significant figure for a level of inbreeding was noted ($F_{IS} = 0.089$, $P = 0.008$) based on genetic differences observed in pairwise analysis. Data for some sites in El Salvador indicate genetic structuring, even in a potentially mobile species such as Pallas's long-tongued bat. Thus, habitat loss and other anthropogenic changes in the country's landscape could induce genetic impacts on *G. soricina* and other mammal species over time.

Collaborative Monitoring to Assess Declines in Oregon Bat Populations via Bat Grid and NABat Monitoring Programs

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The original interagency Bat Grid, led by the US Forest Service and with participation by many partners across Oregon and Washington from 2003–2010, established baseline distributional data for bats throughout Oregon and Washington and provided the foundation for the North American Bat Monitoring Program (NABat). In 2016–2017, collaborative acoustic bat monitoring (referred to locally as "Bat Grid 2.0") was continued across Oregon by state and federal partners at original Bat Grid survey locations and at new locations selected via the NABat master sample. One primary objective was to enable comparisons between 2003–2010 Bat Grid 1.0 baseline and current probabilities of occurrence to evaluate potential population declines in light of the regional expansion of wind energy developments during the intervening years and the recent arrival of white-nose syndrome (WNS) to Washington. Within a Bayesian occupancy modeling framework, we used the occurrence probabilities estimated after 2010 as informative priors to update and map new posterior distributions with data from 2016–2017 for two species (*Myotis lucifugus* and *Lasiurus cinereus*) considered to be vulnerable to these emerging threats. We found evidence of possible decline for *L. cinereus* but not for *M. lucifugus*. WNS arrived in 2016 and may not yet have caused widespread regional impact to *M. lucifugus*. We emphasize that model uncertainty and only two years of additional data make these findings provisional and best considered as testable hypotheses that guide conservation decisions including allocation of resources for further research and monitoring.

Should I Stay or Should I Go? Neighbourhood and Roost Selection in *Ectophylla alba*

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Ectophylla alba, is endemic to a small part of Central America. They roosts in groups, exclusively in leaves modified as tents (inverted boat). A leaf tent is used on average for 7 weeks until it deteriorates and the group moves to a fresh one finished a few days before the current tent gets uninhabitable. *E. alba* feeds only on *Ficus colubrinae*, a small-fruited fig species abundant in riparian habitats that produces fruits 3–4 times a year. Using information generated over the last 12 years, I will explain the roost site selection process, focusing on three interacting dynamic criteria: interspecific interactions (to limit the risk of predation, parasitism or other negative interactions for the roosting bats); microclimate (to keep close to the thermoneutral zone and other environmental constraints), and vegetation composition and structure (to optimize foraging). The interaction between these three criteria determines the quality of the roost. Possibly, the decision-making process involving the three criteria aims to optimize the conditions that allow the bats to maintain the basic conducts linked to the roost (mating, rearing of the young, grooming, resting, etc). Climatic events (i.e, a hurricane) may affect the availability of fresh leaves for tent construction or the abundance of food resources, hence, temporally disrupting the equilibrium of the model. Confronted with these situations, the bats may temporally move out of the "comfort zone" while still following the decision tree along the most economic path in trying to keep the changes to a minimum.

Seasonal Dynamics of Lipid Metabolism and Energy Storage in *Tadarida brasiliensis*

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As flying mammals, insectivorous bats are adapted to operate at extreme levels of energy expenditure. In situations that push the limits of their metabolic capacity, we predict that bats should trade off aspects of their physiology or behavior to maintain energy balance. To test whether bats use physiological compensations to cope with elevated demands, we examined variation in energy storage and pathways for oxidative metabolism in Brazilian free-tailed bats (*Tadarida brasiliensis*) related to costs associated with reproduction and migration. We collected pectoral muscle and liver from female bats at six time points during the summer and fall and measured changes in the

activity of four enzymes involved with lipid metabolism. Body mass varied predictably and dramatically with life-cycle stage, suggesting rapid accumulation and use of fat stores in response to current and anticipated energy demands. Catabolic enzyme activity (CPT, HOAD, and CS) in the muscle was increased during lactation compared to early pregnancy, but exhibited no change prior to fall migration. While there was no temporal change in hepatic fatty acid synthase activity, FAS activity was negatively correlated with body mass. Variation in body mass and enzyme activity in *T. brasiliensis* during the summer suggests mobilization of stored energy and increased lipid oxidative capacity during periods of increased demand, and increased lipid biosynthetic capacity with depletion of fat stores. These results suggest that aerial insectivores may be able to flexibly adjust metabolic capacity based on energy need to maintain energy balance despite extreme levels of expenditure.

Summer Roosting Ecology of *Nycticeius humeralis* on the Gulf Coast of Texas

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Bats spend more time roosting than any other activity and do so in various natural and anthropogenic structures. Few studies have examined bats of the Gulf Coast of Texas and none have analyzed roost selection of evening bats (*Nycticeius humeralis*), a widely distributed species on the southern edge of its range. Evening bats occupy roosts in cavities of live and dead trees, behind exfoliating bark, in tree foliage, buildings, and other locations. Our objective was to determine roost selection of evening bats on the Gulf Coast of Texas. From May to Aug 2018 we mist-netted in bottomland hardwood tracts on San Bernard National Wildlife Refuge and radiotracked six evening bats to five different roosts: two buildings and three tall, large-diameter live oaks (*Quercus virginiana*) (height: 27–31m; dbh: 107–200 cm) located in urban areas. Bats were utilizing the protected areas for foraging yet roosting in urban neighborhoods. Colony size ranged from approximately 48 to 500+ bats. One building roost was shared with Brazilian free-tailed bats (*Tadarida brasiliensis*). All bats stayed in roosts for the full life of the transmitter (5–21 days) and no roost switching occurred. Understanding the complex roosting strategies of evening bats could aid in the conservation of this species, in what is possibly an area of low bat diversity (3 captured species). We plan to radiotrack more evening bats during summer 2019 to further examine roost selection and make comparisons with evening bats from more northern populations.

Finding New Rules for the Patterning of Post-canine Teeth in Mammals: Insights from Noctilionoid Bats

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Teeth are one of the most diverse organs in term of morphology and have become a model to study the development of repeated structures. In particular, the patterning of the molar row is supposed to be established through a signaling cascade in rodents. Recently, the study of other mammalian groups has challenged this view. Moreover, this model cannot predict the patterning of premolars and the diversity of post-canine tooth number observed across mammals. Here, we established a new model for the patterning of the mammalian post-canine dentition using the hyperdiverse Noctilionoid bats as a reference group. We combined morphometric and quantitative data from 117 adult species exhibiting variations in tooth number and size. We showed that the number of post-canine teeth is related to the length of the jaw and that premolar and molar proportions are independent, suggesting distinct developmental mechanisms for their formation. To get insight into these underlying mechanisms, we analyzed the development of 12 different species across 8 developmental stages by µCT scan, tested developmental markers, and linked teeth formation to the growth rate of the jaw. Finally, we proposed a new Turing-based model based on these developmental results to explain the development of premolars and molars rows in our 117 species. Our data reveal that the premolar and molar rows are established by two independent signaling mechanisms and that premolar and molar number and size is linked to the local growth rate of the jaw and provide a testable framework for other bats and mammal species.

The Effect of Vocal Behavior on Roost Finding Tactics

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In social species, individuals tend to either search for resources themselves, or to follow other groupmates towards resources. These tactics can be flexible; however, there is a tendency for individuals to show consistency, suggesting that personality might play a role in the tactic they use. Here, we studied if the vocal behavior of the Spix's disc-winged bat, a species known to have different vocal roles in contact calling, is associated with roost finding tactics. Spix's disc-winged bats use a highly ephemeral roost. Thus, to facilitate roost finding, flying bats produce "inquiry calls" to maintain contact with group members. When a bat finds a roost, it produces "response calls" to recruit group members. In the experiments, we first stablished their vocal behavior (vocal or non-vocal), by playing back inquiry calls. Subsequently, in a flight cage, we placed a roost with a speaker inside to reproduce response calls and we recorded the time spent by each individual entering the roost. Moreover, we color-coded each group member and released them at the same time in the flight cage, this time without reproducing contact calls and we observed the order in which they entered the roost. To determine if these behaviors are consistent, we repeated the experiments over the course of six months. Our results show that vocal behavior plays an important role in defining individual search tactics. This study demonstrates that personality traits are important predictors of foraging tactics in roost finding.

Does Seed Ingestion by Bats Increase Germination? A New Meta-analysis 15 Years Later

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The seed dispersal cycle forms the base of vegetation establishment and population dynamics. Evidence shows varied results for the role of frugivorous bats, where ingestion and gut passage increase seed germination for some plant species, but not for others. Using meta-analysis techniques with a novel database spanning 31 years of study, we answered the following questions: 1) Does seed passage through bat digestive tracts increase seed germination compared to seed pulp removal by humans? 2) Does seed ingestion by bats accelerate seeds´ time until germination compared to seed pulp removal by humans? 3) Is there an effect of germination conditions, bat species and plant species on seed germination? and 4) Is there an effect of fruit bat dietary preferences on seed germination? In general, seed passage through bat digestive tracts neither significantly increased nor accelerated seed germination. However, seed germination varied mainly with plant species and bat species, less than 25% of plant species responded to bat gut passage in a positive or negative way. On the other hand, plant species that were preferred by a species of bat showed higher germination success than non-preferred plant species, in line with the core plant taxa hypothesis. These results suggest that: 1) the principal role of frugivorous bats in seed dispersal is the transport of seeds away from parent plants, 2) bats had a fruit handling that not reduce seed germination, and 3) seed germination of fruits consumed by bats is idiosyncratic to the bat and plant species in question.

Cranial Geometric Morphometrics of the Frugivorous Bat *Sturnira parvidens* (Phyllostomidae: Stenodermatinae)

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Sturnira parvidens belongs to one of the more diverse genera of bats in the Neotropics. Previously, two haplogroups were reported within this species, one located in Eastern Mexico and Central America, and another in the Mexican Pacific Slope. We used geometric morphometric techniques to test if there are differences in the shape of their skulls. We analyzed five different morphological regions in 378 specimens, including samples from its entire geographic range. Landmarks and semilandmarks were used to analyze the shape of the skulls, and we tested for allometry, sexual dimorphism, and differences between haplogroups. The size of specimens does not influence the

shape of skulls, and there are signals of sexual dimorphism. We also found that differences between haplogroups are located in the face, parieto-occipital region and the posterior edge of the palatine. Nevertheless, the differences are subtle, possibly because there has been short time since haplogroups started their differentiation. This evidence indicates that these biological units represent an early stage in the speciation process.

Sublethal Effects of Neurotoxic Pesticides on Bats: from Cells to Behavior

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Agricultural intensification and the consequent increase of pesticide use has been considered a major threat for bat populations in Europe. However, no research on this topic has been conducted in tropical agrosystems, where most of the arable land is frequently treated with pesticides, particularly large monoculture plantations like banana and pineapple. Considering that bats can eat more than 90% of their body mass every night, species that forage preferentially in crops could be highly exposed to pesticides through their prey. This study seeks to determine the sublethal effects of organophosphate pesticides on bat species foraging in or near crops. Organophosphate pesticides are commonly used neurotoxic chemicals that can impair vital functions such as the ability to feed, escape predation, or reproduce. In order to assess the risk of exposure, we have studied foraging activity of bats in crops in Belize, Mexico and Costa Rica, countries known for their great bat diversity and extensive use of pesticides. To estimate intake by bats, we will analyze pesticide levels in insects collected in the same locations. Subsequently we will use an integrative approach to study the toxic effects of organophosphates on captive and wild bats. This approach involves measuring molecular (enzyme activity), physiological (metabolic rate, immune response), and behavioral (echolocation) biomarkers, aiming to extrapolate these responses across levels of biological organization. Understanding the mechanisms and effects at different scales will enable us to better predict the implications on populations and communities and help to inform mitigation strategies.

Fruit-bats Finding Fragrant Fruits

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Frugivorous bats have evolved sensory, morphological, and behavioral adaptations to locate and consume ripe fruit effectively. Previous research has demonstrated that neotropical frugivorous bats rely heavily on olfaction, and therefore on plant chemical signals, to locate ripe fruits. However, little is known about how sensory use and foraging decisions are influenced by the complex diversity of chemical cues that fruiting plants produce. Using wild *Carollia castanea* and *Piper sancti-felicis* as an experimental system, we conducted behavioral trials to test two main hypotheses: (1) foraging decisions in *C. castanea* are primarily driven by ripe fruit scent and its most salient chemical components and (2) *C. castanea* potentially re-weight their sensory inputs to account for available environmental cues, such that bats rely more heavily on other senses (e.g., echolocation) in the absence of adequate scent cues. Our results suggest that *C. castanea* require olfactory information and rely almost exclusively on ripe fruit scent to make foraging attempts. Ripe fruit scent is quantitatively and qualitatively distinct from vegetation scent in *P. sancti-felicis*, with sesquiterpene volatiles (caryophyllene, germacrene-D, β-elemene) dominating the scent profile. *C. castanea* exhibit a strong preference for a few compounds found in ripe fruit scent. Moreover, there was no significant difference in echolocation call parameters when fruit scent or scent constituents were presented during experimental trials. By contrast, bats emitted longer and more frequent echolocation calls when ripe fruit scent was absent. Altogether, these results highlight the adaptations, plasticity, and potential constraints in the sensory system of neotropical fruit bats.

Southeastern *Myotis* and Rafinesque's Big-eared Bats Switch their Roosting Habits Seasonally in Arkansas Bottomlands

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Tree roosts in bottomland forests are an important resource for Rafinesque's big-eared (*Corynorhinus rafinesquii*; CORA) and Southeastern (*Myotis austroriparius*; MYAU) bats. Both bat species are considered rare across their range and little is known about their roost requirements as seasons change from fall to winter. The objective was to characterize roost trees in both seasons in the Cache River National Wildlife Refuge, Arkansas, one of few

remaining tracts of unaltered bottomland hardwoods. In October–December of 2016 and 2017, we radio-tracked 38 bats (21 CORAs and 17 MYAUs) and found 78 confirmed roost trees. Tree species and cavity type (e.g., basal cavity) were recorded for each confirmed roost tree. Both species switched their roosting habits as environmental conditions changed. Various tree cavity types were used for roosting by CORAs until they discontinued using basal cavities entirely late in the season. MYAUs showed no strong preference for cavity types early in the season but progressed to favor upper cavity openings later in the season. This suggests that both CORAs and MYAUs anticipated seasonal flooding that could potentially trap them inside the cavity. Additionally, CORA used Water Tupelo (*Nyssa aquatica;* NYAQ) exclusively, but MYAU shifted from using mainly NYAQ initially to using a variety of tree species as environmental conditions changed. Changing behaviors may coincide with changing priorities from foraging to avoiding seasonally rising flood waters and maintaining homeostatic balance in an increasingly cold time of year.

Using 3D Thermal Videography to Better Understand Bat Fatality Risk at Wind Turbines

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Bat fatalities at wind energy facilities are a major concern, particularly because wind energy development is rapidly expanding into new areas and may impact additional species. Currently, the only scientifically proven impact reduction strategy is operational minimization (i.e., minimizing turbine operation during high risk periods), which is likely to result in additional power loss if changes in turbine technology allow for operation at lower wind speeds. In addition, if turbines become taller with larger rotor-swept zones, then promising impact reduction strategies, such as ultrasonic acoustic deterrents, might need additional research and development to deal with issues such as attenuation of high frequency signals. Given these factors, and to have a diversity of minimization strategies available for varying circumstances (e.g., new species or new turbine technology), more studies need to examine bat behavior around wind turbines in a temporal resolution that allows us to understand risk and potentially build fatality risk models based on real-time observations. To address these needs, we have developed an open-source software program to generate three-dimensional flight paths of bats around wind turbines. We will present a case study showing the value of these methods for testing minimization strategies. We also will discuss other potential applications for this software, such as examining spatial and temporal patterns of bat behavior around wind turbines, which has the potential to result in novel reduction strategies. As we increase our understanding of bat turbine interactions, stakeholders can make more informed decisions on conservation actions needed to avoid population level impacts.

Modeling and Mapping Habitat Suitability for Foraging Activity of Cryptic Foliage-roosting Bats in Central Coastal California

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We detected and modeled bat habitat selection for foraging activity in the Monterey Bay Area, California, to explore a potential method for determining regional distribution of two species of cryptic foliage-roosting bats, hoary bats and red bats. We postulated that foraging activity of these bat species would in part be determined by the extent of forest and grassland cover, and the proximity to urbanization. We walked transects in natural and urban areas and monitored bats using an Echometer Touch bat detector. We also collected data from passive acoustic monitoring and mist netting efforts. All acoustic calls were analyzed to identify bats species using Sonobat software. We will determine available habitat based on a buffer area surrounding each transect, detector, or netting site. Models will be constructed based on chosen land cover covariates at multiple spatial scales and compared using Akaike's Information Criterion. We expect that the results will support the postulate that hoary bats and red bats select specific natural areas at further distances from urbanization for foraging. We will use the results to guide site selection for a more in-depth spatial analysis of habitat use for foraging.

Migratory Bat Roost Use in the Bitterroot Valley
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The roost-site use and migratory habits of silver-haired bats (*Lasionycteris noctivagans*) and hoary bats (*Lasiurus cinereus*) are poorly understood. This study provided some of the first documented roost locations and roost descriptions for silver-haired bats in Montana, and provided one of the first known efforts to attempt to characterize inter-annual site fidelity for these species. We used radio telemetry to track 48 silver-haired bats and 4 hoary bats to their day roost locations between 2016–2018. These tracking efforts resulted in discovery of 70 silver-haired bat roosts, which included a maternity colony of 43 individuals. No hoary bat roosts were documented despite extensive ground and aerial searches. Most silver-haired bat roosts (97%) were located within natural cavities of black cottonwood trees (*Populus trichocarpa*); however, roost trees did not differ in diameter, height, or decay stage compared to available trees. Based on radio telemetry information, hoary bats migrate through the study area in July and August, and silver-haired bats appear to migrate out of the study area in late August and early September. In addition to radio telemetry, we also marked individuals with PIT tags and recaptured 2 silver-haired bats in 2017 that were marked in 2016, suggesting some degree of inter-annual fidelity to summer habitats. The results of this study may be used to guide natural resource management decisions by providing a basic understanding of roost ecology of bats during the maternity period, and the degree of inter-annual fidelity to summer habitats.

Evidence for Multifactorial Processes Underlying Phenotypic Variation in Bat Visual Opsins During Noctilionoid Diversification
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The acquisition of new sensory systems has long been proposed to explain species diversification as the acquisition of new capabilities enables access to new ecological niches. For vision, the acquisition of new wavelengths has been suspected to drive species diversification in primates and fishes due to the resulting advantages in foraging and hunting. However, these studies remained limited to few species and were never carried out within a large taxonomic group. In consequence, the evolution of genomic and developmental mechanisms at the origin of diversification remains largely unknown. Here we perform the first multi-level molecular comparative study of visual ecology evolution across neotropical bats, a group that radiated 40 million years ago, with unparalleled dietary diversification among mammals. Combining data from sequences, gene expression, and immunohistochemistry, we test for correspondence between functional open reading frame, transcript, and protein in two cone opsins, OPN1SW and OPN1LW. In order to decipher the role of these processes in species diversification, we also linked data to ecological parameters. Contrary to expectations, a fifth of taxa possess neither an OPN1SW transcript nor the corresponding S-cone, and four taxa possess the transcript but no protein. S-cones are present in most frugivores but were likely lost independently in several groups, including most flower-visiting species. The highly variable patterns for S-cones contrast strongly with those for OPN1LW and the corresponding long-wavelength sensitive (L-) cones, which were detected in all taxa. Our findings suggest that variation in bat color vision has likely arisen through selection for sensory specialization acting at multiple stages of protein synthesis, and reveal caveats in the inference of phenotype solely from gene sequence. Finally, our results revealed the complex mechanisms at the origin of the evolution of a sensory trait implicated in species diversification in the field.

Habitat Effects on Use and Activity Levels of Bats in Coastal South Carolina
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The southeastern Coastal Plain is projected to have one of the largest urban expansions in the United States. This region marks the northern edge of the rare and understudied northern yellow bat's (*Dasypterus intermedius*) range and the southeastern edge of the threatened northern long-eared bat's (*Myotis septentrionalis*) range. Our objective was to determine habitat use of bats in this region (with focus on northern yellow bats) to inform management and

conservation. During May–August 2018 we placed Anabat Express acoustic detectors at 64 sites in Beaufort County, SC for four nights each. We placed detectors in upland forests, bottomland forests, fields, salt marshes, and ponds, and characterized habitat and forest structure within a 0.05 ha plot surrounding each detector. Overall bat activity at ponds was higher than bottomland forests ($P = 0.02$) and upland forests ($P < 0.001$) and activity in salt marshes was higher than in upland forest ($P = 0.03$). Mean activity decreased significantly with increased basal area and canopy cover, however, R^2 values were low ($R^2 = 0.08$ and $R^2 = 0.12$, respectively). We identified 273 northern yellow bat calls across 34 sites in all habitats. Northern yellow bats were detected at 91% of field and salt marsh sites, and 100% of ponds but, were only detected at 20% and 9% of bottomland and upland hardwood sites. Our results contribute to an increased understanding of habitat use by bats in the Coastal Plain and will allow managers to develop plans to manage important habitat characteristics for bats in this rapidly urbanizing area.

Bat Species Turnover Following White-nose Syndrome Detected by Mobile Bat Acoustic Transects

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Changes to species composition by mass mortality from disease can alter ecosystem functioning. Mass mortalities to white-nose syndrome (WNS) susceptible species are changing bat communities and populations in endemic areas, but species turnover following WNS has only been suggested and not reported. To characterize species composition at a large scale, we used data from mobile bat acoustic routes implemented by Ohio Division of Wildlife in 2011. We hypothesized mobile acoustic route detections between 2011–2017 would indicate an increase in migratory bat abundance, and a decrease in cave-dwelling bat abundance in summer months following the state's emergence of WNS. We predicted migratory species would be utilizing space and resources once used by cave dwelling bats that have greater susceptibility and mortality due to WNS. We created two sets of linear mixed effects models: one to include winter and summer roosting behaviors and another to include species classification. Behaviors and species classifications were not used together since behaviors are nested within species. We used Akaike's Information Criterion to select the best fit model for roosting behavior and species model sets. Relative abundance predictions of cave-dwelling, cavity roosting bats declined, while migratory, cavity roosting bat abundance increased. Relative bat abundance predictions by species indicated potential turnover in summer population structure from *Myotis spp*. and *Eptesicus fuscus* to *Nycticeius humeralis* and *Lasionycteris noctivagans* following WNS. This work provides insight into bat population changes following the emergence of WNS and can inform large-scale management practices for temperate bat conservation in endemic regions.

Effects of Hurricane Maria on the Bat Community on the Caribbean Island of Dominica

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Understanding species' responses to hurricane disturbance can help us predict future impacts and aid in conservation actions, which will become progressively more important with climate change. On 18 September 2017 Hurricane Maria, a category 5 storm, made landfall on the small island (750 km^2) of Dominica, sustaining winds up to 258 kph and causing substantial damage to the vegetation across the island. This presented a unique opportunity to assess the hurricane's impact on bat community structure and composition in the Caribbean. I measured changes in diversity, abundance, reproductive rate, body condition, and habitat use using pre-hurricane data I collected during mist-netting surveys in 2016 and 2017, and post-hurricane data I collected in the same study areas in 2018. Nine species (750 individuals) were captured in the two years prior to the hurricane, with reproductive females documented for eight species. Nine species (79 individuals) were captured post-hurricane, with reproductive females documented for six species across the island. A decline in the number of captures and percent of reproductively active females of several species indicates varying responses within foraging guilds. Preliminary results suggest a stronger sensitivity for species dependent on plants for food, and a failure to reproduce post-hurricane. Analysis is on-going and further results will be presented.

Vocal Learning and Auditory Development in Prenatal Egyptian Fruit Bats
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Vocal learning, the ability to receive and then produce novel sounds, is a critical process in human speech development but has only been demonstrated in a few non-human animals, including bats. The Egyptian fruit bat (*Rousettus aegyptiacus*) is a social, group-living species producing broadband echolocation clicks and various social calls which convey identity and context information. Previous work showed that young fruit bat pups modified the pitch of their calls according to vocalizations of other adults they were exposed to since birth. In this study, we addressed whether the learning period extends to prenatal pups by testing whether pups can hear and learn in utero. We played back temporally and pitch-modified adult calls and pink noise to pregnant bats while monitoring fetal heart rate through an ultrasound. We exposed three other pregnant female groups to control and modified calls for ca. 3.5 months during pregnancy, and assessed the preferences of the pups on Days 5–7 postbirth through acoustic playback tests. We found that by Day 0, Rousettus pups are responsive to both calls and noise, and are highly vocal, producing isolation calls and echolocation. Pups (n = 13) did not show a strong preference to different call types, suggesting that vocal learning of pitch and tempo does not occur prenatally. Further work will include solidifying prenatal auditory capabilities, and determining whether and when postnatal pups are able to discriminate adult calls from noise in the environment.

Assessing the Potential Impacts of Radio Transmitters on Bat Flight in a Controlled Environment
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Telemetry is an effective method for collecting movement and resource use data, however, attached transmitters have the potential to negatively impact the behavior and movement of wildlife, particularly volant species. Studies have suggested that such devices could even have additional implications on bat maneuverability. Despite these concerns, no studies to date have assessed the potential effect of transmitters commonly used in bat telemetry surveys. Thus, we conducted a study on evening bats (*Nycticeius humeralis*) in a controlled environment. We hypothesized that if a transponder affected bat flight, we would observe a decrease in area usage, tortuosity, velocity, and flight duration. Furthermore, if bats habituated to the transponder, we would expect such effects to diminish over time. We housed bats in a flight facility for 4 days in which we recorded bat flight on Cannon infrared camcorders with and without the transmitter attached. We used Ethovision and Track 3D software to create flight paths for each bat to acquire the aforementioned variables. We recorded >30 bats from March 15 to August 31, 2018. In support of our hypothesis, we observed a decrease in flight duration by approximately 56% after the initial transmitter attachment with little to no improvement by the second night (~52%), and observed an improvement by the third night (~24%). Similarly, we found that area usage and velocity followed the same trend. Thus, our study highlights a potential bias in telemetry surveys that could impact data quality and therefore should be taken into consideration when conducting such surveys.

Validating Models for Site Selection in a Population Monitoring Program for Townsend's Big-eared Bats
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Population-level impacts from threats such as disease and disturbance are detectable only through population trend-monitoring programs with adequate statistical power. Efficient survey site selection improves the chances that resources invested result in powerful monitoring, but the use of habitat models for trend-monitoring site selection requires evaluation of predictive accuracy. Therefore, we validated predictions for several habitat models built from multiple datasets for a species of concern, Townsend's big-eared bats (*Corynorhinus townsendii*), threatened by disease (white-nose syndrome) and disturbance in an area with 30 years of survey history (Lava Beds National Monument, Siskiyou County, CA). Hibernating bat abundance was negatively correlated with mean winter cave temperature measured hourly over four years (n = 30). However, the complexity of monitoring over 800 caves renders fine-scale temperature monitoring infeasible. Instead, we explored several cave morphology metrics thought to influence airflow as proxies for cave microclimate. Principal components analysis suggested a link between cave temperature and entrance area, constriction area, and volcanic trench depth, but models built from this small dataset (n = 30) did not perform well in predicting bat abundance. Boosted regression tree models built from a larger dataset

(n = 241) suggested volcanic trench length, maximum ceiling height, and negative slope beyond the entrance predict bat abundance. Extreme overdispersion in the count data resulted in high model deviance and low predictive accuracy, but model deviance was reduced when count data was converted into detection/non-detection data. These models will be useful for identifying sites likely to be occupied, yet precise bat abundance is more difficult to accurately predict.

***Elucidating Patterns of Bat Species Occupancy Across a Disturbed Landscape in California's Central Valley**
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*** Trinity N. Smith** received the **Speleobooks Award.**

California's Central Valley, one of the most productive agricultural regions in the world, is home to 17 species of resident and migratory bats. The Central Valley ecoregion has been identified as a crisis ecoregion, and a high number of species are at risk due to habitat conversion and drought. In response to drought, California Department of Fish and Wildlife implemented the Terrestrial Species Stressor Monitoring (TSM) project, which in part aimed to collect baseline occupancy data and habitat associations for bats. We conducted bat surveys using SM3BAT acoustic detectors at 275 sites spanning the Central Valley in both the driest year on record (2016) and the wettest year on record (2017). The resulting bat species detections were processed using Kaleidoscope software and were then manually vetted. These detection histories will be used to determine species-specific occupancy patterns for bats in the Central Valley, which can be used by managers to assess critical habitat areas.

Importance of Man and Biosphere Reserves for Bat Diversity: Crocker Range MAB in Borneo
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Borneo is a hotspot for chiropteran diversity, hosting over 90 species of bats. The island has undergone extensive deforestation to support growing agricultural demands, leaving isolated fragments behind. The Crocker Range National Park in Sabah, Malaysia is one such fragment, at 139,919ha. UNESCO designated it as a part of the Man and Biosphere Program (MAB) in 2014, with hopes of encouraging sustainable practices that benefit both the people and their environment. Forty-one species were known from the forested core area, but the bat diversity supported by the agricultural lands of the transition zones was unknown. We conducted a survey of two agricultural sites in the transition zone, one forested site in the buffer zone, and two forested sites in the core zone. We hypothesized that the forested areas of the reserve would have greater species richness and abundance. Harp traps and mist nets were used to capture bats at each site. We captured 155 individuals, 95 in forest and 60 in agricultural lands, of 24 species. Twenty species were found in the forest and twelve in agricultural lands. Twelve species were unique to the forest, and four were unique to agriculture. Five species were new locality records (*C. minutus, H. ridleyi, K. intermedia, R. amplexicaudatus,* and *T. pachypus)*. Right now, the core and buffer zones are currently hosting a higher diversity of bats than the transition zones. This survey can act as a baseline when assessing what influence the MAB program has on the conservation of bats in the future.

***Anatomical Diversification of the Bat Calcar**
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The evolution of novel structures is an enduring problem within biology. The calcar is a skeletal element unique to bats that extends from the ankle into the hindlimb membrane. The calcar appears to be morphologically diverse, yet the extent of its variation is unknown. Because understanding anatomical diversity provides clues to homology and function, we completed a broad survey of calcar anatomy to illuminate its evolutionary and functional diversification. We CT scanned calcars from 21 species (16 families), histologically sectioned calcars of 18 species (13 families), and measured calcar length in an average of 6 specimens from 226 species (20 families). We found extensive anatomical variation in calcar size, shape, and tissue composition. The calcar ranges from unmineralized

cartilage (multiple bat lineages) to bone (species within Yangochiroptera). This variation occurs not only across species but also within a single specimen. Bony portions of calcars exhibit internal structure and openings for vascular supply. Calcar length ranges from zero (no calcar) to over 1.5 times the length of the tibia, and some species exhibit particularly unique calcar shapes (*Noctilio leporinus* and *Mystacina tuberculata*). Phylogenetic analyses indicate that calcar length exhibits a high phylogenetic signal and diversified early in bat evolutionary history. This suggests that calcar anatomical diversity emerged as a byproduct of bat systematic diversification. The calcar may serve as an excellent case study for understanding the origin and diversification of novel structures and the evolution of the skeleton in bats and other mammals.

Predicting Habitat Use by Bats to Protect Bats and Inform Wind Energy Development
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Although wind turbines are a clean source of energy, they incidentally kill many bats and birds. Migratory species have the highest mortality; in 2012, ~600,000 bats died from encounters with turbines in the US alone. Arizona has 28 bat species and a high proportion of migratory species that creates a high risk of mortality from interactions at wind energy facilities. Our objectives are to determine the species composition, bat use, and topographic features that might influence bat movement. Our study area encompassed open grassland and shrubland in northern Arizona that were similar to sites considered for wind energy development. We deployed 34 acoustic detectors (SM3BAT) to sample for bat activity at randomly-selected points that represented a range of measures for each habitat covariate. We surveyed points during spring, summer, and fall of 2016 and 2017 and used SonoBat 3 software to identify bat calls to species or species groups. We used occupancy models to evaluate the effects of landscape covariates on bat activity. The highest bat activity occurred in valleys, lower slopes, and evergreen forests. Since most wind energy development in northern Arizona has occurred on flat slopes, shrubland, and grassland, this indicated that best sites for wind energy might not overlap with best sites for bat use. Our predictive map shows bat use in areas of northern Arizona considered best suitable for wind energy development given acoustic activity.

Bats to the Future: The Occurrence and Distribution of *Pipistrellus nathusii* in the North-east of Scotland
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Climate change has negative impacts for many species, but for a select few it can offer new opportunities by expanding available habitats; this is especially the case for *Pipistrellus nathusii*. In both England and Ireland, it is classified as a residential bat with migratory influxes, inhabiting southern areas with warm climates; however, the North-East of Scotland has recently gained an establishing population of *P.nathusii* which is thought to be due to increasing temperatures. Unfortunately, the information regarding the migratory status of this isolated population is both limited and contradictory. It is important to establish the status and trends of this local population, as it is located on the Northern edge of *P.nathusii's* range it would be subject to any future expansion first. To confirm the migratory status, this study recorded echolocation calls in July and September across ten sites with various habitats and locations using SM2+ static detectors and used ArcGIS10.5 to confirm the variables associated with *P.nathusii*'s distribution. Key results showed that significant populations of *P.nathusii* were present in both July and September in the North-East of Scotland, and that with increased distance from the coast, the number of calls reduced. *P.nathusii* is therefore residential in the North East of Scotland, and distance does impact distribution; however, it cannot be confirmed as to why, due to the relationship between distance and habitat. This project has provided a baseline for future generations to monitor the expansion of *P.nathusii*, a now residential and protected species in Scotland.

Population Changes in the Migratory Bats of Calgary, Alberta
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Recent models suggest that factors such as climate change, habitat loss, and especially fatalities at wind turbines, have resulted in declining populations of migratory bat species. In Alberta, silver-haired (*Lasionycteris noctivagans*) and hoary bats (*Lasiurus cinereus*) make up over 80% of bat fatalities at wind turbines. Using mist netting and echolocation recordings, estimates of abundance were made during migration (July–September) from 2006 to 2008 for bats near Calgary, Alberta. In July and August 2018, I replicated those measurements at the same study sites in

Calgary to test the hypothesis that migratory bat populations have declined. Long-term studies of abundance of the migratory species of bats are rare, and have not been conducted in Western Canada. The previous study in Calgary was conducted for other purposes, but offered a unique opportunity to assess population changes over the past ten years. The data on abundance of various species may reveal impacts of renewable energy that are unintended, and therefore the results from this research has the potential to be considered when siting and permitting the building and mitigation measures of more wind facilities. Preliminary capture data suggest significant declines in abundance of both species. I will present further results from captures and acoustic monitoring.

Movement Patterns of Migratory Tree-roosting Bats During Autumn Migration

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Migration routes of long-distance migratory tree-roosting bats (*Lasiurus cinereus, L. borealis and Lasionycteris noctivagans*) in North America are poorly understood. Large numbers of bat fatalities recorded at wind energy facilities are contributing to likely population declines of these species. The majority of documented migratory bat fatalities at wind energy installations occur during autumn migration. There is some urgency to better understand migration patterns of these bats, as the Province of Saskatchewan plans to dramatically increase wind power generation capacity by 2030. We installed passive acoustic detectors in the southern half of Saskatchewan during the migration period to measure migratory bat activity. We placed one set of detectors in a three by three grid pattern across the study area in locations with high wind energy potential and prominent landscape features. We installed a second set of detectors along 5 km transects perpendicular to four of the province's major rivers. Preliminary results indicate higher levels of migratory bat activity in the eastern portion of the province. This may be an indicator that access to roosting habitat is important in bat migration route selection, as that portion of the province contains more forested landscape than other sampling sites located in grassland ecoregions. This information can be used to inform siting decisions for future wind energy projects.

Vegetation Structure and Diet Drive Species Richness of Forest Interior Insectivorous Bats along Mountains in Nigeria

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Bat species richness patterns along elevational gradients vary across mountains and may decrease monotonously, peak at mid-elevation or plateau and decrease sharply. Drivers of bat species richness along elevational gradients include vegetation structure and climatic variables. The role of diet in bat species richness patterns along mountains remains untested. Despite eastern Nigeria being a bat diversity hotspot, species composition and richness patterns at different elevations of the Cameroon/Nigerian mountain range have not been studied. We conducted bat surveys at five and six elevation strata (at 250–400 m intervals) respectively in Afi Mountain Wildlife Sanctuary (AMWS) and Cross River National Park (CRNP) in southeastern Nigeria. Using four-bank harp traps set for two consecutive nights along 200 m transects, we captured bats during 200 and 240 harp trap nights from AMWS and CRNP respectively. We conducted vegetation assessment in 2 m^2 plots around harp traps and trapped insects using light traps on alternating transects. A total of 642 individuals belonging to 12 and 18 species were captured from AMWS and CRNP respectively. We report seven bat species new to the country. Species richness declined monotonically with elevation and was comparable between both areas. Vegetation structure including tree height, foliage height diversity index tree density and canopy cover changed with elevation. Total insect biomass declined monotonically along the elevational gradient. Insect biomass and average dominant tree height per elevational band were important predictors of bat species richness. Our results support the prediction that bat species richness along elevational gradients is resource driven.

Investigating Roost Selection by Indiana Bat and Tri-colored Bat During Fall Swarming

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The Indiana bat and tri-colored bat are two of seven bat species known to be affected by the devastating fungal disease white-nose syndrome (WNS). Since the introduction of this disease, populations of both species have seen dramatic declines. In an effort to improve management and conservation efforts, research has been conducted to further understand ecology and behavior of these species during summer and winter, two critical periods in the life-history of bats. However, the ecology and behavior of the Indiana bat and tri-colored bat during fall swarming have not been fully investigated. Fall is also an extremely critical period for bats because of the energetics associated with reproduction and entering hibernation. During fall swarming there is heightened activity in and around hibernacula, as bats attempt to both mate and build energy reserves to survive winter hibernation. Entering hibernation with substantial energy reserves has become especially important if individuals infected with WNS are to survive winter. Therefore, any effective conservation and management strategy must include provisions to identify, study, and manage fall pre-hibernation bat populations and associated habitat, including diurnal roost sites. During fall (August–October) 2017, we captured bats at hibernacula and used radio telemetry to track seven Indiana bats and five tri-colored bats to their diurnal roosts. We confirmed four tree and three caves roost by tracking each bat for at least three days. We will present the initial results of our study examining diurnal roost selection by these species during fall swarming.

Do Remnant Little Brown Bats Show Increased Evidence of Pre-hibernation Hyperphagia Following Invasion of White-nose Syndrome?

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Little brown bats (*Myotis lucifugus*) suffer high mortality from white-nose syndrome (WNS) following invasion of *Pseudogymnoascus destructans*, and are now endangered in Canada as a result. Mortality from WNS is associated with the early depletion of overwinter fat reserves due to increased frequency of arousals from torpor during hibernation. This predicts that the surviving bats remaining after initial declines from WNS should exhibit traits that help them accumulate large pre-hibernation fat stores. We will test one prediction of this 'fat-bat' hypothesis that, following an initial decline from WNS, remnant bats captured at fall swarms will show elevated levels of plasma triglycerides, which reflect hyperphagia, relative to pre-WNS bats. We captured bats at a fall swarm in central Manitoba Canada throughout August and September 2018. We collected blood samples from little brown bats to measure concentrations of plasma triglyceride using a commercially available kit. We will compare values of plasma triglyceride recorded for our remnant bats to those previously published for pre-WNS bats captured at fall swarms in our study area. These data will shed light on factors that predict the survival of bats following WNS and help determine the potential of evolutionary rescue to help populations recover.

Foraging Range Selection of the Tri-colored Bat in Middle Tennessee

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Tri-colored bats populations are declining in Tennessee and throughout the temperate portions of their range, primarily due to the impacts of white-nose syndrome. The United States Fish and Wildlife Service has been petitioned to protect the species under the Endangered Species Act. However, our limited understanding of the foraging ecology of the species precludes our ability to effectively identify critical summer habitat for listing. The objective of this research was to establish the size of tri-colored bat foraging ranges and to determine if foraging tri-colored bats select certain land cover types significantly more than other available land cover types. During the summers of 2016 and 2017, we radio-tagged 7 male tri-colored bats and biangulated an average of 102 (range 49–177) foraging locations for each bat. The mean 95% minimum convex polygon foraging range was 2,350 (range 234–9,655) ha. To determine land cover selection of foraging tri-colored bats, we created a fixed kernel density estimate of each individual bat's foraging range and generated a 95% and 50% percentage volume contour (PVC).

We compared used versus available land covers at two spatial scales using a MANVO randomization test. Broad level selection of foraging range (95% PVC) within the study area was considered random (Wilk's $\lambda = 0.11$, $P = 0.065$). However, selection of core foraging range (50% PVC) within the overall foraging range was significantly non-random (Wilk's $\lambda = 0.056$, $P = 0.016$). Male tri-colored bats selected core foraging areas over open water and wetlands significantly more than other available land covers.

Endangered Bats in the Greater Toronto Area

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The Greater Toronto Area (GTA) is the largest urban area in Canada, and among the largest in North America, and continues to expand. This creates an added pressure for species on the edge of the expansion, three of which are federally endangered in Canada: *Myotis lucifugus*, *M. septentrionalis,* and *Perimyotis subflavus*. We used acoustic monitoring to detect seasonal activity of bats at 20 conservation areas around the GTA in 2017 and 2018. In 2018 we conducted trapping surveys at a subset of these sites to further investigate the endangered bats. We have confirmed significant acoustic activity of endangered bats, most commonly *M. lucifugus* at 13 sites. We found acoustic evidence of *M. septentrionalis* at one site. We rarely recorded *P. subflavus*. Many of the sites with endangered bats were in the suburbs, or in rural areas surrounding the conurbation, however, because the GTA continues to expand these sites could be affected by urbanisation in the future. Notably, we identified reproductive populations, confirmed by trapping and radio-telemetry, of *M. lucifugus* and *M. septentrionalis* in a forest surrounded by dense urban development and with high recreational usage. We conclude that even highly disturbed, urban sites can support species such as *M. septentrionalis*, which is not typically associated with such anthropogenic landscapes. Consideration for the potential presence of these species should be made during land management and planning.

The Importance of the IAUPR-BC Wetland of Bat Conservation and Citizen Science Education

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The fragmentation of natural ecosystems is a growing reality. After a fragmentation event, the resulting archipelago of habitats often varies in the quality of ecological characteristics that allow it to sustain population of bats. The species diversity and richness of these habitat "islands" is influenced not only by their intrinsic characteristics, but also by the permeability of the matrix on which they stand. We are examining a small wetland habitat along the urban matrix of the northern coast of Puerto Rico, located within the Interamerican University, Bayamon Campus, to assess the conservation value of such habitat remnants. Field work is being conducted using seventy-two meters of mist nets set one week each month in a standardized manner with the help of volunteers, which are recruited through our Facebook site. In addition, acoustic monitoring is being carried out during the night to detect bats that could be avoiding the nets. The following species have been detected so far: *Artibeus jamaicensis*, *Molossus molossus*, *Erophyla bombifrons*, *Brachyphylla cavernarum*, *Noctilio leporunis*, *Pteronotus quadridens*, *Eptesicus fuscus*, and *Tadarida brasiliensis*. Analysis of the bat detector data show a notable difference in the activity and capture rate between the years 2017 and 2018, most likely due to the damaging effects of Hurricane Maria in Puerto Rico. Our preliminary results suggest that the IAUPR-Wetland is an important habitat for bats. During the first year 140 volunteers assisted with field work and learned about the importance of bats in the ecosystem.

When White-nose Syndrome and Mexican Free-tailed Bats Collide

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Mexican free-tailed bats (*Tadarida brasiliensis*) are in the path of the spreading white-nose syndrome (WNS) epidemic, but it is not clear whether they will be a susceptible or resistant species. To be susceptible, the following must be in place: a) the bats must undergo multi-day torpor bouts (hibernate) in temperatures less than 15 C; b) they must hibernate for periods of at least two months in locations where the fungal pathogen for WNS exists; c) the fungus must grow in the skin of the bats; and d) the growing fungus must "stress" the bats physiologically such that morbidity and mortality occur. Although this species may be the most abundant bat in North America, their ability to undergo multi-day torpor bouts has been poorly studied: most are thought to migrate to Mexico and remain active

all winter. As part of a larger study to compare immune responses in WNS-susceptible and WNS-resistant bat species, we first tested the ability of Mexican free-tailed bats to enter and sustain torpor bouts in the summer. Using temperature-sensitive data-loggers to track body temperatures, and oxygen consumption to calculate metabolic rates, we monitored bats (n = 12) at temperatures from 2–22°C, for durations of 6–12 hours. Preliminary results suggest that they could survive these conditions, although it is not clear how well they could arouse themselves from the colder temperatures as passive rewarming was provide. The use of torpor above 10C appeared to be facultative under these conditions, and negatively correlated to body mass.

Does Land-use Change Affect the Interaction between Phyllostomid Bats and their Ectoparasite Flies?

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The family Streblidae is a small group of Diptera specialized as obligate parasites of bats. In this study we tested if this specificity keeps when landscapes change. We captured bats from three different sites: Forest, Orchard, and Urban park. The ectoparasites were collected in 96% ethanol. We performed a bipartite network, rank-abundance curves, and calculated parasitological parameters: prevalence (P), mean abundance (A) and mean intensity (I). We recorded 325 bats from 9 species and 225 streblids from 7 species. For bats, richness was the same for the three environments and abundance was higher in the urban park. *Sturnira hondurensis* was dominant for the forest and crops. Streblids where more abundant in the forest, with *Megistopoda proxima* being the dominant species for all environments. The parasitological parameters were higher in the Forest (P = 37.5%, I = 3.4, A = 1.2). *Megistopoda proxima* and *Paratrichobius longicrus* show inverse patterns in the hosts they parasitize. The bat assemblage changes in the different environments due to the availability of food resources and vegetation cover. The higher diversity of bats in the urban park can be related to the surrounding matrix. The highest abundance of streblids was found in the forest, supporting the idea that bats with better conditions support higher parasite loads. The interaction network supports the high host specificity for *Anastrebla modestini*, but shows how other species like *Paratrichobius longicrus* or *Megistopoda proxima* are apparently flexible species that change hosts when their primary hosts are not available.

Phylogenomics of the *Pteropus hypomelanus* Species Complex in Archipelagic Southeast Asia

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Pteropus hypomelanus is the only *Pteropus* species with a disjunct distribution in the Paleotropics, making its range the widest in the genus despite having small individual home ranges. Range breadth and limited morphologic variability make it difficult to identify subspecies on commonly used diagnostic characteristics, often leading to misidentification with other overlapping *Pteropus* species. It has long been suspected that the *hypomelanus* species complex included cryptic taxa, and questions have been raised as to the validity of the named subspecies. We tested these hypotheses using UCE target capture and mitogenomic data and included material from the type locality of *P. hypomelanus* and other key island populations. Our analyses suggest that *P. hypomelanus* is monophyletic and archipelagic *hypomelanus* lineages each have unique molecular signatures that may be a result of both evolution in isolated island environments and historical introgression with co-occurring *Pteropus* species. To build on this understanding of the species complex in the future, we plan to include historical museum species of other *hypomelanus* subspecies and of the closely allied *P. melanotus* and *P. griseus* species complexes.

Energetics and Foraging Behavior of the Mexican Fishing Bat during Lactation

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The fishing bat *Myotis vivesi* is endemic to desert islands and shores in the Gulf of California where season and daily ambient conditions are extremely variable. Another particularity of these bats is that they fish in the open ocean where food is randomly distributed, so individuals must optimize their search for prey each night. Additionally, during periods energetically expensive such as lactation, bats must invest in tissue production and parental care until weaning, which might represent an important energetic challenge. Accordingly, we hypothesized that energetic expenditure in these animals should increase as lactation period progresses, declining with weaning. We measured daily energy expenditure (DEE) of lactating individuals using doubly labeled water technique. To account for other factors affecting the energetics of bats, we measured time spent foraging, distance traveled each night and ambient temperature, wind speed, and relative humidity. Foraging duration and distance were measured by fitting each bat with a miniature GPS. Our results showed that DEE averaged 57 kJ, from which 70% were allocated to foraging activities. The DEE increased as lactation advanced and was positively correlated with pups' forearms. Individual foraging averaged 6 hours with a total mean distance of ~65 km. This time spent foraging did not increase as lactation advanced, suggesting it is associated with other variables such as food availability, but further studies are needed. We also recommend further energetics studies including milk output, males and other year seasons, to better understand energetics of these bats.

Influence of Farm Structure on Insectivorous Bat Activity in the Vaca Forest Reserve, Belize

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In many agroecosystems, insectivorous bats are predators of crop pests. As a result, they are assumed to provide benefits through pest suppression and facilitation of crop production. As part of the USDA's Research and Extension Experiences for Undergraduates Program, we investigated insectivorous bat activity on farms in the Vaca Forest Reserve (VFR), Belize. The VFR is specifically managed to incorporate some agricultural use and farmers grow fruit and vegetable crops on land within the reserve's boundaries. Our objective was to understand how farm structure influences insectivorous bat activity, the goal being to develop management recommendations that might allow farmers to enhance the pest suppression services bats provide on their lands. During the summer of 2017, we deployed SM2+ acoustic bat detectors (Wildlife Acoustics, Maynard, USA) on 20 farms in the VFR. We programmed these detectors to recorded bat calls from sunrise to sunset for a period of 8 days. Concurrently, we also measured a variety of vegetation characteristics (e.g. canopy cover, stem density, crop richness) within a 0.01 ha plot centered on each detector to assess farm structure. Over the summer, we recorded >7,000 bat calls. We will present the results of our analyses examining the relationship between bat activity and farm structure.

Pollen Identification Provides Evidence that Pallid Bats Visit Agave Species in the Chihuahuan Desert

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Pallid bats, *Antrozous pallidus,* though primarily insectivorous gleaning predators, are known to consume nectar of cardón cactus, *Pachycereus pringlei*, and act as effective pollinators of this species in the Sonoran Desert. It is unknown whether a similar nectar feeding behavior may be occurring in the Chihuahuan Desert of southwest Texas, where several researchers have captured pallid bats covered in pollen. The species of pollen has not been identified. We collected pollen samples from pallid bats in Brewster County, Texas each month between April and August 2018. Clear tape was used to collect samples from the wing membrane on and around the 5th metacarpal. Cubes of glycerine and gelatin with fuchsin stain were used to collect, stain, and preserve the exine characteristics of pollen samples. Tape and cube samples were examined using light microscopy and photographed under 40x and 100x total

magnification. Of the 67 bats sampled 40 were found to have pollen densities ≥1 grain per mm^2 and of these 24 had high pollen densities between 19 and 158 grains per mm^2. We encountered most of the bats covered in high density of pollen in April and August. When compared to a pollen reference collection, the samples were similar in size and exine morphology to *Agave* pollen. Further analysis is needed to distinguish the pollen of the two species that occur in this region of Texas, *Agave havardiana* and *Agave lechuguilla*, and to determine if the pallid bat is consuming nectar from the flowers that it visits.

Studying Populations of *Myotis lucifugus* in Yellowstone National Park through High-frequency Radio-frequency Identification and Mark-resight Analyses

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The spread of white-nose syndrome in North America has created an urgent need to estimate population sizes and connectivity to evaluate the success of current conservation strategies and indicate where management action is required. Although numerous field methods and analytical tools are available for gathering and evaluating population-level data, the dearth of known hibernacula in western North America precludes the use of many of these strategies. Here, we present a novel approach for studying population ecology in the Rocky Mountains by using high-frequency radio-frequency identification (HF-RFID), in combination with an analytical approach previously unused to research bats. For use with these techniques, we subcutaneously implanted 301 female little brown myotis (*Myotis lucifugus*) in Yellowstone National Park with HF-RFID tags and installed 8 continuously scanning HF-RFID readers with 45 antennas inside three maternity roosts. We recorded 2,928,461 detections of 142 HF-RFID tagged bats between June 2017 and August 2018. Using mark-resight models utilizing data from HF-RFID detections and emergence counts, we estimated the pre-parturition population size at one building in 2017 to be 904.13 (95% CI = 775.47–1054.16). In 2018, we estimated this same population to be 715.38 (95% CI = 614.91–832. 25) and estimated a population at a second building to be 199.86 (95% CI = 172.71–231.98). This combination of HF-RFID and mark-resight models provide estimates with relatively narrow confidence intervals, allowing biologists to track long-term population trends and uncover aspects of little brown myotis ecology that will be essential for managing bats populations throughout the region.

Hoary Bats Swarm

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Swarming is a common behavior for many temperate-zone bat species. This behavior is characterized by aggregations of bats engaged in intense flight activity including chasing and social vocalizations. Although its precise function is unresolved and may vary among species and situations, swarming behavior has several unifying characteristics. Swarming occurs during the autumn as bats move between summer and winter habitat. Sex ratios at swarms are typically highly male-biased. Usually a small proportion of individuals hibernate at the same sites where they swarm. Individuals may show fidelity to particular swarming sites but turnover among individuals on consecutive nights at the swarming site is high. To date, swarming behavior has been observed in bats that hibernate in underground sites. Using evidence collected through infrared video, mark-recapture, radio-telemetry, GPS and data-logging tags since 2014, I propose that hoary bats exhibit many of the behaviors associated with swarming. However, in contrast to other swarming studies, the observed behaviors were dispersed over a 6 km stretch of stream channel in a redwood forest in northwestern California. These observations, in concert with observations of a minority of individuals overwintering at this site, serves to expand our knowledge of the behavioral ecology of hoary bats while blurring the distinction between migratory and hibernating bat species.

Using Epigenetic Clocks for Comparative Analyses of Bat Longevity

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Recorded lifespans of bats greatly exceed other placental mammals of similar body size. Moreover, considerable variation in lifespan is present among bats. In this talk, I will present a phylogenetic analysis of potential factors that could explain variation in lifespan among 90 species of bats, such as hibernation, roosting site, diet, sexual conflict –

as estimated by sexual dimorphism, and sociality. I will also describe a method for estimating the age of a bat that takes advantage of patterns of methylation on conserved regions of DNA that change in a predictable way over time. By measuring methylation scores across thousands of sites from individuals of known age a predictive relationship can be obtained. Development of such a "clock" should provide a way to determine the age of any wild bat without previous capture and marking and thereby greatly expand the scope of future longevity analyses.

Understanding Farmer Knowledge of and Attitudes Toward Bats in the Vaca Forest Reserve, Belize

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The Vaca Forest Reserve is a 16,339 ha multi-use reserve in western Belize that supports approximately 50 farming families in and adjacent to its borders. Farmers of the Vaca frequently interact with a variety of wild species, including at least 75 insectivorous, frugivorous, carnivorous, and sanguinivorous bat species. Conversations with farmers indicated they received training on trapping and poisoning bats in hopes of reducing rabies transmission to livestock. To reduce poisoning and promote bat conservation and knowledge of bat-related ecosystem services, we quantified farmer knowledge and attitudes toward bats. During summer 2018, we surveyed 44 farmers in and around the Vaca. The survey was 49 questions addressing knowledge of bat behavior; understanding of ecosystem services and disease risks associated with bats; and emotions and attitudes toward bats; and farmer sociodemographics. Farmers' attitudes toward bats were moderately negative, with farmers thinking they are ugly (70%), worthless (40%), and dangerous (43%). However, our results indicate that these feelings are likely due to economic damages rather than human health concerns. Results also suggest farmers' knowledge of disease risks associated with bats is low, though they interact with them almost daily. When asked about the need for management of bats, 57% of farmers who responded positively to management suggested killing or poisoning bats. In summer 2019, we will use our results to develop bat extension programming in collaboration with local conservation organizations. Additionally, data will be used to develop a global bat attitude and emotion scale that can be adapted to a variety of conditions.

Which Niche? Comparing Niche Metrics for Bat Diets across Prey Taxonomic Levels

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The use of high-throughput amplicon sequencing (HTAS) has transformed the analysis of generalist animal diets, providing identification of prey items that is both broader in overall scope and deeper in taxonomic resolution than was previously possible with morphological methods alone. However, the broader question of how to actually quantify dietary niche breadth based on molecular dietary data remains largely unanswered. To investigate the comparability of dietary niche breadth calculations, we conducted a meta-analysis of relevant literature on little brown (*Myotis lucifugus*) and big brown bat (*Eptesicus fuscus*) diets and used our own molecular analyses to assess total richness, Simpson's diversity, Levin's standardized niche breadth, and Pianka's measure of niche overlap. We calculated these metrics at several prey taxonomic levels, and also considered resource states that included all potential prey items for both bat species versus all potential prey items for each single species. From these analyses, our data suggest that 1) little brown bat dietary niche breadth is driven largely by variation within populations, whereas big brown bat dietary niche breadth was driven by individual niche breadth; and 2) the influence of little brown bats on the dietary niche of big brown bats is greater than the influence of big brown bats on little brown bats. Understanding the links between arthropodivorous bats and their prey remains a particularly salient question as these economically important predators face population declines from white-nose syndrome in North America and from other factors across the globe.

Niche Partitioning in *Carollia* Explained by Divergence in Diet and Olfaction
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Bat-plant mutualisms are critical for maintaining the diversity and distributions of tropical plants, but the strength of this mutualism and whether the interaction has evolved through selection is not well understood. Understanding the extent to which bats are adapted to locate and consume particular plant resources can reveal the evolutionary processes that have led to the evolution of mutualism. We collected fecal samples and sequenced the olfactory receptor repertoires of three sympatric species of *Carollia*, a bat genus that varies in its specialization on the soft fruits of *Piper* plants. We used Bayesian hierarchical modeling to estimate piper preferences based on seed abundances in fecal samples and compared the olfactory receptor repertoires among *Carollia*. The most dedicated *Piper* specialist, *Carollia castanea,* demonstrated a strong preference for three piper plants specifically not preferred by the generalist species and had a unique set of olfactory receptors not shared by the generalist, which may enable the detection of its primary resource to an extent that the other species cannot. Surprisingly, *perspicillata*, the species with the most generalized diet, had a lower diversity of functional receptors, which may result from either a genetic bottleneck or neutral evolution and loss of some receptors. Future work on population dynamics within *Carollia* will shed light on this pattern. Olfactory receptor variation may be a factor in the coexistence of these sympatric species, facilitating the exploitation of different resources. Our study illuminates how gene duplication structures dietary adaptations and reinforces patterns of mutualism interactions between bats and plants.

Bringing the Museum to the High-school Classroom with 3D-printed Bat Skulls
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The examination of biological specimens is critical for students' understanding of anatomy. Whereas teaching collections and commercially available specimens often are sufficient for demonstrating the salient characteristics of higher-level taxa and of representative organisms (i.e., those organisms commonly studied in survey courses), museum collections are much more useful for illustrating the features that distinguish related groups and the variation within species or populations. Nonetheless, often only researchers with experience are permitted hands-on access to museum collections, and working in museums can be constrained by distance to collections, the time and financial costs of travel, and the availability of museum staff. The expanding availability of shared museum resources—such as digitized catalogs, databases, and images—addresses many of these constraints but cannot take the place of hands-on observation and measurement of specimens. The high-school course in Vertebrate Evolution at Choate Rosemary Hall made use of CT images, shared by colleagues with access to museum collections, and on-site 3D-printing technology to create a custom set of phyllostomid bat crania used in an examination of ecomorphology. This novel use of increasingly available resources is recommended for expanding young scientists' access to biological specimens, improving students' ability to address unique and sophisticated morphological questions, and promoting an appreciation of the importance of museum collections.

Long-nosed Bats, Migration, and Parasitism
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Parasites are considered an important selective force acting on local populations and shaping communities and ecosystems. In a broad spectrum, a host represents not only the food resource for the parasite, it is also its habitat and a way to disperse. Host's behavior, geographical range, spatial movement and population density may impact parasitic transmission and parasite abundance, being important drivers of parasite variability, therefore our aim was to measure the variability and changes in parasitic loads among long-nosed bat species over their distribution ranges. From April 2017 to June 2018 we investigated the ectoparasites associations of two batflies species and wing mites in twelve caves along the migratory routes of Long-nosed bats. We inspected a total of 650 bats and collected more than 10,000 ectoparasites. We analyzed the data using General Linear Mixed Models, Molecular and Geometric Morphometric Analysis. Our preliminary results show that parasites tend to be more abundant on different host species at specific localities along their distribution, additionally, the larger host has more parasites than smaller

hosts. Other factors as the interaction between sex and reproductive status might have an important impact over parasitic abundance. Geometric morphometric shows evidence of coevolution and species divergence on wing mites, following the phylogeny of its host. Even though, our knowledge of main factors that shape the interactions between the bat hosts and its parasites remains elusive, bats and their parasites may play an important role in providing guidelines for conservation and a better understanding of the disease transmission and infectivity.

Ecological and Environmental Drivers of Variation in Bat Echolocation Calls

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Sensory traits are used by organisms to perceive and respond to information about their environment and their variation directly impacts individual fitness. Bat echolocation is an important sensory trait used for navigation and communication that influences species survival and reproduction. However, little is known about the patterns and causes of variation in bat echolocation pulses. Here, we analyzed the patterns and triggers for variation of echolocation pulses in 13 bat species. Animals were sampled using a standardized protocol across contrasting environments and geographic extent in Mexico. The resulting audio collection was manually annotated and call events were transformed to a constant dimensional feature representation composed by time/frequency samples at positions evenly spaced over the shape's longitude. We used Generalized Linear Mixed Effects Models to assess the influence of variables related to geography, environment, and evolutionary history over call variation. The influence of each predictor was estimated by grouping the calls by different taxonomic levels and guilds. Evolutionary variables had the largest coefficients within families, indicating greater influence over variation. The highest ranked coefficients at guild level were longitudinal range and mean annual precipitation. Genus and species levels had fewer predictors since some of the variables were constant for most cases and had maximum overall coefficients for latitudinal range and mean annual precipitation. Our study highlights the influence of evolutionary history and environmental discontinuities on call plasticity and how they influence calls based on different grouping levels.

RECENT LITERATURE

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ANATOMY/HISTOLOGY

Gol'din, P., L. Godlevska, and M. Ghazali. 2018. Age-related changes in the teeth of two bat species: Dental wear, pulp cavity and dentine growth layers. Acta Chiropterologica, 20(2): 519-530. **[**Schmalhausen Institute of Zoology, National Academy of Sciences of Ukraine, 15 Bogdan Khmelnytskyi Street, Kiev, 01030, Ukraine]

BEHAVIOR

Petersen, H., N. Finger, A. Bastian, and D. Jacobs. 2018. The behaviour and vocalisations of captive Geoffroy's horseshoe bats, *Rhinolophus clivosus* (Chiroptera: Rhinolophidae). Acta Chiropterologica, 20(2): 439-453. [Animal Evolution and Systematics Group, Department of Biological Sciences, University of Cape Town, Rondebosch, Cape Town, 7700, South Africa]

Wu, X., Y. Pang, B. Luo, M. Wang, and J. Feng. 2018**.** Function of distress calls in least horseshoe bats: A field study using playback experiments. Acta Chiropterologica, 20(2): 455-464. **[**Key Laboratory of Southwest China Wildlife Resources Conservation of Ministry of Education, China West Normal University, Nanchong 637009, China]

Zhao, X., T. Jiang, H. Liu, Y. Wang, Y. Liu, and J. Feng. 2019. Acoustic signalling of aggressive intent in the agonistic encounters of female Asian particoloured bats. Animal Behaviour, 149: 65-75. [jiangtl730@nenu.edu.cn]

BIOGEOGRAPHY

Barrios-Gómez, K. M., R. López-Wilchis, J. Díaz-Larrea, and L. M. Guevara-Chumacero. 2019. Spatial distribution of bat richness in Mexico at different taxonomic levels: biogeographical and conservation implications. Therya, 10(1): 11-23. [rlw@xanum.uam.mx]

CONSERVATION

Angell, R. L., S. D. Langton, M. A. MacDonald, J. Skates, and K. A. Haysom. 2019. The effect of a Welsh agri-environment scheme on bat activity: A large-scale study. Agriculture, Ecosystems and Environment, 275: 32-41. [karen.haysom@arc-trust.org]

Benvindo-Souza, M., R. E. Borges, S. M. Pacheco, and L. R. de Souza Santos. 2019. Genotoxicological analyses of insectivorous bats (Mammalia: Chiroptera) in central Brazil: The

oral epithelium as an indicator of environmental quality. Environmental Pollution, 245: 504-509. [lia.santos@ifgoiano.edu.br]

Nystrom, G. S., and V. J. Bennett. 2019. The importance of residential swimming pools as an urban water source for bats. Journal of Mammalogy, gyz020, https://doi.org/10.1093/jmammal/gyz020 [v.bennett@tcu.edu]

Starik, N., T. Göttert, E. Heitlinger, and U. Zeller. 2018. Bat community responses to structural habitat complexity resulting from management practices within different land use types — A case study from north-eastern Germany. Acta Chiropterologica**,** 20(2): 387-405. **[**Systematic Zoology Division, Albrecht Daniel Thaer-Institute of Agricultural and Horticultural Sciences, Humboldt-Universität zu Berlin, Unter den Linden 6, 10099 Berlin, Germany]

DEVELOPMENT/ONTOGENY

Varela-Boydo, F., L. G. Ávila-Torresagatón, A. Rizo-Aguilar, and J. A. Guerrero. 2019. Variation in echolocation calls produced by *Myotis velifer* (Chiroptera: Vespertilionidae) during postnatal development. Therya, 10(1): 55-58. [aguerrero@uaem.mx]

DISEASE

Benvindo-Souz, M., R. E. Borges, S. M. Pacheco, L. R. de Souza Santos. 2019. Micronucleus and other nuclear abnormalities in exfoliated cells of buccal mucosa of bats at different trophic levels. Ecotoxicology and Environmental Safety, 172: 120-127. [lia.santos@ifgoiano.edu.br]

McDougall, F., W. Boardman, M. Gillings, and M. Power. 2019. Bats as reservoirs of antibiotic resistance determinants: A survey of class 1 integrons in grey-headed flying foxes (*Pteropus poliocephalus*). Infection, Genetics and Evolution, 70: 107-113. [fiona.mcdougall@hdr.mq.edu.au]

Sánchez-Hernández, C., S. S. Zalapa, S. Guerrero, M. de L. Romero-Almaraz, L. M. Sil-Berra, G. D. Schnell. 2018**.** Ocular lesions and diseases in bats from Jalisco and Oaxaca, Mexico. Acta Chiropterologica, 20(2): 485-492. **[**Departamento de Zoología, Instituto de Biología, Universidad Nacional Autónoma de México, A.P. 70-153, Coyoacán, Ciudad de México, México]

Wolkers-Rooijackers, J. C. M., K. Rebmann, T. Bosch, and W. C. Hazeleger. 2018. Fecal bacterial communities in insectivorous bats from the Netherlands and their role as a possible vector for foodborne diseases. Acta Chiropterologica, 20(2): 475-483. [judith.wolkers-rooijackers@wur.nl]

DISTRIBUTION/FAUNAL STUDIES

De Carvalho, W. D., L. A. C. Gomes, I. J. De Castro, A. C. Martins, C. E. L. Esbérard, and K. Mustin. 2018. Beyond the Amazon forest: richness and abundance of bats in the understory of savannahs, campinaranas and terra firme forest. Acta Chiropterologica, 20(2): 407-419. **[**Programa de Pós-Graduação em Biodiversidade Tropical, Universidade Federal do Amapá, Rodovia Juscelino Kubitscheck, S/N, Jardim Marco Zero 68903-419, Macapá, Amapá, Brazil]

Hoppe, J. P. M., G. Marchezi, and A. D. Ditchfield. 2019. First record of the white-winged vampire bat, *Diaemus youngii* (Jentink, 1893) (Chiroptera, Phyllostomidae) for the state of Goiás, Brazil, with a revised distribution map. Check List, 15(1): 55-64. [jpmhoppe@gmail.com]

Kazakov, D, A. Shumkina, A. Botvinkin, and O. Morozov. 2018**.** Bat swarming in the eastern Palaearctic (eastern Siberia). Acta Chiropterologica, 20(2): 427-438. **[**International Complex Research Laboratory for Study of Climate Change, Land Use and Biodiversity, Tyumen State University, 25 Lenin Street, 625003 Tyumen, Russia]

Layng, A. M., A. M. Adams, D. E. Goertz, K. W. Morrison, B. A. Pond, and R. D. Phoenix. 2019. Bat species distribution and habitat associations in northern Ontario, Canada. Journal of Mammalogy, 100(1): 249-260. [am.layng@gmail.com]

Palacios-Mosquera, L., Y. del C. Copete-Mosquera, A. M. Jiménez-Ortega, H. Mantilla-Meluk, and P. M. Velazco. 2019. New record of *Artibeus aequatorialis* Andersen, 1906 (Chiroptera: Phyllostomidae) for northwestern Colombia. Therya, 10(1): 45-47. [lepamo8@gmail.com]

Soares, F. A. M., P.A. da Rocha, A. Bocchiglieri, and S. F. Ferrari. 2018. Structure of a bat community in the xerophytic Caatinga of the state of Sergipe, Northeastern Brazil. Mammalia, 83(2): 125-133. [fabiosoares9@gmail.com]

Willig, M. R., S. J. Presley, J.-L. Plante, C. P. Bloch, S. Solari, V. Pacheco, and S. C. Weaver. 2019. Guild-level responses of bats to habitat conversion in a lowland Amazonian rainforest: species composition and biodiversity. Journal of Mammalogy, 100(1): 223-238. [michael.willig@uconn.edu]

ECHOLOCATION

Ren, M., H. Sun, S. Bo, S. Zhang, and P. Hua. 2018. Parallel amino acid deletions of prestin protein in two dramatically divergent bat lineages suggest the complexity of the evolution of echolocation in bats. Acta Chiropterologica, 20(2): 311-317.

ECOLOGY

Anthony, C. R., and D. M. Sanchez. 2019. Resource selection and space use of *Myotis evotis* in a western juniper woodland in Oregon. Journal of Mammalogy, 100(1): 239-248. [Dana.Sanchez@oregonstate.edu]

Flores-Abreu, I. N., R. E. Trejo-Salazar, L. L. Sánchez-Reyes, S. V. Good, S. Magallón, A. Garcíza-Mendoza, and L. E. Eguiarte. 2019. Tempo and mode in coevolution of *Agave sensu lato* (Agavoideae, Asparagaceae) and its bat pollinators, Glossophaginae (Phyllostomidae). Molecular Phylogenetics and Evolution, 133: 176-188. [fruns@unam.mx]

Kipson, M., M. Šálek, R. Lučan, M. Uhrin, E. Maxinová, T. Bartonička, M. Andreas, K. Kipson, A. Pušić, D. Rnjak, L. Naďo, and I. Horáček. 2018. Foraging habitat, home-range size and diet

of a Mediterranean bat species, Savi's pipistrelle. Acta Chiropterologica, 20(2): 351-360. [Department of Zoology, Faculty of Science, Charles University in Prague, Viničná 7, 128 44 Prague, Czech Republic]

Maas, B., S. Heath, I. Grass, C. Cassano, A. Classen, D. Faria, P. Gras, K.Williams-Guillén, M. Johnson, D. S. Karp, V. Linden, A. Martínez-Salinas, J. M. Schmack, and S. Kross. 2019. Experimental field exclosure of birds and bats in agricultural systems —Methodological insights, potential improvements, and cost-benefit trade-offs. Basic and Applied Ecology, 35: 1-12**.** **[**beamaas@gmx.at]

Michaelsen, T. C., K. H. Jensen, and G. Högstedt. 2018. Does light condition affect the habitat use of soprano pipistrelles *Pipistrellus pygmaeus* at the species northern extreme? Acta Chiropterologica, 20(2): 377-385. [Department of Biology, University of Bergen, P.O. Box 7800, NO-5020 Bergen, Norway]

Parolin, L. C., F. A. Hansel, G. V. Bianconi, and S. B. Mikich. 2019. Chemical compounds in Neotropical fruit bat-plant interactions. Mammalian Biology, 94: 92-97. [lays.parolim@pucpr.br]

Ruadreo, N., C. C. Voigt, and S. Bumrungsri. 2018. Large dietary niche overlap of sympatric open-space foraging bats revealed by carbon and nitrogen stable isotopes. Acta Chiropterologica, 20(2): 329-341. [sara.b@psu.ac.th]

Rydell, J., J. Eklöf, H. Fransson, and S. Lind. 2018**.** Long-term increase in hibernating bats in Swedish mines — Effect of global warming? Acta Chiropterologica, 20(2): 421-426. [Biology Department, Lund University, SE-223 62 Lund, Sweden]

Slider, R., and A. Kurta. 2018. Big brown bat trapped by common burdock. Michigan Birds and Natural History, 25(1&2): 5-7. [rslider5@ycschools.us]

Smith, P. G. and P. A. Racey. 2018. The itinerant Natterer: Dynamics of summer roost occupancy by *Myotis nattereri* (Chiroptera, Vespertilionidae). Acta Chiropterologica, 20(2) 361-376. [p.racey@abdn.ac.uk]

Torres-Flores, J. W., and R. López-Wilchis. 2018**.** Trophic niche and diet of *Natalus mexicanus* (Chiroptera: Natalidae) in a tropical dry forest of western Mexico. Acta Chiropterologica, 20(2): 343-350. **[**Departamento de Biología, Universidad Autónoma Metropolitana Iztapalapa, Avenida San Rafael Atlixco No. 186, Col. Vicentina, Del. Iztapalapa, C.P. 09340, Ciudad de México, México]

EVOLUTION

Rakotoarivelo A. R, S. M. Goodman, M. C. Schoeman, and S. Willows-Munro. 2019. Phylogeography and population genetics of the endemic Malagasy bat, *Macronycteris commersoni* s.s. (Chiroptera: Hipposideridae) PeerJ 7:e5866 https://doi.org/10.7717/peerj.5866. [andrinajoro@moov.mg]

HIBERNATION

Haase, C. G., N. W. Fuller, C. R. Hranac, D. T.S. Hayman, S. H. Olson, R. K. Plowright, and L. P. McGuire 2019. Bats are not squirrels: Revisiting the cost of cooling in hibernating mammals. Journal of Thermal Biology, 81: 185-193. [catherine.haase@montana.edu]

IMMUNOLOGY

Cabrera-Martinez, L. V., L. G. Herrera M., and A. P. Cruz-Neto. 2019. Food restriction, but not seasonality, modulates the acute phase response of a Neotropical bat. Comparative Biochemistry and Physiology (A), 229: 93-100. [gherrera@ib.unam.mx]

Ruoss, S., N. I. Becker, M. S. Otto, G. Á. Czirják, and J. A. Encarnação. 2019. Effect of sex and reproductive status on the immunity of the temperate bat *Myotis daubentonii*. Mammalian Biology, 94:120-126. [J.Encarnacao@bio.uni-giessen.de]

PALEONTOLOGY

Czaplewski, N. J., G. S. Morgan, and R. A. Martin. 2018. New specimens of Pliocene bats (Mammalia, Chiroptera, Vespertilionidae and Molossidae) from the Meade Basin, Kansas, U.S.A. Journal of Vertebrate Paleontology, 38:2, DOI: 10.1080/02724634.2018.1430034. [nczaplewski@ou.edu]

PARASITOLOGY

Barros, J. H. S., L. Lima, A. O. Schubach, and M. M.G. Teixeira. 2019. *Trypanosoma madeirae* sp. n.: A species of the clade *T. cruzi* associated with the neotropical [sic] common vampire bat *Desmodus rotundus*. International Journal of Parasitology: Parasites and Wildlife, 8: 71-81. [juliana.barros@ioc.fiocruz.br]

Durán, A. A., R. A. Saldaña-Vázquez, G. Graciolli, and L. C. Peinado. 2018. Specialization and modularity of a bat fly antagonistic ecological network in a dry tropical forest in northern Colombia. Acta Chiropterologica, 20(2): 503-510. **[**Grupo de Investigación en Zoología y Ecología Universidad de Sucre, Sincelejo — Sucre, Colombia]

Holz, P. H., L. F. Lumsden, A. R. Legione, and J. Hufschmid. 2019. *Polychromophilus melanipherus* and haemoplasma infections not associated with clinical signs in southern bent-winged bats (*Miniopterus orianae bassanii*) and eastern bent-winged bats (*Miniopterus orianae oceanensis*). International Journal of Parasitology: Parasites and Wildlife, 8:10-18. [holzp@student.unimelb.edu.au]

Reeves, W. K., and J. E. Lloyd. 2019. Chapter 20 – Louseflies, keds, and bat flies (Hippoboscoidea). Pp. 421-438 in G. R. Mullen and L. A. Durden (Eds.), Medical and Veterinary Entomology (3rd Edition), Academic Press, 792 pp. [ISBN 978-0-12-814043-7]

Rodrigues, M. S., L. Lima, S. C. das Chagas Xavier, H. M. Herrera, F. L. Rocha, A. L. R. Roque,

M. M. G. Teixeira, and A. M. Jansen. 2019. Uncovering *Trypanosoma* spp. diversity of wild mammals by the use of DNA from blood clots. International Journal of Parasitology: Parasites and Wildlife, 8: 171-181. [jansen@ioc.fiocruz.br]

Urbieta, G. L., J. M. Torres, E. A. C. Dos Anjos, C. M. E. Carvalho, and G. Graciolli. 2018. Parasitism of bat flies (Nycteribiidae and Streblidae) on bats in urban environments: Lower prevalence, infracommunities, and specificity. Acta Chiropterologica, 20(2): 511-518. **[**Programa de Pós-Graduação em Biologia Animal, Laboratório de Sistemática, Ecologia e Evolução (LSEE), Instituto de Biociências (INBIO), Universidade Federal de Mato Grosso do Sul (UFMS), 79090-900, Campo Grande, MS, Brazil]

Wang, L-J. H.-J. Hana, M. Zhao, J.-W. Liu, L.-M. Luo, H.-L. Wen, X.-R. Qin, C.-M. Zhou, R. Qi, H. Yu, and X.-J. Yu. 2019. *Trypanosoma dionisii* in insectivorous bats from northern China. Acta Tropica, 193: 124-128. [yuxuejie@whu.edu.cn]

PHYSIOLOGY

Pretorius, M., T. Kearney, M. Keith, W. Markotter, E. Seamark, and H. Broders. 2018. Increased body mass supports energy compensation hypothesis in the breeding female Natal long-fingered bat *Miniopterus Natalensis* [sic]. Acta Chiropterologica, 20(2): 319-328. [hugh.broders@smu.ca]

REPRODUCTION

Campolina-Silva, G. H., R. A. Hess, and C. A. Oliveira 2019. Seasonal variation of cell proliferation and apoptosis in the efferent ductules and epididymis of the Neotropical bat *Artibeus lituratus* (Chiroptera, Phyllostomidae). General and Comparative Endocrinology, 273: 3-10. [cleida@icb.ufmg.br]

Viana, P. I. M., T. O. Farias, S. A. Talamoni, and H. P. Godinho. 2018. Sertoli cell efficiency of the Neotropical bats *Anoura geoffroyi*, *Artibeus lituratus* and *Myotis levis* (Mammalia: Chiroptera). Acta Chiropterologica, 20(2): 493-501. **[**Programa de Pós-graduação em Biologia de Vertebrados, Departamento de Ciências Biológicas, Pontifícia Universidade Católica de Minas Gerais, Avenida Dom José Gaspar, 500, Belo Horizonte, Minas Gerais, Brazil]

TAXONOMY/SYSTEMATICS/PHYLOGENETICS

Görföl, T., N. M. Furey, P. J. J. Bates, and G. Csorba. 2018. The identity of '*Falsistrellus' affinis* from Myanmar and Cambodia and new records of *Hypsugo dolichodon* from these countries. Acta Chiropterologica, 20(2): 301-309. [gorfol.tamas@nhmus.hu]

Javier Juste, J., M. Ruedi, S. J. Puechmaille, I. Salicini, and C. Ibáñez. 2018. Two new cryptic bat species within the *Myotis nattereri* species complex (Vespertilionidae, Chiroptera) from the western Palaearctic. Acta Chiropterologica, 20(2): 285-300. [juste@ebd.csic.es]

Lausen, C. L., M. Proctor, D. W. Nagorsen, D. Burles, D. Paetkau, E. Harmston, K. Blejwas, P. Govindarajulu, and L. Friis. 2019. Population genetics reveal *Myotis keenii* (Keen's myotis) and

Myotis evotis (long-eared myotis) to be a single species. Canadian Journal of Zoology, 97(3): 267-279. [corilausen@netidea.com]

Martínez-Cerón, J. M., E. Patiño-Castillo, S. Carvalho-Madrigal, and J. F. Díaz-Nieto. 2019. Molecular and morphological identification of *Phylloderma stenops* Peters, 1865 (Chiroptera, Phyllostomidae) and new records for Colombia. Check List 15 (1): 37–44. [juanmceron@gmail.com]

Najafi, N., V. Akmali, and M. Sharifi. 2019. Historical explanation of genetic variation in the Mediterranean horseshoe bat *Rhinolophus euryale* (Chiroptera: Rhinolophidae) inferred from mitochondrial cytochrome-b and D-loop genes in Iran. Mitochondrial DNA (Part A), 30: 135-147. [sharifimozafar2012@gmail.com]

Sánchez, R. T., M. E. Montani, I. H. Tomasco, M. M. Díaz and R. M. Barquez. 2019. A new species of *Eptesicus* (Chiroptera, Vespertilionidae) from Argentina. Journal of Mammalogy, 100(1): 118-129. [mmonicadiaz@yahoo.com.ar]

Velazco, P. M., L. Guevara, and J. Molinari. 2018. Systematics of the broad-nosed bats, *Platyrrhinus umbratus* (Lyon, 1902) and *P. nigellus* (Gardner and Carter, 1972) (Chiroptera: Phyllostomidae), based on genetic, morphometric, and ecological niche analysis. Neotropical Biodiversity, 4(1): 119-133. [pvelazco@amnh.org]

TECHNIQUES FOR STUDYING BATS

Richardson, S. M. P. R. Lintott, D. J. Hosken, and F. Mathews. 2019. An evidence-based approach to specifying survey effort in ecological assessments of bat activity. Biological Conservation, 231: 98-102. [F.Mathews@sussex.ac.uk]

Rojas, V. G., S. C. Loeb, and J. M. O'Keefe. 2019. False-positive occupancy models produce less-biased occupancy estimates for a rare and elusive bat species. Journal of Mammalogy, 100(1): 212-222. [vanessaxrojas@gmail.com]

Suárez, P., A. Iglesias, and A. Gálvez. 2019. Make robots be bats: specializing robotic swarms to the Bat algorithm. Swarm and Evolutionary Computation, 44: 113-129. [iglesias@unican.es]

Womack-Bulliner, K. M., S. K. Amelon, F. R. Thompson, and J. J. Lebrun. 2018. Performance of hierarchical abundance models on simulated bat capture data. Acta Chiropterologica, 20(2): 465-474. **[**Missouri Department of Conservation, Northeast Regional Office, 3500 S. Baltimore Street, Kirksville, MO 63501, USA]

VIROLOGY

Guzmán, C., A. Calderón, C. Martinez, M. Oviedo, and S. Mattar. 2019. Eco-epidemiology of the Venezuelan equine encephalitis virus in bats of Córdoba and Sucre, Colombia. Acta Tropica, 191, 178-184. [mattarsalim@hotmail.com]

Lin-Fa Wang and Danielle E Anderson. 2019. Viruses in bats and potential spillover to animals and humans. Current Opinion in Virology, 34: 79–89. [linfa.wang@duke-nus.edu.sg]

Yu, P., B. Hu, Z.-L. Shi, and J. Cui. 2019. Geographical structure of bat SARS-related coronaviruses. Infection, Genetics, and Evolution, 69: 224-229. [jiecui@wh.iov.cn]

ANNOUNCEMENTS

Reminder—Renewal Time!

Just a reminder that this is the last issue of the 2018 series of *Bat Research News*. That means some of you will be receiving renewal information in your e-mail inbox fairly soon. We hope you will continue to support *BRN* for the 2019 volume-year.

Back Issues

Are you missing any back issues of the print edition of *Bat Research News*? If you would like to replace them, please contact Margaret Griffiths (margaret.griffiths01@gmail.com). Most are available from Volume 45, 2004 to Volume 58, 2017. Depending on what you need, we may ask you to cover postage. Beginning in 2019, we will be reducing the inventory of back issues, beginning with the oldest (i.e., Vol. 45: no. 2, 2004).

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Original research/speculative review articles, short to moderate length, on a bat-related topic would be most welcomed. Please submit manuscripts as .rtf documents to Allen Kurta, Editor for Feature Articles (akurta@emich.edu). Also please consider submitting short articles, notes, or letters on a bat-related topic. If you have questions, please contact Al. Thank you for considering *BRN*.

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FUTURE MEETINGS and EVENTS

2019

The 18th International Bat Research Conference (IBRC) will be held 28 July–2 August 2019, in Phuket, Thailand , at the Slate. Registration and abstract submission are open. Please visit the IBRC website for information — https://www.ibrc2019.com/.

The 49th Annual NASBR will be held 23–26 October 2019, in Kalamazoo, Michigan, at the Radisson Plaza Hotel & Suites. Check the NASBR website for future updates — http://www.nasbr.org/.

2020

The 15th European Bat Research Symposium will be held 3–7 August 2020, in Turku, Finland. Please visit https://www.ebrs2020.fi/ for updates and information.

The NASBR will celebrate their 50th anniversary where it all began, in Arizona. The annual meeting will be held 28–31 October 2020, in Tempe, Arizona. The NASBR also plans to publish an edited volume that highlights bat biology research to coincide with their 50th annual meeting. Check the NASBR website for more information and future updates — http://www.nasbr.org/.

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Gray Bats (*Myotis grisescens*) in storm drain under the city park in Eldorado Springs, Cedar County, Missouri. Photo by Lynn Robbins. Thanks for sharing, Lynn!

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Bat Research News is published four times each year, consisting of one volume of four issues. *Bat Research News* publishes short feature articles and general interest notes that are reviewed by at least two scholars in that field. *Bat Research News* also includes abstracts of presentations at bat conferences around the world, letters to the editors, news submitted by our readers, notices and requests, and announcements of future bat conferences worldwide. In addition, *Bat Research News* provides a listing of recent bat-related articles that were published in English. *Bat Research News* is abstracted in several databases (e.g., BIOSIS).

Communications concerning feature articles and "Letters to the Editor" should be addressed to Dr. Al Kurta (akurta@emich.edu), recent literature items to Dr. Tom Griffiths (thomas.alan.griffiths@gmail.com), and all other correspondence (e.g., news, conservation, or education items; subscription information; cover art) to Dr. Margaret Griffiths (margaret.griffiths01@gmail.com).

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An Overlooked Specimen of the Brazilian Funnel-eared Bat (*Natalus macrourus*) from the Early 19th Century

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The Brazilian Funnel-eared Bat (*Natalus macrourus*) was first described by Paul Gervais in 1855 (Gervais, 1856a, 1856b), based on a single specimen collected in Bahia, Brazil, during the expedition of 1843–1847 by Francis de Castelnau. Gervais named it *Spectrellum macrourum*, although the species was later placed in the genus *Natalus* (Dobson, 1878). Over time, the species was variously referred to as *N. stramineus* and *N. espiritosantensis*, although the nomenclatural confusion was eventually settled by Garbino and Tejedor (2013).

Today, *N. macrourus* is the most southerly species of this New World genus and is the only one found south of the Amazon River (Delgado-Jaramillo et al., 2018; da Rocha et al., 2013; Taddei and Uieda, 2001; Tejedor, 2006, 2011). Although it has a wider geographic distribution than other species in the genus, specimens of *N. macrourus* are few, and significant gaps occur within its known range. *N. macrourus* has been negatively affected by habitat loss and degradation, and this mammal is listed as near threatened by the International Union for the Conservation of Nature and is one of Brazil's most threatened bats (Teixeira, 2014). In this note, we describe a specimen of this rare species that pre-dates the original description by Gervais.

The Finnish naturalist Reinhold Ferdinand Sahlberg (1811–1874) made two expeditions to Brazil during the 19th century (Huldén, 2011; Saalas, 1958). Sahlberg was primarily an entomologist, but he also collected a few other animals, including about 30 mammals, some of which are in the collection of the Finnish Museum of Natural History (FMNH) in Helsinki. During his first visit to Brazil in September–October 1840, Sahlberg spent a few weeks in the area of Rio de Janeiro. His second visit to Brazil was longer and lasted from September 1849 to January 1851. As before, Sahlberg mainly traveled in areas near Rio de Janeiro, including Pétropolis, but he also made some excursions to southern parts of the state of Minas Gerais (Saalas, 1958).

Sahlberg's Brazilian mammals include the single skin of a bat, which has FMNH catalog number UN 806 (Figure 1). The specimen is identified only as "Vespertilionidae," and the locality is simply given as "Brazil," with no date of collection. The bat is preserved with wings folded close to the body, although the left wing is slightly extended laterally and anteriorly. Ventrally, the belly has been opened, and the axial skeletal elements removed and replaced with cotton. The cranium remains inside the skin; the mouth is open, and part of the dentition is visible but not easily accessible for measurement. The specimen is a male, as evidenced by presence of a penis.

We encountered UN 806 during a general survey of bats in the FMNH in 2018 and identified it as *N. macrourus*, based on several characteristics. The ears display the typical nataline funnel-like ear shape (Tejedor, 2011;

Figure 1. Specimen UN 806. Main figure) Dorsal view of body. Inset) Frontal view of ears. Photos by K. Meramo.

Fig. 1), with a deeply concave medial margin and a greater maximum width than length (ca.10.2 mm and 9.0 mm, respectively, based on measurements of the dried skin). The pelage is uniformly yellowish brown. The rostrum is flat and triangular-shaped in dorsal view, and lacks a nose leaf. The caudal vertebrae are still in place, and the tail is long relative to the body, and although exact length cannot be determined, due to the tail being slightly curled, its length is ca. 48.6 mm and approximately equal to the combined head and body length of 49.1 mm. The tail does not extend beyond the uropatagium. Forearm length (39.9 mm) is consistent with published measurements of male *N. macrourus*, which range from 37.0 to 42.1 mm (Goodwin, 1959; Leal et al., 2012; da Silva et al., 2015; Taddei and Uieda, 2001; Tejedor, 2006, 2011). We acknowledge that the various species of *Natalus* are superficially quite similar to each other and that *N. macrourus* has been described as lacking "external and cranial diagnostic features" (Tejedor, 2011:43), but only this member of the genus has ever been recorded from the parts of Brazil that Sahlberg is known to have visited.

Although the exact locality is unknown, UN 806 almost certainly originated from southeastern Brazil. It also is unknown whether this individual was collected during Sahlberg's first Brazilian expedition of 1840 or during his second expedition of 1849–1851. However, the latter is more probable, because Sahlberg brought skins of Brazilian mammals to Finland from that expedition (Saalas, 1958). Nevertheless, UN 806 remains one of the earliest collected individuals of *N. macrourus*, pre-dating publication of the scientific description of the species (Gervais, 1856a, b). Even today, *N. macrourus* is rare in zoological collections (Delgado-Jaramillo et al., 2018; Tejedor, 2011) and appears rare and possibly endangered in the wild, so the existence of this overlooked specimen is of historical interest, as one of the earliest scientifically collected individuals of *N. macrourus*.

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Literature Cited

Delgado-Jaramillo, M., E. Barbier, and E. Bernard. 2018. New records, potential distribution, and conservation of the near threatened cave bat *Natalus macrourus* in Brazil. Oryx, 52:579–586.

Dobson, G. E. 1878. Catalogue of the Chiroptera in the collection of the British Museum. Taylor and Francis, London, United Kingdom.

Garbino, G. S. T., and A. Tejedor. 2013. *Natalus macrourus* (Gervais, 1856) (Chiroptera: Natalidae) is a senior synonym of *Natalus espiritosantensis* (Ruschi, 1951). Mammalia, 77:237–240.

Gervais, P. 1856a. Deuxième mémoire. Documents zoologiques pour servir à la monographie des chéiroptères sud-américains. Pp. 25–88 *in* Animaux nouveaux ou rares recueillis pendant l'expédition dans les parties centrales de l'Amérique du Sud, de Rio de Janeiro à Lima, et de Lima au Para (F. de Castelnau, ed.). P. Bertrand, Paris, France.

Gervais, P. 1856b. Documents zoologiques pour servir à la monographie de chéiroptères sud-américains. Comptes Rendus de l'Académie des Sciences, Paris, 42:1–11.

Goodwin, G. G. 1959. Bats of the subgenus *Natalus*. American Museum Novitates, 1977:1–22.

Huldén, L. 2011. Reinhold Ferdinand Sahlberg och historia naturalis. Pp. 41–53 *in* R. F. Sahlberg: Anteckningar från en resa kring jorden 1839–1843 (P. Berg, ed.). Svenska litteratursällskapet i Finland, Helsingfors, Finland.

Leal, E. S. B., D. de F. Ramalho, B. G. Miller, P. de B. P. Filho, J. G. do P. Neto, F. V. P. V. Nova, R. M. de Lyra-Neves, G. J. B. de Moura, and W. R. Telino-Júnior. 2012. Primeiro registro da família Natalidae (Mammalia: Chiroptera) para a Caatinga do Estado da Paráiba, Nordeste do Brasil. Revista Brasileira de Zoociências, 14:243–253.

da Rocha, P. A., J. Simanas Mikalauskas, A. Bocchiglieri, J. Anderson Féijo, and S. F. Ferrari. 2013. An update on the distribution of the Brazilian funnel-eared bat, *Natalus macrourus* (Gervais, 1856) (Mammalia, Chiroptera), with new records from the Brazilian northeastern. Check List, 9:675–679.

Saalas, U. 1958. Reinhold Ferdinand Sahlberg: tutkimusmatkailija, luonnontieteilijä, lääkäri ja tilanomistaja 1811–1874. Acta Entomologica Fennica, 14:1–255.

da Silva, S. S. P., D. Dias, M. A. Martins, P. G. Guedes, J. C. de Almeida, A. P. da Cruz, N. M. Serra-Freire, J. dos S. Damascena, and A. L. Peracchi. 2015. Bats (Mammalia: Chiroptera) from the Caatinga scrublands of the Crateus Region, northeastern Brazil, with new records for the State of Ceará. Mastozoologica Neotropical, 22:335–348.

Taddei, V. A., and W. Uieda. 2001. Distribution and morphometrics of *Natalus stramineus* from South America (Chiroptera, Natalidae). Iheringia, Série Zoologia, 91:123–132.

Teixeira, I. 2014. Portaria n° 444, de 17 de dezembro de 2014. Available at: http://www.icmbio.gov.br/sisbio/images/stories/instrucoes_normativas/PORTARIA_Nº_444_DE_17_DE_DEZEMBRO_DE_2014.pdf.

Tejedor, A. 2006. The type locality of *Natalus stramineus* (Chiroptera: Natalidae): implications for the taxonomy and biogeography of the genus *Natalus*. Acta Chiropterologica, 8:361–380.

Tejedor, A. 2011. Systematics of funnel-eared bats (Chiroptera: Natalidae). Bulletin of the American Museum of Natural History, 353:1–140.

RECENT LITERATURE

Authors are requested to send reprints (PDF files) of their published papers to the Editor for Recent Literature, **Dr. Thomas A. Griffiths**, (e-mail: **thomas.alan.griffiths@gmail.com**) for inclusion in this section. Receipt of reprints is preferred, as it will facilitate complete and correct citation. However, if reprints and/or PDF files are unavailable, please send a complete citation (including complete name of journal and corresponding author e-mailing address) by e-mail. The Recent Literature section is based on several bibliographic sources and for obvious reasons can never be up-to-date. Any error or omission is inadvertent. Voluntary contributions for this section, especially from researchers outside the United States, are most welcome and appreciated.

ANATOMY/HISTOLOGY

Aoyama, A., N. Kurihara, and S. Sugita. 2019. Innervation of wing membrane in Japanese little horseshoe bats, *Rhinolophus cornutus*. Journal of Veterinary Medical Science, 81(5): 653-656. [no e-mail provided]

Bernardi, L. F. O., X. Prous, M. S. Ribeiro, J. Mascarenhas, S. M. C. Genelhú, M. H. Simões, and T. Bezerra. 2019. First record of albinism for the doglike bat, *Peropteryx kappleri* Peters, 1867 (Chiroptera, Emballonuridae). Subterranean Biology, 30: 33–40. https://doi.org/10.3897/subtbiol.30.34223 [leopoldobernardi@gmail.com]

Cristancho, P., and D. Steven. 2019. Descripción y comparación morfométrica, morfológica externa e histológica de la hoja nasal en *Carollia brevicauda* y *C. perspicillata* (Chiroptera: Phyllostomidae). Licenciatura en Biologia: http://hdl.handle.net/11349/14975. [no email provided]

Dragu, A., G. Csorba, and R. Bancila. 2019. Ecological character displacement in mandibular morphology of three sympatric horseshoe bats. Hystrix, the Italian Journal of Mammalogy, doi:10.4404/hystrix-00120-2018 [bancila_ralucaioana@yahoo.com]

El-Mansi, A. A., M. A. Al-Kahtani, and M. M. A. Abumandour. 2019. Comparative phenotypic and structural adaptations of tongue and gastrointestinal tract in two bats having different feeding habits captured from Saudi Arabia: Egyptian fruit bat (*Rousettus aegyptiacus*) and Egyptian tomb bat (*Taphozous perforatus*). Zoologischer Anzeiger, 281: 24-38. [aelmansi@kku.edu.eg]

Falana, B. A., and K. E. Olubayode. 2019. Comparative anatomy of the heart and lungs of the rat (*Rattus norvegicus*), bat (*Manis tricuspis*) [*sic*], and pangolin (*Eidolon helvum*) [*sic*]. Journal of Surgical Research and Therapeutics, 2(1): 11-16. [benedict.falana@uniosun.edu.ng]

Santana, S. E., J. H. Arbour, A. A. Curtis, and K. E. Stanchak. 2019. 3D digitization in functional morphology: where is the point of diminishing returns? Integrative and Comparative Biology,icz101, https://doi.org/10.1093/icb/icz101 [ssantana@uw.edu]

BEHAVIOR

Ancillotto, L., G. Venturi, and D. Russo. 2019. Presence of humans and domestic cats affects bat behaviour in an urban nursery of greater horseshoe bats (*Rhinolophus ferrumequinum*). Behavioural Processes, 164: 4-9. [danrusso@unina.it]

Zeppelini, C. G., L. M. M. Azeredo, and L. C. S. Lopez. 2019. Bats like dimmer lights: lunar phobia as a luminosity threshold phenomenon on Neotropical bats (Mammalia: Chiroptera). Acta Ethologica, 22(2): 125-128. [czeppelini@gmail.com]

BIOGEOGRAPHY

Barrios-Gómez, K. M., R. López-Wilchis, J. Díaz-Larrea, and L. M. Guevara-Chumacero. 2019. Spatial distribution of bat richness in Mexico at different taxonomic levels: biogeographical and conservation implications. Therya, 10(1): 11-23. [rlw@xanum.uam.mx]

Onstein, R. E., W. D. Kissling, L. Chatrou, and T. L. P. Couvreur, H. Morlon, and H. Sauquet. 2019. Which frugivory-related traits facilitated historical long-distance dispersal in the custard apple family (Annonaceae)? Journal of Biogeography. DOI 10.1111/jbi.13552. [onsteinre@gmail.com]

CONSERVATION

Alpízar, P, B. Rodríguez-Herrera, and K. Jung. 2019. The effect of local land use on aerial insectivorous bats (Chiroptera) within the two dominating crop types in the Northern-Caribbean lowlands of Costa Rica. PLoS ONE 14(1): e0210364. https://doi.org/10.1371/journal.pone.0210364, [prialp55@gmail.com]

Alston, J. M., I. M. Abernethy, D. A. Keinath, and J. R. Goheen. 2019. Roost selection by male northern long-eared bats (*Myotis septentrionalis*) in a managed fire-adapted forest. Forest Ecology and Management, 446: 251-256. [jalston@uwyo.edu]

Banner, K. M., K. M. Irvine, T. J. Rodhouse, D. Donner, and A. R. Litt. 2019. Statistical power of dynamic occupancy models to identify temporal change: Informing the North American Bat Monitoring Program. Ecological Indicators, 105: 166-176. [katharine.banner@montana.edu]

Briones-Salas, M., M. C. Lavariega, C. E. Moreno, and J. Viveros. 2019. Responses of phyllostomid bats to traditional agriculture in Neotropical montane forests of southern Mexico. Zoological Studies 58**:**9: 10 pp., doi:10.6620/ZS.2019.58-09. [jbv666999@hotmail.com]

Brook, C. E., H. C. Ranaivoson, D. Andriafidison, M. Ralisata, J. Razafimanahaka, J.-M. Heraud, A. P. Dobson, and C. J. Metcalf. 2019. Population trends for two Malagasy fruit bats. Biological Conservation, 234: 165-171. [cbrook@berkeley.edu]

Caldwell, K. L., T. C. Carter, and J. C. Doll. 2019. A comparison of bat activity in a managed central hardwood forest. The American Midland Naturalist, 181(2): 225-244. [tccarter@bsu.edu]

Cely-Gomez, M. A., and D. Castillo-Figueroa. 2019. Diet of dominant frugivorous bat species in an oil palm landscape from Colombian Llanos: implications for forest conservation and recovery. THERYA, 10(2): 149-153. [alejandracelygomez@gmail.com]

Claireau, F., Y. Bas, J. Pauwels, K. Barré, N. Machon, B. Allegrini, S. J. Puechmaille, and C. Kerbiriou. 2019. Major roads have important negative effects on insectivorous bat activity. Biological Conservation, 235: 53-62. [f.claireau@naturalia-environnement.fr]

Grilliot, M. E., J. L. Hunt, and C. G. Sims. 2018. Organochloride pesticides present in animal fur, soil, and streambed in an agricultural region of southeastern Arkansas. Journal of the Arkansas Academy of Science, 72 (19), https://scholarworks.uark.edu/jaas/vol72/iss1/19 [huntj@uamont.edu]

Hermes, R., T. B. Hildebrandt, F. Göritz, N. J. Fasel, and S. Holtze. 2019. First cryopreservation of phyllostomid bat sperm. Theriogenology, 131: 28-31. [hermes@izw-berlin.de]

Khan, F. A. A., N. Shazali, N. Latip, and I. Azhar. 2019. Into the heart of Borneo: mammals of Upper Baleh, Sarawak. Journal of Sustainability Science and Management, 14(2): 171-180. [akfali@unimas.my]

Lawson, K. J., C. L. Lausen, K. A. Mancuso, L. A. Volkmann, TJ Gooliaff, J. Hutchen, K. J. Teichman, A. J. Kelly, and K. E. Hodges. 2019. Bat activity and richness in beetle-killed forests in southern British Columbia. Journal of Mammalogy, 100: 510-517. [kirstie.lawson09@gmail.com]

Nystrom, G. S., and V. J. Bennett. 2019. The importance of residential swimming pools as an urban water source for bats. Journal of Mammalogy, 100: 394-400. [v.bennett@tcu.edu]

Rodríguez-San Pedro, A., C. Rodríguez-Herbach, J. L. Allendes, P. N. Chaperon, C. A. Beltrán, and A. A. Grez. 2019. Responses of aerial insectivorous bats to landscape composition and agave heterogeneity in organic vineyards. Agriculture, Ecosystems and Environment, 277: 74-82. [ar.sanpedro@gmail.com]

Umadi, R.; S. Dookia, and J. Rydell. 2019. The monumental mistake of evicting bats from archaeological sites—a reflection from New Delhi. Heritage, 2: 553-567. [jens.rydell@telia.com]

DEVELOPMENT/ONTOGENY

López-Aguirre, C., S. J. Hand, D. Koyabu, N. T. Son, and L. A. B. Wilson. 2019. Postcranial heterochrony, modularity, integration and disparity in the prenatal ossification in bats (Chiroptera). BMC Evolutionary Biology, 17 pp., https://doi.org/10.1186/s12862-019-1396-1 [c.lopez-aguirre@unsw.edu.au]

DISEASE

Bandelj, P., T. Knapič, J. Rousseau, M. Podgorelec, P. Presetnik, M. Vengust, and J. S. Weese. 2019. *Clostridioides difficile* in bat guano. Comparative Immunology, Microbiology and Infectious Diseases, 65: 144-147. [jsweese@uoguelph.ca]

DISTRIBUTION/FAUNAL STUDIES

Ancillotto, L., E. Mori, L. Bosso, P. Agnelli, and D. Russo. 2019. The Balkan long-eared bat (*Plecotus kolombatovici*) occurs in Italy – first confirmed record and potential distribution. Mammalian Biology, 96: 61-67. [danrusso@unina.it]

Debata, S., and S. K. Palita. 2019. Odisha's first record of a free-tailed bat (Mammalia: Chiroptera: Molossidae): what could it be? Journal of Threatened Taxa, 11(8): 14071-14074. [skpalita@gmail.com] [*note: a juvenile free-tailed bat that could not be positively identified*]

García, F. J., H. J. Cabrera Peña, G. Flórez, O. Vásquez-Parra, M. Machado, and D. Araujo-Reyes. 2018. First records of *Thyroptera lavali* (Chiroptera, Thyropteridae) for the Guiana Shield with an updated distribution of *Thyroptera* species in Venezuela. Mammalia, 83(3): 219-226. Retrieved 17 Jun. 2019, from doi:10.1515/mammalia-2018-0020 [cormura@yahoo.com]

Sachanowicz, K., M. Ciechanowski, P. Tryjanowski, and J. Z. Kosicki. 2018. Wintering range of *Pipistrellus nathusii* (Chiroptera) in central Europe: has the species extended to the north-east using urban heat islands?. Mammalia, 83(3): 260-271. Retrieved 17 Jun. 2019, from doi:10.1515/mammalia-2018-0014 [kubako@amu.edu.pl]

Tumlison, R., D.B. Sasse, H. W. Robison, M. B. Connior, C. T. McAllister, K. Jobe, and M. Anderson. 2018. Vertebrate natural history notes from Arkansas, 2018. Journal of the Arkansas Academy of Science, 72 (7): https://scholarworks.uark.edu/jaas/vol72/iss1/7 [tumlison@hsu.edu]

Voyta, L. L., F. N. Golenishchev, and E. A. Petrova. 2019. Putjata's expedition to Chinese Khingan in 1891 and its small mammal collection from "Tongjia Yingzi" kept at the Zoological Institute in St. Petersburg, Russia. Russian Journal of Theriology, 18(1): 56-66. [leonid.voyta@zin.ru]

Zhigalin, A. 2019. New data on David's myotis, *Myotis davidii* (Peters, 1869) (Mammalia, Chiroptera, Vespertilionidae), in Siberia and the Urals. Biodiversity Data Journal, 7, doi: 10.3897/BDJ.7.e34211 [ur.liam@nilagihz-xela]

ECHOLOCATION

Feijó, A., H. Nunes, E. M. Vilar, and P. A. da Rocha. 2018. Blindness in echolocating bats. Mammalia, 83(3): 272-275. Retrieved 17 Jun. 2019, from doi:10.1515/mammalia-2018-0034 [anderson@ioz.ac.cn]

Matsuo, H. 2019. Echolocation of bats and dolphins and its application. Pp. 257-271 *in* A. Miyauchi and M. Shimomura, Eds. Industrial Biomimetics, CRC Press, 294 pp. [ISBN 0429608276, 9780429608278]

ECOLOGY

Aung, M. M., and T. T. Htay. 2019. Dietary analysis of the Indian flying fox *Pteropus giganteus* (Brunnich, 1782) (Chiroptera: Pteropodidae) in Myanmar through the analysis of faecal and chewed remnants. Journal of Threatened Taxa, 11(8): 13977-13983. [no e-mail provided]

Hernández-Pérez, E. L., G. Castillo-Vela, G. García-Marmolejo, M. S. López, and R. Reyna-Hurtado. 2019. Wild pig (*Sus scrofa*) as prey of the common vampire bat (*Desmodus rotundus*). THERYA, 10(2): 195-199. [e.hperez@hotmail.com]

Johnson, J. S., M. J. Lacki, and S. A. Fulton. 2019. Foraging patterns of Rafinesque's big-eared bat in upland forests managed with prescribed fire. Journal of Mammalogy, 100: 500-509. [jjohnson@ohio.edu]

Kemp, J., A. López-Baucells, R. Rocha, O. S. Wangensteen, Z. Andriatafika, A. Nair, and M. Cabeza. 2019. Bats as potential suppressors of multiple agricultural pests: A case study from Madagascar. Agriculture, Ecosystems and Environment, 269: 88-96. [jamesrussellkemp@gmail.com]

Liu, Y., Y. Wang, Z. Zhang, Y. Bu, and H. Niu. 2019. Roost selection and ecology of Stoliczka's trident bat, *Aselliscus stoliczkanus* (Hipposideridae, Chiroptera) in China. Mammalian Biology, 95: 143-149. [hongxingniu@htu.cn]

Mancini, M. C. S., R. de S. Laurindo, F. Hintze, R. de M. Mello, and R. Gregorin. 2019. Different bat guilds have distinct functional responses to elevation. Acta Oecologica, 96: 35-42. [mthmancini@gmail.com]

Nguyen, T. N., A. Ruangwiset, and S. Bumrungsri. 2019. Vertical stratification in foraging activity of *Chaerephon plicatus* (Molossidae, Chiroptera) in Central Thailand. Mammalian Biology, 96: 1-6. [sara.b@psu.ac.th]

Polyakov, A. Y., T. J. Weller, and W. D. Tietje. 2019. Remnant trees increase bat activity and facilitate the use of vineyards by edge-space bats. Agriculture, Ecosystems and Environment, 281: 56-63. [polyakov@berkeley.edu]

Parolin, L. C., F. A. Hansel, G. V. Bianconi, and S. B. Mikich. 2019. Chemical compounds in Neotropical fruit bat-plant interactions. Mammalian Biology, 94: 92-97. [lays.parolim@pucpr.br]

Silva, S. S. P. d., Q. F. Neves, P. G. Guedes, J. C. de Almeida and M. de C. Brasil-Sato. 2019. Diet and parasites of *Lonchophylla inexpectata* Moratelli & Dias, 2015 (Chiroptera, Lonchophyllinae) in the threatened Caatinga scrublands from Ceará (northeastern Brazil), Studies on Neotropical Fauna and Environment, DOI: 10.1080/01650521.2019.1587212 [batshirley@gmail.com]

EVOLUTION

Burger, J. R., M. A. George, jr., C. Leadbetter, and F. Shaikh. 2019. The allometry of brain size in mammals. Journal of Mammalogy, 100: 276-283. [jrb130 @duke.edu]

Rodríguez-Herrera, B., P. Rodríguez, W. Watson, G. F. McCracken, R. A. Medellín, and I. Galván. 2019. Sexual dichromatism and condition-dependence in the skin of a bat. Journal of Mammalogy, 100: 299-307. [galvan@ebd.csic.es]

GENERAL REFERENCE

Zagmajster, M. 2019. Chapter 13 – Bats, Pp. 94-101 *in* White, W. B., D. C. Culver, and T. Pipan. Encyclopedia of Caves, 3rd Edition. Academic Press, 1250 pp. [ISBN E-Book: 9780128141250; ISBN paper: 9780128141243]

IMMUNOLOGY

Ruoss, S., N. I. Becker, M. S. Otto, G. Á. Czirják, and J. A. Encarnação. 2019. Effect of sex and reproductive status on the immunity of the temperate bat *Myotis daubentonii*. Mammalian Biology, 94: 120-126. [J.Encarnacao@bio.uni-giessen.de]

PALEONTOLOGY

Amador, L. I., N. B. Simmons, and N. P. Giannini. 2019. Aerodynamic reconstruction of the primitive fossil bat *Onychonycteris finneyi* (Mammalia: Chiroptera). Biology Letters, 15(3): https://doi.org/10.1098/rsbl.2018.0857 [ngiannini@amnh.org]

Brown, E. E., D. D. Cashmore, N. B. Simmons, and R. J. Butler. 2019. Quantifying the completeness of the bat fossil record. Palaeontology. https://doi.org/10.1111/pala.12426 [emilyb62@hotmail.com]

Morgan, G. S., N. J. Czaplewski, and N. B. Simmons. 2019. A new mormoopid bat from the Oligocene (Whitneyan and early Arikareean) of Florida, and phylogenetic relationships of the major clades of Mormoopidae (Mammalia: Chiroptera). Bulletin of the American Museum of Natural History: 434, 1-146. [gary.morgan1@state.nm.us]

Ubilla, M., P. Gaudioso, and D. Perea. 2019. First fossil record of a bat (Chiroptera, Phyllostomidae) from Uruguay (Plio-Pleistocene, South America): a giant desmodontine. Historical Biology, https://doi.org/10.1080/08912963.2019.1590352 [martinubilla@gmail.com]

PARASITOLOGY

Barbier, E., G. Graciolli, and E. Bernard. 2019. Structure and composition of Nycteribiidae and Streblidae flies on bats along an environmental gradient in northeastern Brazil. Canadian Journal of Zoology, 97(5): 409-418. [barbier.eder@gmail.com]

Jensen, K. M., L. Rodrigues, T. Pape, A. Garm, S. Santamaria, A. S. P. S. Reboleira. 2019. Hyperparasitism in caves: bats, bat flies and ectoparasitic fungus interaction. Journal of Invertebrate Pathology, 166: 107206. [sreboleira@snm.ku.dk]

Rahman, A., and P. Choudhury. 2019. Report on three ectoparasites of the Greater Short-nosed fruit bat *Cynopterus sphinx* Vahl, 1797 (Mammalia: Chiroptera: Pteropodidae) in Cachar District of Assam, India. Journal of Threatened Taxa, 11(8): 13984-13991. [parthankar@rediffmail.com]

Souza, A. J. S. d., A. Pinheiro Malheiros, M. M. Alves, A. A. C. das Chagas, L. R. M. de Sá, and M. do C. P. Soares. 2019. A paruterinid metacestode in the liver of a Neotropical bat (*Molossus molossus*). Parasitology International, 70: 46-50. [souzajralex@gmail.com]

PHYSIOLOGY

Pretorius, M., T. Kearney, M. Keith, W. Markotter, E. Seamark, and H. Broders. 2018. Increased body mass supports energy compensation hypothesis in the breeding female Natal long-fingered bat *Miniopterus Natalensis* [*sic*]. Acta Chiropterologica, 20(2): 319-328. [hugh.broders@smu.ca]

REPRODUCTION

Carvalho, W. D de, M. A. Martins, D. Dias, R. A. Saldana-Vázquez, J. M. Palmeirim, and C. E. L. Esbérard. 2019. Reproductive constraints in frugivorous phyllostomid bats: seasonal and elevational variation in reproductive rates in the Brazilian Atlantic forest. Journal of Mammalogy, 100: 487-499. [wilruoca@hotmail.com]

Culina, A., D. M. Linton, R. Pradel, S. Bouwhuis, and D. W. Macdonald. 2019. Live fast, don't die young: survival–reproduction trade-offs in long-lived income breeders. Journal of Animal Ecology, 88: 746–756. [a.culina@nioo.knaw.nl]

TAXONOMY/SYSTEMATICS/PHYLOGENETICS

Solari, S., C. G. Sotero-Caio, and R. J. Baker. 2019. Advances in systematics of bats: towards a consensus on species delimitation and classifications through integrative taxonomy. Journal of Mammalogy, 100(3): 838-851. [sergio.solari@udea.edu.co]

Morgan, G. S., N. J. Czaplewski, and N. B. Simmons. 2019. See listing under **PALEONTOLOGY**.

Teta, P. 2018. The usage of subgenera in mammalian taxonomy. Mammalia, 83(3): 209-211. Retrieved 17 Jun. 2019, from doi:10.1515/mammalia-2018-0059 [antheca@yahoo.com.ar]

Velazco, P. M., and B. D. Patterson. 2019. Small mammals of the Mayo River basin in northern Peru, with the description of a new species of *Sturnira* (Chiroptera: Phyllostomidae). Bulletin of the American Museum of Natural History, No. 429, 67 pp. [ISSN 0003-0090]

TECHNIQUES FOR STUDYING BATS

López-Baucells, A., L. Torrent, R. Rocha, P. E. D. Bobrowiec, J. M. Palmeirim, and C. F. J. Meyer. 2019. Stronger together: combining automated classifiers with manual postvalidation optimizes the workload vs reliability trade-off of species identification in bat acoustic surveys. Ecological Informatics, 49: 45-53. [adria.baucells@gmail.com]

Morgan, C. N., L. K. Ammerman, K. D. Demere, J. B. Doty, Y. J. Nakazawa, and M. R. Mauldin. 2019. Field identification key and guide for bats of the United States of America. Occasional Papers, Museum of Texas Tech University, No. 360, 1-25 pp. [loren.ammerman@angelo.edu]

VIROLOGY

Bennett, A. J., T. Bushmaker, K. Cameron, A. Ondzie, F. R. Niama, H.-J. Parra, J.-V. Mombouli, S. H. Olson, V. J. Munster, and T. L. Goldberg. 2018. Diverse RNA viruses of arthropod origin in the blood of fruit bats suggest a link between bat and arthropod viromes. Virology, 1: 64-72. [tony.goldberg@wisc.edu]

Doysabas, K. C. C., M. Oba, M. Furuta, K. Iida, T. Omatsu, T. Furuya, T. Okada, K. Sutummaporn, H. Shimoda, M.-L. Wong, C.-H. Wu, Y. Ohmori, R. Kobayashi, Y. Hengjan, K. Yonemitsu, R. Kuwata, Y.-K. Kim, S.-H. Han, J.-H. Sohn, S.-H. Han, K. Suzuki, J. Kimura, K. Maeda, H.-S. Oh, D. Endoh, T. Mizutani, and E. Hondo. 2019. Encephalomyocarditis virus is potentially derived from eastern bent-wing bats living in East Asian countries. Virus Research, 259: 62-67. [ehondo@agr.nagoya-u.ac.jp]

Feng, H., A.-L. Sander, A. Moreira-Soto, D. Yamane, J. F. Drexler, and S. M. Lemon. 2019. Hepatovirus 3ABC proteases and evolution of mitochondrial antiviral signaling protein (MAVS). Journal of Hepatology, 71: 25-34. [smlemon@med.unc.edu]

ANNOUNCEMENTS

Reminder—Renewal Time!

Just a reminder that this is the last issue of the 2018 series of *Bat Research News*. That means some of you will be receiving renewal information in your e-mail inbox fairly soon. We hope you will continue to support *BRN* for the 2019 volume-year.

Back Issues

Are you missing any back issues of the print edition of *Bat Research News*? If you would like to replace them, please contact Margaret Griffiths (margaret.griffiths01@gmail.com). Most are available from Volume 45, 2004 to Volume 59, 2018. Depending on what you need, we may ask you to cover postage. Beginning in 2019, we will be reducing the inventory of back issues, beginning with the oldest (i.e., Vol. 45: no. 2, 2004).

Request for News

Please consider submitting news from your lab group, your field work, or any bat-related news. Thank you in advance for considering us as a place for bat, bat worker, and bat lab news items.

Request for Manuscripts — *Bat Research News*

Original research/speculative review articles, short to moderate length, on a bat-related topic would be most welcomed. Please submit manuscripts as .rtf documents to Allen Kurta, Editor for Feature Articles (akurta@emich.edu). Also please consider submitting short articles, notes, or letters on a bat-related topic. If you have questions, please contact Al. Thank you for considering *BRN*.

Change of Address Requested

Will you be moving in the near future? If so, please **send** your **new postal and e-mail addresses** to Margaret Griffiths (margaret.griffiths01@gmail.com), and include the date on which the change will become effective. Thank you in advance for helping us out!

FUTURE MEETINGS and EVENTS

2019

The 18th International Bat Research Conference (IBRC) will be held 28 July–2 August 2019, in Phuket, Thailand, at the Slate. Registration and abstract submission are open. Please visit the IBRC website for information — https://www.ibrc2019.com/.

The 49th Annual NASBR will be held 23–26 October 2019, in Kalamazoo, Michigan, at the Radisson Plaza Hotel. Check the NASBR website for future updates — https://www.nasbr.org/welcome19.

2020

The 15th European Bat Research Symposium will be held 3–7 August 2020, in Turku, Finland. Please visit https://www.ebrs2020.fi/ for updates and information.

The **NASBR** will celebrate their **50th anniversary** where it all began, in Arizona. The annual meeting will be held 28–31 October 2020, in Tempe, Arizona. The NASBR also plans to publish an edited volume that highlights bat biology research to coincide with their 50th annual meeting. Check the NASBR website for more information and future updates — http://www.nasbr.org/.

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An extraordinary "mountain" of *Pteronotus* bat pups in Campanario Bat Cave (top), with a close-up of the bat pups (bottom). Campanario Bat Cave is a sea cave on the Osa Peninsula, Costa Rica, that contains a large population of three species of *Pteronotus* bats. It is managed by the Campanario Biological Station. Keith Christenson encountered this scene on his first visit. Nearly all the bat pups were found on these two ridges on a shelf and he had to stop exploration of the cave as there was no way around the pups. Although an unusual locale for a large bat colony, the bats were doing quite well given the number of pups in residence. Photo by Keith Christenson, March 2019.

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A Cost-effective Guano Trap for Artificial Bat Roosts

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Indirect methods of assessing habitat selection are common within the wildlife field and often are chosen because of the ease and efficiency of data collection (McDonald et al., 2012). As a notable example, fecal material is often readily accessible, can be collected with little or no stress to animals, and can be used for various applications, such as determining species presence, dietary studies, and genetic applications (Kohn and Wayne, 1997). Considering the benefits afforded by indirect sampling approaches, we sought to develop a cost-effective guano trap that would allow frequent, standardized collection of fecal material from bats and also be suitable for different types of artificial roosts that have been installed for these mammals in eastern North America.

Our guano trap attaches to a standard "4-by-4" wooden post (actual dimensions: 3.5 by 3.5 inches or 8.9 by 8.9 cm) that is commonly used for mounting artificial bat roosts (Fig. 1), although the trap easily can be altered to mount to a larger pole. Traps are made from polyvinylchloride (PVC) pipe (3/4 inch or 19.1 mm in diameter), PVC fittings, and other affordable materials and are constructed as two L-shaped halves for ease of installation and removal (Fig. 2). The joints that connect the triangular halves are not permanently connected so that they can easily be separated, for monitoring the roost (e.g., spotlight checks) or for eventual removal.

To construct a trap (Fig. 2), we first built the sides from pieces of PVC pipe (18 inches or 45.7 cm in length), connected via tee connectors and PVC cement; the four corners were then connected using 90°-elbow pieces, making sure that we did not cement the L-shaped frames to each other. We then attached "arms" made from pieces of pipe (17 inches or 43.2 cm in length) to the center of the tee connectors, to brace the trap against the post; different lengths of pipe can be used for these braces to allow mounting on different-sized poles. We covered the surface of the trap with a 3.5-ft^2 (1.06-m^2) piece of black, fiberglass, window screen to catch guano. The screen was cut into triangular halves to fit the L-shaped frames and attached to the frames using a zip tie on each side of every connector joint and one on each post brace (20 zip ties total). We also cut a small triangle (half square) in the center of each half of the screen to fit the square-shaped post.

To affix a trap to the post, we used 16-guage bailing wire. We first screwed an eyebolt into pre-drilled pilot holes on each side of the post, 56 inches (1.4 m) above the ground and then drilled a hole (3/8 inch or 9.5 mm in diameter) in each of the central tee connectors. A strand of bailing wire (30 inches or 76.2 cm in length) was threaded through these holes and attached to the eyebolts (Fig. 1). The result was a guano trap positioned about 36 inches (0.9 m) above the ground. Each L-shaped half was installed separately and connected upon completion.

Using this design, we created 20 replicates of the trap for less than US$300. Following Adams et al. (2015) and Hoeh et al. (2018), we deployed these guano traps beneath 16 rocket boxes and 18 artificial bark roosts, on 1 May 2019 (Fig. 1). As of 4 July 2019, the traps had been in place for 65 days and had been subjected to 57.1 cm of total rainfall, wind speeds up to 36 km/h, and ambient temperatures ranging from 2.7 to 32.9°C.

Figure 1. Guano trap mounted on 4-by-4 post.

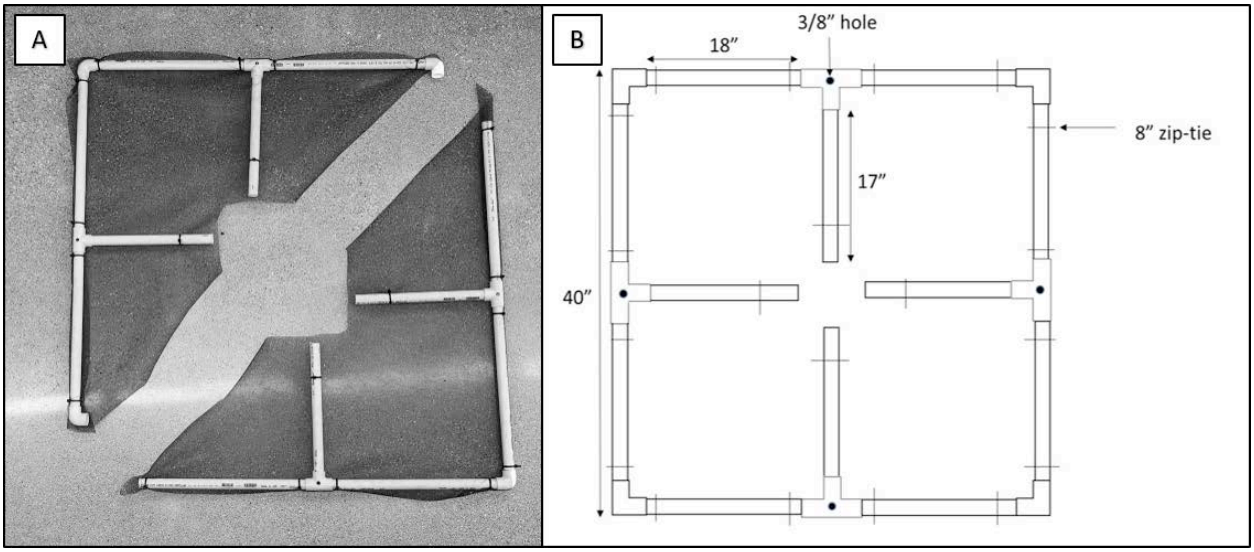

Figure 2. Details of trap construction. (A) L-shaped halves of trap allow for attachment to existing roosts. (B) Dimensions of trap. Metric values are provided in text.

Nevertheless, all traps remained intact and functional, with one trap catching as many as 1,052 pellets over two nights at an artificial bark roost.

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Literature Cited

Adams, J., P. Roby, P. Sewell, J. Schwierjohann, M. Gumbert, and M. Brandenburg. 2015. Success of Brandenbark™, an artificial roost structure designed for use by Indiana bats (*Myotis sodalis*). Journal of the American Society of Mining and Reclamation, 4:1−15.

Hoeh, J. P. S., G. S. Bakken, W. A. Mitchell, and J. M. O'Keefe. 2018. In artificial roost comparison, bats show preference for rocket box style. PLoS ONE, 13(10):e0205701

Kohn, M. H., and R. K. Wayne. 1997. Facts from feces revisited. Trends in Ecology & Evolution, 12:223–227.

McDonald, L. L., W. P. Erickson, M. S. Boyce, and J. R. Alldredge. 2012. Modeling vertebrate use of terrestrial resources. Pp. 410–428 *in* The Wildlife Techniques Manual, Volume 1 (N. J. Silvy, ed.). John Hopkins University Press, Baltimore, Maryland.

RECENT LITERATURE

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ANATOMY/HISTOLOGY

Amador, L. I., N. P. Giannini, N. B. Simmons, and V. Abdala. 2018. Morphology and evolution of sesamoid elements in bats (Mammalia: Chiroptera). American Museum Novitates, 3905: 1–38. [available for download free from the AMNH publications website]

Reis, A. d. S., R. d. A. Zampaulo, and S. A. Talamoni. 2019. Frequency of leucism in a colony of *Anoura geoffroyi* (Chiroptera: Phyllostomidae) roosting in a ferruginous cave in Brazil. Biota Neotropica, 19(3): e20180676. https://dx.doi.org/10.1590/1676-0611-bn-2018-0676 [alineambiental@yahoo.com.br]

Stanchak, K. E., J. H. Arbour, and S. E. Santana. 2019. Anatomical diversification of a skeletal novelty in bat feet. Evolution, 73(8): 1591–1603. [stanchak@uw.edu]

BEHAVIOR

Hemingway, C. T., M. J. Ryan, and R. A. Page. 2019. Transitive foraging behavior in frog-eating bats. Animal Behaviour, 154: 47–55. [cheming@utexas.edu]

BIOGEOGRAPHY

López-Aguirre, C., S, J. Hand, S. W. Laffan, and M. Archer. 2019. Zoogeographical regions and geospatial patterns of phylogenetic diversity and endemism of New World bats. Ecography, 42(6): 1188–1199. [c.lopez-aguirre@unsw.edu.au]

CONSERVATION

Chattopadhyay, B., K. M. Garg, R. Ray, and F. E. Rheindt. 2019. Fluctuating fortunes: Genomes and habitat reconstructions reveal global climate-mediated changes in bats' genetic diversity. Proc. R. Soc. B 286: http://doi.org/10.1098/rspb.2019.0304 [no e-mail provided]

Claireau, F., Y. Bas, S. J. Puechmaille, J.-F. Julien, B. Allegrini, and C. Kerbiriou. 2019. Bat overpasses: An insufficient solution to restore habitat connectivity across roads. Journal of Applied Ecology, 56(3): 573–584. [f.claireau@naturalia-environnement.fr]

Haddock, J. K., C. G. Threlfall, B. Law, and D. F. Hochuli. 2019. Responses of insectivorous bats and nocturnal insects to local changes in street light technology. Austral Ecology, 44(6): 1052–1064. [joanna.haddock@sydney.edu.au]

Lavery, T. H., and J. Fasi. 2019. Buying through your teeth: Traditional currency and conservation of flying foxes *Pteropus* spp. in Solomon Islands. Oryx, 53(3): 505–512. [tlavery@fieldmuseum.org]

Law, B., A. Kathuria, M. Chidel, and T. Brassil. 2019. Long-term effects of repeated fuel-reduction burning and logging on bats in south-eastern Australia. Austral Ecology, 44(6): 1013–1024. [brad.law@dpi.nsw.gov.au]

Leeuwerck, E. 2019. Monitoring, roost occupancy, and diet of the strawcolored [*sic*] fruit bat *Eidolon helvum* in Kigali, Rwanda. African Bat Conservation News, 48: 4–7. [eleeuwerck@yahoo.fr]

Meierhofer, M. B., J. S. Johnson, S. J. Leivers, B. L. Pierce, J. E. Evans, and M. L. Morrison. 2019. Winter habitats of bats in Texas. PLoS ONE, 14(8): e0220839. https://doi.org/10.1371/journal.pone.0220839 [melissa.meierhofer@ag.tamu.edu]

Struebig, M., J. S. P. Froidevaux, M. Broyles, G. Jones, K. L. Boughey, and C. L. Hawkins. 2019. Managing hedgerows for nocturnal wildlife: Do bats and their insect prey benefit from targeted agri-environmental schemes? Journal of Applied Ecology, 56(7): 1610–1623. [jeremy.froidevaux@bristol.ac.uk]

Taylor, P. J., C. Denys, and F. P. D. Cotterill. 2019. Taxonomic anarchy or an inconvenient truth for conservation? Accelerated species discovery reveals evolutionary patterns and heightened extinction threat in Afro-Malagasy small mammals. Mammalia, 83(4): 313–329. [Peter.Taylor@univen.ac.za]

Thomas, J. F., M. L. Reid, T. S. Jung, and R. M. R. Barclay. 2019. Site occupancy of little brown bats (*Myotis lucifugus*) in response to salvage logging in the boreal forest. Forest Ecology and Management, 451: 1–9. [julie.thomas@gov.yk.ca]

Tollington S., Z. Kareemun, A. Augustin, K. Lallchand, V. Tatayah, and A. Zimmermann. 2019. Quantifying the damage caused by fruit bats to backyard lychee trees in Mauritius and evaluating the benefits of protective netting. PLoS ONE, 14(8): e0220955. https://doi.org/10.1371/journal.pone.0220955 [Simon.Tollington@gmail.com]

Tolme, P. 2019. Shifting winds. National Wildlife (world edition), 57(5): 32–37. [no e-mail provided]

Vleut I., G. G. Carter, and R. A. Medellín. 2019. Movement ecology of the carnivorous woolly false vampire bat (*Chrotopterus auritus*) in southern Mexico. PLoS ONE, 14(7): e0220504. https://doi.org/10.1371/journal.pone.0220504 [ivar8207@gmail.com]

Wentzel, J. J., P. A. Barber, G. E. Hardy, P. A. Fleming, and M. D. Craig. 2019. Microbat responses to forest decline. Austral Ecology, 44(2): 265–275. [t.fleming@murdoch.edu.au]

DEVELOPMENT/ONTOGENY

Carter, R. T., A. Stuckey, and R. A. Adams. 2019. Ontogeny of the hyoid apparatus in Jamaican fruit bats (Chiroptera: Phyllostomidae) in unraveling the evolution of echolocation in bats. Journal of Zoology, 308(4): 301–307. https://doi.org/10.111/jzo.12679 [carterrt@etsu.edu]

López-Aguirre, C., S. J. Hand, D. Koyabu, N. T. Son, and L. A. B. Wilson. 2019. Postcranial heterochrony, modularity, integration and disparity in the prenatal ossification in bats (Chiroptera). BMC Evolutionary Biology, 17 pp., https://doi.org/10.1186/s12862-019-1396-1 [c.lopez-aguirre@unsw.edu.au]

DISEASE

Brook, C. E., H. C. Ranaivoson, C. C. Broder, A. A. Cunningham, J.-M. Héraud, A. J. Peel, L. Gibson, J. L. N. Wood, C. J. Metcalfe, A. P. Dobson, and A. Fenton. 2019. Disentangling serology to elucidate henipa- and filovirus transmission in Madagascar fruit bats. Journal of Animal Ecology, 88(7): 1001–1016. [cbrook@berkeley.edu]

Cote, A., R. M. Wallace, D. A, Jackson, M. A. Said, K. Musgrave, C. H. Tran, C. van Houten, A. Harrist, D. Buttke, A. Busacker, V. Pickens, and S. A. J. Guagliardo. 2019. Evaluating the public health response to a mass bat exposure—Wyoming, 2017. Zoonoses & Public Health, 66(5): 504–511. [Andrea.cote@usda.gov]

Gharout-Sait, A., A. Touati, M. Ahmim, L. Brasme, T. Guillard, A. Agsous, and C. de Champs. 2019. Occurrence of carbapenemase-producing *Klebsiella pneumoniae* in bat guano. Microbial Drug Resistance: Mechanism, Epidemiology, & Disease, 25(7): 1057–1062. [gharoutalima@gmail.com]

Kramer, A. M., C. S. Teitelbaum, A. Griffin, and J. M. Drake. 2019. Multiscale model of regional population decline in little brown bats due to white-nose syndrome. Ecology & Evolution, 9(15): 8639–8651. [amkramer@usf.edu]

Mbu'u, C. M., W. F. Mbacham, P. Gontao, S. L. Sado Kamdem, A. M. N. Niôga, M. H. Groschup, A. Wade, K. Fischer, and A. Balkema-Buschmann. 2019. Henipaviruses at the interface between bats, livestock and human populations in Africa. Vector Borne & Zoonotic Diseases, 19(7): 455–465. [wfmbacham@yahoo.com]

McDougall, F., W. Boardman, M. Gillings, and M. Power. 2019. Bats as reservoirs of antibiotic resistance determinants: A survey of class 1 integrons in Grey-headed flying foxes (*Pteropus poliocephalus*). Infection, Genetics & Evolution, 70: 107–113. [fiona.mcdougall@hdr.mq.edu.au]

DISTRIBUTION/FAUNAL STUDIES

Alfaro-Lara, H., D. Villalobos-Chaves, J. I. Castillo-Gómez, A. F. Zuniga-Montero, and W. Pineda-Lizano. 2018. Rediscovery of *Furipterus horrens* (Chiroptera: Furipteridae) in Costa Rica. Mammalia, 83(4): 352–356. [dvillaloboschaves@gmail.com]

Catzeflis, F., G. Issartel, and J. Jemin. 2018. New data on the bats (Chiroptera) of Martinique island (Lesser Antilles), with an emphasis on sexual dimorphism and sex ratios. Mammalia, 83(5): 501–514. [francois.catzeflis@umontpellier.fr]

Dar, T. H., M. Kamalakannan, C. Venkatraman, and K. Chandra. 2018. New record of *Hipposideros speoris* (Chiroptera: Hipposideridae) from Myanmar hidden in the National Zoological Collections of the Zoological Survey of India. Mammalia, 83(5): 515–517. [kamalakannanm1@gmail.com]

ECHOLOCATION

Beetz, M. J., M. Kössl, and J. C. Hechavarria. 2019. Adaptations in the call emission pattern of frugivorous bats when orienting under challenging conditions. Journal of Comparative Physiology A: Neuroethology, Sensory, Neural & Behavioral Physiology, 205(4): 457–467. [jerome.beetz@uni-wuerzburg.de]

Carter, R. T., A. Stuckey, and R. A. Adams. 2019. Ontogeny of the hyoid apparatus in Jamaican fruit bats (Chiroptera: Phyllostomidae) in unraveling the evolution of echolocation in bats. Journal of Zoology, https://doi.org/10.1111/jzo.12679. [carterrt@etsu.edu]

Geipel, I., J. Steckel, M. Tschapka, D. Vanderelst, H.-U. Schnitzler, E. K. V. Kalko, H. Peremans, and R. Simon. 2019. Bats actively use leaves as specular reflectors to detect acoustically camouflaged prey. Current Biology, 29(16): 2731–2736. [inga.geipel@gmail.com]

ECOLOGY

Aldasoro, M., I. Garin, N. Vallejo, U. Baroja, A. Arrizabalaga-Escudero, U. Goiti, and J. Aihartza. 2019. Gaining ecological insight on dietary allocation among horseshoe bats through molecular primer combination. PLoS ONE, 14(7): e0220081. https://doi.org/10.1371/journal.pone.0220081 [oxerra.aihartza@ehu.eus]

Andriollo, T., F. Gillet, J. R. Michaux, and M. Ruedi. 2019. The menu varies with metabarcoding practices: A case study with the bat *Plecotus auritus*. PLoS ONE, 14(7): 1–17. e0219135. https://doi.org/10.1371/journal.pone.0219135 [manuel.ruedi@ville-ge.ch]

Baroja, U., I. Garin, J. Aihartza, A. Arrizabalaga-Escudero, N. Vallejo, M. Aldasoro, and U. Goiti. 2019. Pest consumption in a vineyard system by the lesser horseshoe bat (*Rhinolophus hipposideros*). PLoS ONE, 14(7): e0219265. https://doi.org/10.1371/journal.pone.0219265 [urtzi.goiti@ehu.eus]

Chang, Y., S. Song, A. Li, Y. Zhang, Z. Li, Y. Xiao, T. Jiag, J. Feng, and A. Lin. 2019. The roles of morphological traits, resource variation and resource partitioning associated with the

dietary niche expansion in the fish-eating bat *Myotis pilosus*. Molecular Ecology, 28(11): 2944–2954. [fengj@nenu.edu.cn]

Laurindo, R. d. S., and R. Gregorin. 2019. Temperature and resource availability drive the seasonal abundance of *Artibeus lituratus* (Chiroptera: Phyllostomidae) in Atlantic Forest remnants of southeastern Brazil. Mammalia, 83(4): 383–389. [rafaelslaurindo@gmail.com]

Linden, V. M. G., I. Grass, E. Joubet, T. Tscharntke, S. M. Weier, P. Taylor, and M. Struebig. 2019. Ecosystem services and disservices by birds, bats and monkeys change with macadamia landscape heterogeneity. Journal of Applied Ecology, 56(8): 2069–2078. [linden.vmg@gmail.com]

Ripperger, S. P., S. Rehse, S. Wacker, E. K. V. Kalko, S. Schulz, B. Rodriguez-Herrera, and M. Ayasse. 2019. Nocturnal scent in a 'bird-fig': A cue to attract bats as additional dispersers? PLoS ONE, 14(8): e0220461. https://doi.org/10.1371/journal.pone.0220461 [simon.ripperger@gmail.com]

Saldaña-Vazquez, R. A., J. H. Castaño, J. Baldwin, and J. Pérez-Torres. 2019. Does seed ingestion by bats enhance germination? A new meta-analysis 15 years later. Mammal Review, 49(3): 201–209. [romeo.saldana@gmail.com]

FLIGHT

Cichocki, J., M. Warchałowski, A. Ważna, I. Gottfried, A. Bator-Kocoł, T. Gottfried, A. Kościelska, J. Bojarski, M. Pietraszko-Warchalowska, and G. Gabryś. 2019. Frequent or scarce? Damage to flight-enabling body parts in bats (Chiroptera). PLoS ONE, 14(7): e0219783. https://doi.org/10.1371/journal.pone.0219783 [cichocki@wnb.uz.zgora.pl]

Guigueno, M. F., A. Shoji, K. H. Elliott, and S. Aris-Brosou. 2019. Flight costs in volant vertebrates: A phylogenetically-controlled meta-analysis of birds and bats. Comparative Biochemistry & Physiology A: Molecular and Integrative Physiology, 235: 193–201. [melanie.guigueno@mcgill.ca]

Sekhar, S., P. Windes, X. Fan, and D. K. Tafti. 2019. Canonical description of wing kinematics and dynamics for a straight flying insectivorous bat (*Hipposideros pratti*). PLoS ONE, 14(6): 1–45. e0218672. https://doi.org/10.1371/journal.pone.0218672 [dtafti@exchange.vt.edu]

HIBERNATION

Gottfried, I., T. Gottfried, and K. Zając. 2019. Bats use larval galleries of the endangered beetle *Cerambyx cerdo* as hibernation sites. Mammalian Biology, 95: 31–34. [iwona.gottfried@uwr.edu.pl]

Uzenbaeva, L. B., A. G. Kizhina, V. A. Ilyukha, V. V. Belkin, and E. A. Khizhkin. 2019. Morphology and composition of peripheral blood cells during hibernation in bats (Chiroptera, Vespertilionidae) of northwestern Russia. Biology Bulletin, 46(4): 398–406. [golubewa81@yandex.ru]

IMMUNOLOGY

Ruoss, S., N. I. Becker, M. S. Otto, G. Á. Czirják, and J. A. Encarnação. 2019. Effect of sex and reproductive status on the immunity of the temperate bat *Myotis daubentonii*. Mammalian Biology, 94: 120–126. [J.Encarnacao@bio.uni-giessen.de]

MIGRATION

Sasse, D. B. 2019. Gray bat day roosts in concrete barriers on bridges during migration. The American Midland Naturalist, 182: 124–128. [blake.sasse@agfc.ar.gov]

PALEONTOLOGY

Amador, L. I., N. B. Simmons, and N. P. Giannini. 2019. Aerodynamic reconstruction of the primitive fossil bat *Onychonycteris finneyi* (Mammalia: Chiroptera). Biology Letters, 15(3): https://doi.org/10.1098/rsbl.2018.0857 [ngiannini@amnh.org]

Brown, E. E., D. D. Cashmore, N. B. Simmons, and R. J. Butler. 2019. Quantifying the completeness of the bat fossil record. Palaeontology, 62(5): 757–776. https://doi.org/10.1111/pala.12426 [emilyb62@hotmail.com]

Merino, A., J. J. Fornós, A. Mulet, and J. Ginés. 2019. Morphological and mineralogical evidence for ancient bat presence in Cova des Pas de Vallgornera (Llucmajor, Mallorca,Western Mediterranean). International Journal of Speleology, 48(2): 115–131. [tonymerinoj@gmail.com]

Morgan, G. S., N. J. Czaplewski, and N. B. Simmons. 2019. A new mormoopid bat from the Oligocene (Whitneyan and early Arikareean) of Florida, and phylogenetic relationships of the major clades of Mormoopidae (Mammalia: Chiroptera). Bulletin of the American Museum of Natural History: 434, 1–146. [gary.morgan1@state.nm.us]

Ubilla, M., P. Gaudioso, and D. Perea. 2019. First fossil record of a bat (Chiroptera, Phyllostomidae) from Uruguay (Plio-Pleistocene, South America): A giant desmodontine. Historical Biology, https://doi.org/10.1080/08912963.2019.1590352 [martinubilla@gmail.com]

PARASITOLOGY

Batista, J. M. N., C. d. Carvalho, W. A. Pedro, B. N. Santana, V. S. Camargo, E. D. Ferrari, I. G. Nascimento, and M. V. Meireles. 2019. Identification of *Crypotosporidium* bat genotypes XVI-XVIII in bats from Brazil. Parasitology Research, 118(7): 2183–219. [marcelo@fmva.unesp.br]

Reis, A. d. S., R. d. A. Zampaulo, L. F. d. O. Bernardi, and S. A. Talamoni. 2019. *Monunguis streblida* (Neothrombidiidae) in Brazil and its parasitic relationships with dipteran ectoparasites (*Anastrebla* and *Trichobius*) of bats. Parasitology Research, 118(9): 2467–2473. [alineambiental@yahoo.com.br]

Rosskopf, S. P., J. Held, M. Gmeiner, B. Mordmüller, P.-B. Matsiégui, I. Eckerle, N. Weber, K. Matuschewski, and J. Schaer. 2019. *Nycteria* and *Polychromophilus* parasite infections of bats in central Gabon. Infection, Genetics & Evolution, 68: 3–34. [schaerju@hu-berlin.de]

Silva, S. S. P. d., Q. F. Neves, P. G. Guedes, J. C. d. Almeida, and M. d. C. Brasil-Sato. 2019. Diet and parasites of *Lonchophylla inexpectata* Moratelli & Dias, 2015 (Chiroptera, Lonchophyllinae) in the threatened Caatinga scrublands from Ceará (northeastern Brazil). Studies on Neotropical Fauna and Environment, 54(2): 107–113. [batshirley@gmail.com]

PHYSIOLOGY

Heffner, R. S., G. Koay, and H. E. Heffner. 2019. Bats are unusually insensitive to brief low-frequency tones. Journal of Comparative Physiology A: Neuroethology, Sensory, Neural & Behavioral Physiology, 205(4): 583–594. [Rickye.Heffner@utoledo.edu]

REPRODUCTION

Gaona O, E. S. Gómez-Acata, D. Cerqueda-García, C. X. Neri-Barrios, and L. I. Falcón. 2019. Fecal microbiota of different reproductive stages of the central population of the lesser-long nosed [*stet*] bat, *Leptonycteris yerbabuenae*. PLoS ONE, 14(7): e0219982. https://doi.org/10.1371/journal.pone.0219982 [falcon@ecologia.unam.mx]

TAXONOMY/SYSTEMATICS/PHYLOGENETICS

Demos, T. C., P. W. Webala, S. M. Goodman, J. C. K. Peterhans, M. Bartonjo, and B. D. Patterson. 2019. Molecular phylogenetics of the African horseshoe bats (Chiroptera: Rhinolophidae): Expanded geographic and taxonomic sampling of the Afrotropics. BMC Evolutionary Biology, 19: https://doi.org/10.1186/s12862-019-1485-1 [tdemos@fieldmuseum.org]

Hawkins, J. A., M. E. Kaczmarek, M. A. Müller, C. Drosten, W. H. Press, and S. L. Sawyer. 2019. A metaanalysis of bat phylogenetics and positive selection based on genomes and transcriptomes from 18 species. Proceedings of the National Academy of Sciences of the United States of America, 116(23): 11351–11360. [wpress@cs.utexas.edu]

Liu, T., K. Sun, G. Csorba, K. Zhang, L. Zhang, H. Zhang, L. Jin, V. D. Thong, Y. Xiao, and J. Feng. 2019. Species delimitation and evolutionary reconstruction within an integrative taxonomic framework: A case study on *Rhinolophus macrotis* complex (Chiroptera: Rhinolophidae). Molecular Phylogenetics & Evolution, 139: https://doi.org/10.1016/j.ympev.2019.106544 [sunkp129@nenu.edu.cn]

Vivas-Toro, I., and O. E. Murillo-Garcia. 2019. Taxonomic identity of an insular population of sac-winged bat *Saccopteryx* (Chiroptera: Emballonuridae). Revista de Biologia Tropical, 67(3): 396–405. [isabela.vivas@correounivalle.edu.co]

TECHNIQUES FOR STUDYING BATS

Scherrer, D., P. Christe, and A. Guisan. 2019. Modelling bat distributions and diversity in a mountain landscape using focal predictors in ensemble of small models. Diversity and Distributions, 25: 770–782. [daniel.scherrer@unil.ch]

VIROLOGY

Forbes, K. M., P. W. Webala, A. J. Jääskeläinen, S. Abdurahman, J. Ogola, M. M. Masika, I. Kivistö, H. Alburkat, I. Plyusnin, L. Levanov, E. M. Korhonen, E. Huhtamo, D. Mwaengo, T. Smura, A. Mirazimi, O. Anzala, O. Vapalahti, and T. Sironen. 2019. Bombali virus in *Mops condylurus* bat, Kenya. Emerging Infectious Diseases, 25(5): 955–957. [kmforbes@uark.edu]

Kajihara, M., B. M. Hang'ombe, K. Changula, H. Harima, M. Isono, K. Okuya, R. Yoshida, A. Mori-Kajihara, Y. Eto, Y. Orba, H. Ogawa, Y. Qiu, H. Sawa, E. Simulundu, D. Mwizabi, M. Munyeme, D. Squarre, V. Mukonka, A. Mweene, and A. Takada. 2019. Marburgvirus in Egyptian fruit bats, Zambia. Emerging Infectious Diseases, 25(8): 1577–1580. [atakada@czc.hokudai.ac.jp]

Mendenhall, I. H., D. L. H. Wen, J. Jayakumar, V. Gunalan, L. Wang, S. Mauer-Stroh, Y. C. F. Su, and G. J. D. Smith. 2019. Diversity and evolution of viral pathogen community in cave nectar bats (*Eonycteris spelaea*). Viruses, 11(3): 250. https://www.mdpi.com/1999-4915/11/3/250. [ian.mendenhall@duke-nus.edu.sg]

Yadav, P. D., A. M. Shete, A. G. Kumar, P. Sarkale, R. R. Sahay, C. Radhakrishnan, R. Lakra, P. Pardeshi, N. Gupta, R. R. Gangakhedkar, V. R. Rajendran, R. Sadanandan, and D. T. Mourya. 2019. Nipah virus sequences from humans and bats during Nipah outbreak, Kerala, India, 2018. Emerging Infectious Diseases, 25(5): 1003–1006. [dtmourya@gmail.com]

ANNOUNCEMENTS

Back Issues

Are you missing any back issues of the print edition of *Bat Research News*? If you would like to replace them, please contact Margaret Griffiths (margaret.griffiths01@gmail.com). Most are available from Volume 45, 2004 to Volume 59, 2018. Depending on what you need, we may ask you to cover postage. We are reducing the inventory of back issues, beginning with the oldest (i.e., Vol. 45: no. 2, 2004).

Request for News

Please consider submitting news from your lab group, your field work, or any bat-related news. Thank you in advance for considering us as a place for bat, bat worker, and bat lab news items.

Request for Manuscripts — *Bat Research News*

Original research/speculative review articles, short to moderate length, on a bat-related topic would be most welcomed. Please submit manuscripts as .rtf documents to Allen Kurta, Editor for Feature Articles (akurta@emich.edu). Also please consider submitting short articles, notes, or letters on a bat-related topic. If you have questions, please contact Al. Thank you for considering *BRN*.

Change of Address Requested

Will you be moving in the near future? If so, please **send** your **new postal and e-mail addresses** to Margaret Griffiths (margaret.griffiths01@gmail.com), and include the date on which the change will become effective. Thank you in advance for helping us out!

FUTURE MEETINGS and EVENTS

2019

The 49th Annual NASBR will be held 23–26 October 2019, in Kalamazoo, Michigan, at the Radisson Plaza Hotel. Check the NASBR website for future updates — https://www.nasbr.org/welcome19.

2020

The 15th European Bat Research Symposium will be held 3–7 August 2020, in Turku, Finland. Please visit https://www.ebrs2020.fi/ for updates and information.

The **NASBR** will celebrate their **50th anniversary** where it all began, in Arizona. The annual meeting will be held 28–31 October 2020, in Tempe, Arizona. The NASBR also plans to publish an edited volume that highlights bat biology research to coincide with their 50th annual meeting. Check the NASBR website for more information and future updates — https://www.nasbr.org/annual-meetings.

2021

The 51st Annual NASBR will be held in Winnipeg, Manitoba, Canada, dates to be determined. Check the NASBR website for updates — https://www.nasbr.org/annual-meetings.

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Small-footed bat (*Myotis leibii*) caught near Otter Creek Wilderness in West Virginia. Photo courtesy of Keith Christenson.

BAT RESEARCH NEWS

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Bat Research News is published four times each year, consisting of one volume of four issues. *Bat Research News* publishes short feature articles and general interest notes that are reviewed by at least two scholars in that field. *Bat Research News* also includes abstracts of presentations at bat conferences around the world, letters to the editors, news submitted by our readers, notices and requests, and announcements of future bat conferences worldwide. In addition, *Bat Research News* provides a listing of recent bat-related articles that were published in English. *Bat Research News* is abstracted in several databases (e.g., BIOSIS).

Communications concerning feature articles and "Letters to the Editor" should be addressed to Dr. Al Kurta (akurta@emich.edu), recent literature items to Dr. Tom Griffiths (thomas.alan.griffiths@gmail.com), and all other correspondence (e.g., news, conservation, or education items; subscription information; cover art) to Dr. Margaret Griffiths (margaret.griffiths01@gmail.com).

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Abstracts of Papers Presented at the

49th Annual Symposium of the
North American Society for Bat Research
Kalamazoo, Michigan, USA
October 23rd – 26th, 2019

The following abstracts are from papers presented at the 49th Annual Symposium of the North American Society for Bat Research (NASBR). The local hosts for the meeting were Amy Russell and Maarten Vonhoff. Meeting abstracts were submitted by Gary Kwiecinski, Shahroukh Mistry, Riley Bernard, Luis Viquez-R., and Emma Wilcox, Program Directors for NASBR. Abstracts are arranged in alphabetical order by first author and, except for minor formatting changes, are published as received. **Student award recipients** are indicated by an **asterisk** (*****) next to the title of their paper. E-mail contact information for authors is not available.

Bat Longevity is Predicted by Genome Methylation Rate
Danielle M. Adams[1], Josephine Reinhardt[2], Steve Horvath[3] and Gerald S. Wilkinson[1]
[1]Department of Biology, University of Maryland, College Park, USA; [2]Department of Biology, State University of New York, Geneseo, USA; [3]Department of Human Genetics, University of California, Los Angeles, USA

Recorded lifespans of bats exceed other placental mammals of similar body size. Moreover, considerable variation in lifespan is present among bats with at least four lineages exhibiting extreme longevity. The underlying mechanisms of increased longevity are still unknown, but humans and other model species exhibit consistent age-related change in DNA methylation patterns across thousands of conserved sites. Using a custom microarray, we obtained methylation scores at more than 20,000 genomic sites from over 700 individuals of known age from 28 bat species representing six families. Using a machine-learning technique we derive a highly predictive relationship for estimating age in each species from a subset of these sites. We then use this relationship, or epigenetic clock, to estimate the age of unknown individuals as well as compare patterns of age-specific methylation acceleration and deceleration among species. We find that among species the rate of methylation change is significantly associated with maximum longevity, such that longer-lived species show slower rates of methylation change. In addition, using methylation data from six species with published genomes, we find that the majority of age-related methylation sites are near the transcription start sites of genes that are important for transcription regulation. We then further explore how the genomic regions with age-dependent methylation patterns vary among long and short-lived species.

Improving Urban Habitats for Bats: What Makes a Bat-friendly Residential Swimming Pool?
Elizabeth J. Agpalo and Victoria J. Bennett
Department of Environmental Sciences, Texas Christian University, Fort Worth, USA

For urban environments to support an abundant and healthy bat community, resources for a diversity of species need to be readily available, including roosting sites, foraging opportunities, commuting routes, and water sources. For example, bats typically have been recorded using water sources in urban areas, such as drainage ditches, lakes, and ponds. However, in areas where temperatures are consistently high and rainfall limited, these sources tend to be ephemeral. During these periods, bats have been observed utilizing an alternative water source in the form of residential swimming pools. Thus, if such pools can be made more attractive to bats, this could be a strategy implemented to improve urban habitats. We, therefore, set out to determine what features, primarily size, shape (round or square), lighting, and treatment (chlorine, salt, mineral) encouraged bats to drink at pools. From June to September 2016 and 2019, we conducted behavioral surveys at 14 pools in suburban Fort Worth, Texas. Using thermal cameras and acoustic detectors, we recorded bat foraging and drinking activity. Our results to date demonstrated that while shape did not influence pool use, treatment type, lighting, and size did. For example, bats were observed drinking more readily at mineral pools. Pools with flood lights on all night were avoided entirely by bats, and all species (7 in total) were recorded at pools that exceeded 40 m^2 in size. With this information, we can better advise interested residents in urban neighborhoods how to make their backyards more bat-friendly.

Population Genetic Analysis of the Big Brown Bat in the Eastern United States
Juan Pablo Aguilar Cabezas and Joseph S. Johnson
Department of Biological Sciences, Ohio University, Athens, USA

The big brown bat (*Eptesicus fuscus*) is an ideal species for population genetic analyses because it is widely distributed, is believed to have a partial migratory strategy, and appears to be minimally affected by white-nose syndrome (WNS). In this study, we estimated genetic diversity, population structure, population connectivity, and population size trends by analyzing the cyt-b gene from big brown bats sampled across seven states in the eastern United States. We found some genetic differentiation among populations and high haplotype diversity. Bayesian clustering using the program Structure and model-based-distance clustering revealed two subpopulations. A Bayesian skyline plot analysis showed a decline in populations of big brown bats over time. In addition, we found a signal of positive selection in the cyt-b gene, concordant with the hypothesis that OXPHOS genes are under selection in bats because of the importance of energy demand. Also, the haplotypes differed from the cyt-b gene deposited in the National Center for Biotechnology in six amino acid substitutions, such as a cysteine/glycine to alanine. These data show high dispersal and connectivity among big brown populations, although some regional clustering does occur, and that although the species is thought to suffer low mortality from WNS, populations have been declining for around 2,000 years with a recent acceleration in this process. Given the importance of bats as pollinators, seed dispersers, and plague controllers, these findings of positive selection and population contraction encourage additional investigation to identify the selective pressures and the extent of population decline using nuclear data.

The Role of Temperature in Assemblage Structure of Overwintering Insectivorous Bats
Brett R. Andersen[1], Richard D. Stevens[1,2] and Liam P. McGuire[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, USA; [2]Department of Natural Resources Management, Texas Tech University, Lubbock, USA

While community structure is typically considered to result from long-term ecological and evolutionary processes, behavior and physiology of temperate bats combined with variable environmental conditions can result in dynamic assemblages that vary from day to day. Overwintering insectivorous bat assemblages in temperate regions are one example, although the rules governing their structure are poorly understood. When faced with elevated thermoregulatory costs and reduced prey availability in winter, many bats opt to hibernate or migrate, but some populations, especially at southern latitudes, regularly fluctuate between using torpor and remaining active depending on environmental conditions. This effectively removes or reintroduces species on a nightly basis resulting in a dynamic assemblage. In this study, we aim to understand the role of ambient temperature in determining bat activity based on species-specific thresholds. From December through March 2018 and 2019, we recorded bat activity at 72 sites in managed conifer forests of central Louisiana and eastern Texas. Over 1,568 detector nights of recording yielded approximately 37,000 bat passes representing all 12 species expected to occur in the region. Species richness was highly correlated with temperature and species-specific activity profiles were characterized by temperature thresholds. These results suggest that temperature significantly influences community structure in overwintering bats potentially due to species-specific morphological, behavioral, or phylogenetic characteristics. Future research will investigate how temperature affects bats across a latitudinal gradient and how species characteristics and local adaptations combine to structure bat communities.

Factors Influencing Bat Occupancy of Artificial Roost Boxes
Michelle Arias[1], Sarah Gignoux-Wolfsohn[1], Kathleen Kerwin[2] and Brooke Maslo[1,2]
[1]Department of Ecology, Evolution and Natural Resources, Rutgers, State University of New Jersey, New Brunswick, USA; [2]Rutgers Cooperative Extension, Rutgers, State University of New Jersey, New Brunswick, USA

Provisioning bats evicted from man-made structures with artificial roost boxes is a common strategy for mitigating the negative impacts exclusions have on bats; however, formal assessment of the effectiveness of this practice is rare. Using data from two bat conservation programs in New Jersey (Rutgers University Wildlife Conservation and Management Program and Conserve Wildlife Foundation of New Jersey), we explored factors significantly affecting occupancy rate of artificial roost boxes. We extracted from the dataset information on roost box occupancy, age (time since installation), placement (building, tree, or pole), and whether or not an exclusion had been performed in the property. We also tested the influence of multiple physical characteristics (i.e., color) of the roost box, as well as landscape factors (i.e., distance to water). Overall, 27% of roost boxes were occupied by bats. Predictor variables

explaining the majority of variation in occupancy included roost box age, placement, and exclusion history. Roost boxes mounted on buildings had a significant positive effect on occupancy and increased with time since roost box installation. Occupancy was also highly dependent on whether or not an exclusion had been performed on the property; 86% of roost boxes installed on a building after an exclusion were occupied. Our results provide support for installing artificial roost boxes to mitigate negative impacts to evicted bats and provide justification for mounting roost boxes on structures close to the original roost entrance.

A Cross-taxa Test of Hypotheses for Why Bats Are Killed by Wind Turbines
Erin F. Baerwald, Simon A. H. Fense and R. Mark Brigham
Department of Biology, University of Regina, Regina, CAN

Wind turbines are a rapidly increasing means of generating electricity, and although wind energy is relatively environmentally friendly, it is not without ecological impacts. One concern is the large number of bats killed at some wind energy facilities. While there are many hypotheses that have been proposed to explain these fatalities, currently there are no definitive answers. We took a novel approach to evaluate the various hypotheses by using data on fatality rates of Nightjars (Order: Caprimulgiformes), a threatened avian Order that are ecologically similar to the bats killed most frequently at turbines across North America, the Lasiurine bats. We predicted that if the reason for collisions is general to nocturnal aerial-hawking insectivores, fatality rates at wind turbines should be similar across taxa. If fatality rates differ across taxa, then the reasons for fatalities are more specific to the Lasiurine bats. We used the Bird Studies Canada Wind Energy Bird and Bat Monitoring Database for data on fatality rates within Canada and the American Wind Wildlife Information Centre Database for data on fatality rates within the United States. These data indicate that fatalities of Nightjars at wind turbines are three orders of magnitude lower than for bats, even at the same sites. This lends support to the idea that the reason for high numbers of bat fatalities is related to being a bat (e.g., roost attraction, mating behavior, and/or anatomy) and not to being a nocturnal aerial-hawking insectivore (i.e., foraging).

Preliminary Analyses of the Roosting and Foraging Ecology of *Myotis lucifugus* on Prince Edward Island
Evan W Balzer[1], Catherine Kennedy[2] and Hugh G Broders[1]
[1]*Biology, University of Waterloo, Waterloo, CAN;* [2]*Environmental Studies, University of Prince Edward Island, Charlottetown, CAN*

The behavioral ecology of post white-nose syndrome *Myotis lucifugus* on Prince Edward Island (PEI) is poorly understood, but the geography of Prince Edward Island National Park (PEINP) represents a unique opportunity to examine the habitat use of these endangered bats. The national park is long and narrow, abutting the ocean along its entire northern border and populated farms and towns to the south. Unlike other study areas which are often strictly forested or residential, PEINP has ocean, forest, and populated regions within the foraging range of *M. lucifugus*. We anticipate that the roosting behavior of bats foraging in the park can give insight to roost preference. If *M. lucifugus* prefer anthropogenic roosts to natural ones, then we expect our tracked bats will generally leave the park to roost in areas with a higher density of buildings. We netted for bats using mist nets at sites across PEINP from June 5 until August 13, 2019, and tracked a subset of the captured bats to diurnal roosts using radio telemetry. We primarily caught female bats, and most tracked bats used anthropogenic roosts outside the park. We propose using our second field season to sample at non-park sites comparable to park ones to see if roost preference is influenced by tree cover and housing density. Additionally, we hope to characterize important characteristics of anthropogenic roost structures. Early evidence supports the contention that PEINP represents important foraging habitat, and that the relationship between homeowners and roosting bats is key to the persistence of *M. lucifugus* on PEI.

Bats Draw Undergraduates into Studying Mathematics and Biology Together
Krista Beck, Karissa Rico and Jason E. Miller
California State University Channel Islands, Camarillo, USA

Once upon a time, a biology major could graduate with a B.S. degree with little or no mathematics on their college transcript. Times have changed. Accessibility to low cost data storage and high-speed computing power has transformed the academic study of biology, and the open source software movement has made world-class statistical and modeling software available to biologists in every area (e.g., R, Octave, Python). While the undergraduate curriculum in biology has been slow to keep pace with these changes, professional societies and professional societies and foundations have invested in programs that aim to transform undergraduate degree programs to reflect

the reality of the 21st century. This poster describes how we have used the beauty of bats (and NSF seed funding) to develop an interdisciplinary training program to prepare undergraduates to work at the intersection of the life and mathematical sciences. We describe how the natural history of bats provides an excellent platform for motivating students in biology and mathematics to work in an interdisciplinary fashion. Specifically, we use the question of finding (foraging) bats, acquiring their foraging acoustics, and then identifying them to species using machine learning techniques (e.g., discriminant function analysis).

Multi-dimensional Resource Use by a Southern Appalachian Bat Assemblage

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[1]Center for Bat Research, Outreach, and Conservation, Indiana State University, Terre Haute, USA; [2]Institute for Bird Populations, University of Missouri, Columbia, USA

Ecological niches are multi-dimensional, but multi-dimensional analyses of bat resource use are uncommon. Understanding how bat assemblages are structured may be enhanced by multi-dimensional, assemblage-wide studies of resource use. We conducted such an analysis for a Southern Appalachian bat assemblage via a spatially-distributed acoustic survey at 50 random sites in Great Smoky Mountains National Park, sampling from May–August 2015–2016. We deployed Pettersson D500X detectors on trails and early successional openings, parsing calls into Myotis, Mid, and Low phonic groups. We tested 12 generalized linear mixed-effect models quantifying bat acoustic activity as a function of distance to water, proportion of forest in 500-m buffer, basal area, and canopy closure, using an information theoretic approach to compare models. We assessed use of 4 major habitat types via ANOVA. We used a non-parametric kernel density estimation procedure to describe trends and examine degree of temporal overlap in activity among phonic groups. Myotis and Mid bats exhibited the greatest proportion of temporal overlap, but differed spatially. Myotis focused activity at sites with more forest in a 500-m buffer and used northern hardwood forest most often and early successional habitat least often. Mid bats used early successional habitat most often and spruce-fir forests least often. Temporally, Low bats overlapped least with Myotis, but Low bats showed no significant spatial variation in habitat use. This Southern Appalachian bat assemblage uses resources in complex ways that may not be apparent by spatial analyses alone. Future studies should examine temporal and dietary dimensions of resource use.

Microbiome Classification Studies of *Myotis sodalis* with Further Identification of Microbiome Chitinase-producing Bacteria

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Bats serve a very valuable role within the environmental and human world. They are responsible for a multitude of beneficial processes, such as aiding in the control of disease, pollination, and seed dispersal. Since its emergence in 2006, white-nose syndrome (WNS) has caused a large decline in bat populations. Interestingly, some bat species experience illness from *Pseudogymnoascus destructans* while other species do not. Could it be the microbiome plays a role in protecting bats? We aimed to collect and characterize bacteria from the microbiome of WNS-affected *Myotis sodalis* and identify any chitinase-producing bacteria that have the ability to break down chitin. We collected samples from *M. sodalis* via swabs of the surface skin in the oral, wing, and genital regions of bats caught by harp trapping and mist netting in Missouri and Indiana. The characterization of the microbiome and identification of chitinase-producing bacteria is done through isolation and differential hands-on lab techniques. Bacteria will be characterized down to genus. Results gathered from this work will be beneficial to aide in the relation of bats and their microbiome influence to possible disease susceptibility or defense. With the detrimental decline of bat populations, especially within the endangered North American species, research to broaden what we know has only become even more prevalent.

Multi-species Roosting May Bias Emergence Count Surveys in Eastern North America

Scott M. Bergeson and Austin Motz
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Emergence counts are frequently used as a low-impact method of monitoring bat populations. However, it is difficult to identify the species of individual bats when employing this method. Thus, most researchers assume that all bats that emerge from a roost are the same species. This is a risky assumption that, if proven false, could greatly impact estimates of population size. To determine the prevalence in which this assumption is broken, we requested

data from bat biologists working in the eastern United States. We received data from nine researchers that confirmed the occurrence of roosts containing multiple species of bats on a single day (multi-species roost). Reported multi-species roosts included large bridge roosts, bat boxes, BrandenBark artificial roosts, and tree roosts. These roosts contained combinations of nine bat species; *Myotis sodalis*, *M. lucifugus*, *M. septentrionalis*, *M. grisescens*, *M. leibii*, *M. austroriparius*, *Nycticeius humeralis*, *Corynorhinus rafinesquii*, and *Eptesicus fuscus*. Within these multi-species roosts, one individual bat species was typically found in numbers that comprised the majority of occupants, while other species of bats were found in numbers higher than anticipated (i.e., more than one individual bat/outlier) The average percent composition of an individual species within a multi-species roost was 38.6 ± 0.3%. These results suggest that multi-species roosts do occur, and the number of bats of non-target species in each roost may not be negligible. Biologists should consider this potential bias whenever employing emergence counts as a method to survey bat populations.

Is There a Silver Bullet for Managing White-nose Syndrome? Comparing Management Decisions across Pathogen Emergence Zones

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In the last decade, federal, state, and provincial agencies, tribal and private organizations, and academic institutions have collaborated on developing surveillance, monitoring, research, and management programs for white-nose syndrome (WNS). As a result, scientists and managers have learned a great deal about variations in host ecology and pathogen dynamics; however, effective mitigation measures to combat the disease remain elusive. To address this mismatch between research and management, we used decision analysis to assist wildlife managers located within each WNS pathogen zone (i.e., WNS Confirmed, *Pd* Detected, and *Pd* Not Detected) to identify management strategies for bat populations of concern. Across these decisions, we identified differences in how each manager approaches and implements actions to prepare for, or combat, WNS. We completed three workshops and found that management objectives and actions were consistent across managers and pathogen zones. Here, we present common themes and risk profiles that may aid in the development of conservation strategies in other management jurisdictions, as well as other disease systems.

Midnight Snack: Investigating the Consumption of Prey by Bats during Hibernation in Tennessee

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Temperate North American bat species use seasonal hibernation to conserve energy when ambient temperature is low and food resources are scarce. Previous research suggests that migratory species, such as tree bats, and species known to roost in thermally unstable locations are more likely to remain active throughout winter. Recently, studies conducted in the southeastern United States. documented emergence activity of cave roosting species throughout the hibernation period. To determine if individuals were foraging during periodic winter arousals, we captured bats emerging from five caves in Tennessee over the course of six winters (October–April 2012–2018). We used NextGen sequencing to analyze guano from 454 individuals, representing 10 species of bats. We analyzed 116 samples using the Ion Torrent platform for guano collected during winters 2012–2014 and 338 samples using the Illumina MiSeq platform for guano collected during winters 2014–2018. Our objectives were to 1) determine the composition of prey consumed by bats during winter; 2) identify the differences in the consumption of prey consumed among species. A total of 2,440 Operational Taxonomic Units (OTUs) were consumed by bats active in winter, with 1,135 (~ 47%) identified to species or order in BOLD. Bats captured during winter consumed a much wider variety of insects than expected. By gaining a better understanding of what bats are consuming during winter, we may be able to manage for, and promote the availability of, targeted insect prey known to be consumed during a time when bats are most vulnerable to disturbance or disease.

Response of Bats and Nocturnal Food Webs to Mountain Pine Beetle Outbreaks

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Climate change is causing increasing severity and frequency of disturbance events, altering community compositional structure and food web interactions. Bat ensembles exert top down food web influences and are sensitive to disturbance events that alter prey composition and habitat structure. Severe outbreaks of mountain pine beetle (*Dendroctonous ponderosae*) in Colorado impacted over 1.3 million hectares of lodgepole pine (*Pinus contorta*) forests, resulting in widespread defoliation. The secondary successional stages that ensue are linked with changes in insect composition, and bats limited by ecomorphology are expected to respond to changes in habitat structure and prey availability. We conducted an exploratory survey in Roosevelt National Forest, Colorado to identify how mountain pine beetle (MPB) affected lodgepole pine forests have disrupted bat habitat-specific foraging patterns and nocturnal insect abundance and composition. We expect activity of maneuverable, gleaning bats and insect abundances to be greater in severely affected stands than in unaffected stands. We deployed SM2 Wildlife Acoustics bat detectors in severely affected (≥50% stand mortality) and unaffected (≤10% mortality) lodgepole pine stands from June to August 2019 to survey bat activity. We used a Townes Style Malaise trap to determine nocturnal flying insect abundance and composition and quantified understory and overstory vegetation structure at each detector location. Preliminary analyses showed high bat activity in severely affected stands with higher degrees of coarse woody debris (CWD) and understory cover. We hope to quantify how the progression of large-scale successional changes of beetle affected forests alter competitive interactions among foothill bat ensembles.

***Myotis sodalis* and *M. septentrionalis* Captures and Roosting Preferences in Post White-nose Syndrome Missouri 2017–2019**

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North American bats are facing precipitous declines from climate change, energy development, and white-nose syndrome (WNS). WNS was first detected in Missouri in 2010 and since 2012 there have been large population declines among the cave hibernating species. We conducted mist-net surveys during the summer maternity season at six Missouri Department of Conservation lands in northern Missouri over three years. A total of 632 bats representing 9 species were captured over 500 mist-net nights. Thirty-nine *Myotis sodalis* were captured in 2017, 9 in 2018, and 8 in 2019 whereas 5 *M. septentrionalis* were captured in 2017, 1 in 2018, and 0 in 2019. We compare roost radio telemetry results with resource use studies for *M. sodalis* and *M. septentrionalis*. Of note, *M. sodalis* maternity colonies roosted in cracks and crevices in snags with little or no bark on a lake rather than roosting beneath exfoliating bark. Wildlife managers can use this information and approach to evaluate bat population trends in the post-WNS Midwestern landscapes to design and implement appropriate conservation strategies.

Specialized Landing Maneuvers in *Thyroptera tricolor* Reveal Linkage between Roosting Ecology and Landing Biomechanics

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Disk-winged bats (*Thyroptera* spp.) are the only mammals that use suction to cling to smooth surfaces, having evolved suction cups at the bases of the thumbs and feet that facilitate attachment to specialized roosts: the protective funnels of ephemeral furled leaves. We predicted that this combination of specialized morphology and roosting ecology is coupled with concomitantly specialized landing maneuvers. We tested this prediction by investigating landings in *Thyroptera tricolor* using high-speed videography and a force-measuring landing pad disguised within a furled leaf analogue. We found that their landing maneuvers are distinct among all bats observed to date. Landings comprised three phases: 1) approach, 2) ballistic descent, and 3) adhesion. During approach, bats adjusted trajectory until centered in front of and above the landing site, typically the leaf's protruding apex. Bats

initiated ballistic descent by arresting the wingbeat cycle and tucking their wings to descend toward the leaf, simultaneously extending the thumb-disks cranially. Adhesion commenced when the thumb-disks contacted the landing site. Significant body reorientation occurred only during adhesion, and only after contact, when the thumb-disks acted as fulcra about which the bats pitched 75.02 ± 26.17º (mean ± s.d.) to swing the foot-disks into contact. Landings imposed 6.98 ± 1.89 bodyweights of peak impact force. These landing mechanics are likely influenced by the orientation, spatial constraints, and compliance of furled leaf roosts. Roosting ecology influences critical aspects of bat biology, and taken as a case-study, this work suggests that roosting habits and landing mechanics could be functionally linked across bats.

Bat Activity at Vernal Pools in California

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Vernal pools are a protected yet diminishing habitat in the Central Valley of California. These shallow, ephemeral wetlands have an impervious hardpan, filling with rainwater during winter and spring, but are dry throughout the summer and fall. They are home to several rare and endemic species of plants and animals. Vernal pools may provide a habitat for bats to forage as well as access to water during the spring, especially as surrounding habitats dry, yet there are no studies of bat activity at vernal pools in California. We hypothesized that bats would utilize these habitats to forage and drink. Acoustic recorders were deployed at Pool 22 of the Vina Plains Preserve in Tehama County to record nightly, starting on April 20, 2019. There was significant bat activity—almost exclusively *Tadarida brasiliensis*—at the vernal pool during the spring, and this reduced in summer as the pools dried. Activity at the pool was considerably higher than at a control site one km away—averaging 43 and 5 passes per night respectively. Bat activity also surprisingly rebounded during late July and August, perhaps indicating changes in insect availability. Peak *Tadarida* activity was 8:00 to 10:00 pm and then again at 4:00 am, whereas *Myotis* spp. were most active between 1:00 and 3:00 am. Preliminary analysis indicates at least 20%, and up to 60%, of nightly bat passes included feeding buzzes, suggesting that vernal pools are actively used by bats as foraging habitat.

Synchronous Muscle Recruitment for Stable Flight Control in Egyptian Fruit Bats

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Bats demonstrate a remarkable capacity to recover flight stability after perturbations from the environment. This ability is likely supported by the precisely-timed recruitment of wing muscles, which modulate the production of aerodynamic forces. However, we know little about neuromuscular control mechanisms in bat flight. Studies of limb movement in response to perturbations during terrestrial locomotion show a proximo-distal control gradient in which performance of muscles that control proximal joints is insensitive to perturbations, in contrast to activity of muscles controlling more distal joints. We hypothesized that when flight is asymmetrically perturbed, the activity of left and right pectoralis major muscles would remain synchronized. To test this, we recorded electrical activity of the pectoralis muscles using wireless dataloggers (Vesper Pipistrelle, 4.1g) from five *Rousettus aegyptiacus* trained to fly along a corridor (1.5 x 6.0 x 2.0m). Bats passed through a window that divided the corridor's length in half en route to a landing pad; in perturbed flights, a jet of air was delivered to one wing (2.5X body weight) as bats flew through the window. We tracked the 3D position of 15 markers on each individual using six high-speed cameras. We compared the timing of muscle recruitment with kinematics for all flights. Results show symmetrical recruitment in all flight trials, demonstrating that recovery of stable flight after perturbation does not alter the recruitment symmetry of the pectoralis in *Rousettus aegyptiacus*. This supports the idea that proximo-distal limb muscle activation gradients are a fundamental characteristic of vertebrate neuromechanical control.

Size Matters: Evidence of Resource-defense Polygyny in a Subtropical Bat
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Understanding social structure and animal behavior is critical for effective species conservation. Many tropical bat species form harems, where males play key social roles by defending groups of females directly (female-defense polygyny) or the resources that females need (resource-defense polygyny). *Eumops floridanus* (Florida bonneted bat) is an endangered subtropical species thought to form harems, but our understanding of its social structure, reproduction, and behavior is rudimentary. We evaluated demographic variation in morphology and behavior of *E. floridanus* to determine if this species may exhibit female or resource-defense polygyny. We used a three-year dataset of 341 individuals uniquely marked with Passive Integrated Transponders (PIT tags), coupled with tri-annual capture records, to track bats at 5 roosts fitted with PIT tag readers. We identified likely dominant males in each roost using morphometric and reproductive status characteristics. We assessed differences among sex, and status categories in three primary metrics: roost activity, emergence times, and foray duration per night. Large, dominant males were more active at roosts, spent less time foraging and returned to roosts more frequently during the night than females and other smaller males. Females spent the most time foraging regardless of reproductive status. We provide evidence that *E. floridanus* forms small harem groups that are active year-round and exhibits resource-defense polygyny, with the largest males defending the roost at the expense of time spent foraging. We suggest that roost sites represent critical resources for male *E. floridanus* to recruit and gain access to females, which has important implications for conservation.

Do Bats Use Olfactory Cues to Locate Potential New Roosts?
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Understanding how bats select roosts is crucial to their management. This knowledge could help exclude bats from buildings and attract them to protected areas. Research on how bats locate roosts has focused on acoustic cues. Other studies have found effects of scent-marking. However, inadvertent chemical cues in bat guano and urine might also influence roost-finding. To test this hypothesis, I ran a series of tests to see if bats chose to roost in sites stained with guano and urine, using vampire bats (*Desmodus rotundus*) and velvety free-tailed bats (*Molossus molossus*) in Panama and big brown bats (*Eptesicus fuscus)* in Ohio. To measure attraction to scent cues, I filmed captive bats (24 *Desmodus* and 18 *Molossus*) in an experimental arena. To count visits to roosts in the field, I used paired ultrasonic microphones installed within two adjacent experimental roosts, where one roost entryway was stained with guano and urine, while the other served as an unscented control. Roosts were deployed at 16 sites in Panama and seven sites in Ohio. To test the impact of acoustic cues, I played back calls of bats between the two roosts. Preliminary analysis suggests that 1) scent from guano is not a strong enough attractant to draw bats into new roosts and 2) captive bats are not immediately attracted to guano scent, but they appear to show a preference to roost in the scented sites after longer time intervals. Our work gives insight on the capacity for scent cues as a tool for bat management.

Integrative Maps for Bats of the World
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Spatial data are essential for visualizing the distribution of bats, environmental gradients, landscape genetics, and temporal changes to promote and inform research and sustainable management decisions. As known bat species diversity continues to increase, spatial data to create geographic distribution models are in high demand. Recognizing the limitations of all spatial data is essential as there are many primary open source data sets available. In an effort to visualize the most probable distribution for each species represented on the Bats of the World: A Taxonomic and Geographic Database (www.Batnames.org), two open source spatial data sets were used for the species distribution maps. The IUCN Red List polygon data represent the conservative distribution layer, while gbif point data were incorporated using a more discriminatory approach by developing a "potential outlier" layer for all points that exist outside of the IUCN polygons. ArcGIS Pro Version 2.4 was used to create the geospatial layers in a

coordinate system based on each species geographic range in an effort to reduce distortion for shape, area, distance, and direction. Metadata were updated for all species-specific map layers and then configured to a species Webmap through the Portal into ArcGIS Online. Species Webmaps were reprojected to the WGS 1984 Web Mercator Auxilliary Sphere prior to being linked to the website as interactive species maps. We hope to update all the bat species Webmaps prior to the next biannual review by the Global Bat Taxonomy Working Group of the IUCN Bat Specialist Group in the fall of 2019.

Bats of the California Channel Islands: New Records with New Methods

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Eight bat species were known and documented from the California Channel Islands when J.C. Von Bloeker (1967) presented at the First California Islands Symposium in 1965. Methods of detecting and identifying bats have changed over the past century (Brown and Rainey 2018). Museum collection methods using shotguns have been replaced by mist netting and recording of echolocation signals. Currently, capture or acoustic records have identified 14 bat species (56% of the 25 species known to occur in California) on six of the eight California Channel Islands, with occasional sightings of flying bats on the other two. Bats now compose 78% of the native mammals on the islands (Collins 2012). Recorded echolocation signals are now recognized as valid "vouchers" if the species emits calls that are separable from others. For year-round monitoring, the authors have installed long-term acoustic recording equipment on three of the islands. For example, echolocation signals have identified western red bat (*Lasiurus blossevillii*), hoary bat (*Lasiurus cinereus*), western yellow bat (*Lasiurus xanthinus*), and Mexican free-tailed bat (*Tadarida brasiliensis*) from San Nicolas Island, and western mastiff bat (*Eumops perotis*) and canyon bat (*Parastrellus hesperus*) from Santa Cruz Island. Acoustic data have identified three new species for the California Channel Islands, as well as several new records on individual islands. As acoustic monitoring and other techniques are used more extensively, the number of species documented will increase and the proportions that are resident, vagrant, or transient on each island can be better resolved.

Effect of Flight Duration on ß-hydroxybutyrate Concentration in Blood Plasma of *Eptesicus fuscus*

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Insectivorous bats alter relative use of metabolic substrates to match requirements of their activities, including energetically expensive flight. The "fasting while foraging" hypothesis states that the metabolic demands of flight often exceed energy intake while foraging, hence bats may metabolize fat stores (especially early in the night) to power flight with ketones, a byproduct of the normal oxidation of fatty acids. Previous studies in bats found increases in the plasma ketone ß-hydroxybutyrate following food consumption paired with or without flight, but no study has explored whether increases in plasma ß-hydroxybutyrate occur following flight without food consumption. We used metabolite analysis to examine changes in plasma ß-hydroxybutyrate as a function of flight duration in 2 groups (fall and spring) of captive big brown bats (*Eptesicus fuscus*). We fasted bats for 12 hours prior to flight (exercise treatment) or rest (control), and then collected interfemoral vein blood. Exercise activity was quantified as flight time. For the fall group, we collected three rest and one flight sample. Results for the fall group were mixed and the interpretation of data patterns may be complicated by changes in metabolism that occur in the Fall when bats physiologically prepare for hibernation. To control for seasonal effects, group 2 bats were tested in the spring, and we collected two rest and three flight samples. We found a positive correlation between flight duration and levels of plasma ß-hydroxybutyrate in the spring group, which supports the fasting while foraging hypothesis.

Anthropogenic Effects on Landscape Connectivity in Bat Communities of Puerto Rico

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The current biodiversity crisis is driven by anthropogenic (e.g., habitat transformation) and natural (e.g., hurricanes) disturbances that can disrupt connectivity and lead to extirpation or extinction. The Caribbean is a biodiversity

hotspot with a high rate of mammal diversity loss since the Last Glacial Maximum. Puerto Rico, one of the most isolated islands in the Caribbean, is home to 13 bat species that inhabit three different ecosystems: tropical moist and dry forests, and Bahamian-Antillean mangrove forests. These ecosystems have been subjected to different levels of disturbance over time, providing a living laboratory to investigate the effects of anthropogenic and natural disturbances, and evaluate potential threats to bat dispersal, survival, and population recovery. Here, we use circuit and graph theory to quantify structural connectivity between 53 unique localities on Puerto Rico across these ecosystems. We built a network of bat communities using similarity and geographic distances to identify important localities that serve as community connectivity corridors. Our results identify several urban (e.g., San Juan, Bayamón, and Toa Alta) and forest (e.g., Arecibo, Adjuntas, Lares, and Orocovis) localities that create corridors from East to West, with poor connectivity from North to South across the Central Cordillera. Northern urban localities still provide suitable habitat in small fragmented forest remnants, in contrast with localities with intense agricultural pressure in the south of the island. By defining and quantifying bat communities and connectivity, we can assess population changes and recovery in the face of global change.

Hydrogen Isotopes Reveal Complex Seasonal Migratory Structure in At-risk Tree-roosting Bats in North America

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Understanding migratory patterns is essential to predicting the impacts of, and organismal tolerance to, global environmental change. Several species of bat migrate long distances within North America, exhibiting potentially complex migratory structure. These species have been negatively impacted by human development during migration, and some might be at risk of extinction. However, bat migration has thus far been very difficult to study by traditional means. Stable isotope signatures present a promising alternative, but bat movement patterns have thus far been too complex to summarize within the context of small regions or distinct management units. Understanding of bat abundance and habitat usage is also limited, so it is difficult if not impossible to identify distinct regions of seasonal habitat. We used stable hydrogen isotope analysis in conjunction with emerging methods of analytically comparing probabilistic assignment models of animal origin to examine migratory structure in three species of North American tree-roosting bat. Our results indicate a strong signal of migratory structure in two of the three species, and the presence of partial migration (year-round residency of some individuals, up to very long-distance migration in others) in all three species. These results have important implications for understanding the migratory ecology, evolutionary ecology, and conservation risks facing these species.

Bats and Apples: Bat Ecosystem Services in Apple Orchards in Central New York

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New York is the second largest producer of apples in the United States. Conventional farmers reduce pest damage using pesticides. However, in addition to high economic costs, pesticides are toxic and decrease natural enemies and pollination services. Thus, many farmers have opted to use organic systems, but they experience higher crop damages. For years, we have known that insectivorous bats can suppress nocturnal insects. However, because this is not an obvious service, their value is not placed on its magnitude. Moreover, although multiple studies have looked at bat pest-control services in a variety of crops, the importance of bats in New York apple orchards has not been evaluated. Thus, we monitored presence of bats and pests in apple orchards, to estimate their pest-control value. So far, we have detected 8 bat species foraging in both conventional and organic orchards. The most common species is *Eptesicus fuscus*. This species is more active from 9 pm to midnight, corresponding with the activity peak of the codling moth, the most common apple pest in the area. This suggests that *E. fuscus* is probably the most important pest-control species in the area. Currently, we are evaluating density and activity of pests and collecting bat pellets to estimate bat diet at apple orchards. With these data, we want to estimate the monetary contribution of bats as pest control. We are confident that our estimates will resonate in the scientific community, the general public, and policy-makers.

Vampire Bats that Cooperate in the Lab Re-form their Social Networks when Back in the Wild
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Behavioral ecologists disagree about the concept of 'social bonds.' Some authors argue that many animals form social relationships similar in form and function to human friendships. Others point out that such bonds are often defined using correlational social network data and many nonsocial effects can create these same patterns. Other authors argue that these patterns might be based on stable options of partners rather than on partner fidelity. Here we present a framework for resolving this controversy: social bonds exist but their existence alone cannot explain why animals cooperate because they vary along a spectrum of stability. Measuring relationship stability is therefore necessary to test the roles of partner control, partner choice, and threat of partner switching. We apply this framework to vampire bats. If social bonds actually cause social network structure, then social preferences tested under controlled conditions should predict association even in a drastically different physical and social environment. Using a recently-developed high-resolution automated proximity sensor system, we show that vampire bats that cooperate in the lab reform their social networks when released into the wild. Allogrooming and food-sharing induced in captivity among female vampire bats over 22 months predicted their assortativity and association rates in the wild. Not all social bonds survived. On one hand, social bonds are not an emergent byproduct of a stable captive environment and they are a cause rather than a mere consequence of spatial structure. On the other hand, the social environment matters and even strong social bonds are not entirely stable.

Mineralization of the Trachea and Larynx in Laryngeally Echolocating and Nonecholocating Bats
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Cartilage that forms the structural basis of the trachea and larynx in echolocating bats is often relatively heavily mineralized compared to those of other mammals. Mineralization is thought to reinforce the cartilage in response to forces applied through echolocation and possibly flight. Using computed tomography, I assessed the relative levels of mineralization of tracheal rings, cricoid, thyroid, and arytenoid cartilages in nonecholocating, low intensity low duty cycle, high intensity low duty cycle, and high intensity high duty cycle echolocating bats. All individuals showed evidence of tracheal ring mineralization. Larger bats exhibited more extensive tracheal ring mineralization compared to smaller bats irrespective of the ability to laryngeally echolocate. Surprisingly, nonecholocating bats had extensively mineralized cricoids and thyroids and no evidence of mineralization of the arytenoids. Low intensity low duty cycle bats only had mineralized cricoids. High intensity low duty cycle bats had patchy mineralization of the cricoids, thyroids, and arytenoids. High intensity high duty cycle bats had extensively mineralized cricoids and arytenoids and large sections of mineralization of the thyroids. The degree of laryngeal mineralization matched the presumed workload associated with the echolocation system, in that low intensity low duty cycle bats had the least amount of mineralization and high intensity high duty cycle bats had the most. None of the echolocating bats had completely mineralized thyroids, which may reflect a dynamic function, moving and distorting during sonar signal production. Whereas, the thyroids of nonecholocating bats may play a larger role in maintaining the airway during ventilation and require more rigidity.

1406 Reasons Why Diversity is Important
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What if biologists chose to study only one bat species in the world? Despite gaining tremendous understanding of the animal, this species would define our knowledge of Chiroptera. Everything we identified about behavior, diet, disease, echolocation, evolution, habitat use, hibernation, physiology, and reproduction would be focused through the lens of a single species. As biologists, we recognize this is a ridiculous proposition. Why then, should we be any less concerned about representing the full range of human qualities and attributes in our profession? A variety of genders, ethnicities, sexual orientations, perspectives, areas of expertise, and cultures leads to better science. Increases in productivity, creativity, and quality rise when women and historically underrepresented groups participate. Problem solving and collaboration among groups of people with diverse backgrounds and experiences leads to more innovative outcomes. Diverse groups of people raise different questions; questions drive science, and that moves science forward. For example, a First Nations woman wildlife biologist who studied gene flow and population structure developed a non-invasive approach to sample DNA. She helped establish the practice of using

fecal samples for DNA collection. Despite these and other examples, we struggle to ensure equal representation. We are drawn to people who are like us. What challenges do women and minorities face to entering and excelling in science and the study of bats? What are practical approaches to increase, recognize, and encourage contributions of diverse people into this profession? We must recognize our biases, create connections, take action, and be allies to underrepresented groups. Those in leadership roles can recruit and train women and minorities, foster an open work culture, mentor, encourage cross-job communication and nonhierarchical structures, make sure women and underrepresented minorities represent 15 to 30% of team members to gain critical mass. We drive science forward when "we" represents all of us.

Collaborative Monitoring Strengthens Macro-scale Assessments of White-nose Syndrome Impacts for North American Bats

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In order to understand macro-scale population dynamics and impacts from perturbations operating at large spatial scales, monitoring at broad scales is imperative. The invasive fungal pathogen, *Pseudogymnoascus destructans* (*Pd*), causing the disease, white-nose syndrome (WNS) in hibernating bats, has caused severe, local declines and extirpations in several species of hibernating bats throughout North America. However, in order to examine macro-scale impacts of WNS on North American bat species, monitoring and assessment must be conducted at broad scales. The North American Bat Monitoring Program (NABat) was initiated in 2015 as the first broad-scale coordinated effort to monitor bat species across North America. Leveraging efforts by NABat, we used winter count data of five species of hibernating bats (*Myotis lucifugus*, *M. sodalis*, *M. septentrionalis*, *Perimyotis subflavus*, and *Eptesicus fuscus*) collected from the US and Canada at over 200 sites across 25 states and provinces, and spanning 23 years from 1995–2018. For four out of five species (*M. septentrionalis*, *P. subflavus*, *M. lucifugus, M. sodalis*), we found that WNS caused sustained declines greater than or equal to 90% and extirpations throughout their ranges following the invasion of *Pd.* Results at the macro-scale also indicate losses by an order of magnitude (log-scale) difference following *Pd* invasion for the same four species. Our study highlights the strength of macro-scale assessments that can only be derived from broad-scale monitoring efforts, and which are needed to implement greater global, national, and state/province-level protection for the most impacted species.

Genetic Approaches Improve our Understanding of Bat-wind Turbine Impacts

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Understanding the impacts of wind energy mortality on bats requires accurate assessments of species and sex, but this is not always possible in the field. This study applied a genetic approach to identify sex and species using bat carcasses collected during post-construction fatality monitoring from two wind energy facilities in south Texas in 2017 and 2018. This region has a diverse bat community with morphologically similar species, and early reports suggested that both *Lasiurus intermedius* and *Lasiurus ega* would be impacted. From these facilities, we obtained wing tissue samples from 440 bats identified as *L. intermedius* (66%) or *L. ega* (33%) in the field. Following DNA extraction, regions of the X and Y chromosomes were amplified using PCR to determine sex (n = 412) and a region of the mitochondrial COI gene was sequenced to verify species identification (n = 426). Field sex assignments were 18% female, 19% male, and 63% unknown, with no difference between species. Molecular data indicated a 53% female-biased sex ratio. *L. ega* had more field misidentifications than *L. intermedius* with 24% versus 8%, respectively. Sequencing data also revealed *L. xanthinus* (n = 36) and *L. blossevillii* (n = 3), two species that were not known to occur in this region of Texas. Our data indicate that molecular sex determination is necessary for studies investigating influences of sex on collision risk. We also recommend DNA barcoding be used for species identification in regions with morphologically similar bat species and where species of conservation concern could be impacted.

Understanding Migration Diversity: Connecting Migratory Patterns to Functional Motivations
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Each year billions of animals migrate between seasonally disconnected habitats, influencing the ecological properties of their temporary habitats and filling important ecological roles. Some species make 'to-and-fro' migrations, where all individuals move between seasonal habitats. But, for many species, migration patterns are more complex, involving partial and/or differential migration. Landscape-level patterns of migration are the cumulative result of the collective behaviors of individual migrants (migration is an adaptive trait expressed by individuals). Thus, to understand the adaptive drivers of population level migratory patterns, we must consider the functional motivations (i.e., the current fitness utility of a behavior) of migrating individuals, and how varied functional motivations within populations give rise to the observed diversity of landscape-level patterns of migration. Here, we will first describe a conceptual framework linking the functional motivations of migrants to landscape-level patterns of migration. The framework includes considerations of varied migration strategies that result in different flight and stopover behaviors throughout migration. We apply the framework to a system of long-distance migratory hoary bats (*Lasiurus cinereus*) that exhibit both partial and differential patterns of migration. We find that differences in reproductive contribution throughout the annual cycle between hoary bat sexes are a primary driver of the observed migratory diversity, demonstrating the influence of life history traits on migration. We conclude that our framework is useful for identifying critical natural history gaps, setting meaningful research trajectories for migration conservation, and understanding the evolution of migratory diversity.

Bat Activity on a Gulf Coast Refuge: Understanding Activity Patterns
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There is a lack of knowledge of bat ecology on the Texas Coast, which can guide conservation and management. Our objective was to compare bat activity on the San Bernard National Wildlife Refuge as a response to habitat type (bottomland hardwood, saline prairie, and upland prairie); habitat structure (field, open water, and corridor); and time of night. Preliminary data in a telemetry study suggested evening bats (*Nycticeius humeralis*—a species known to be relatively flexible in roost site selection) are not using the refuge for roosting; however, we predicted bats are traveling to the refuge to forage. We predicted bat activity would be greatest in the bottomland hardwood habitat, open water structure, and equally active throughout the night. We recorded activity with Pettersson D500X detectors on the refuge in summer of 2018 (n = 53 sites). We defined "high level of activity" as being above the 70th percentile of activity. We compared habitat type and structure using percent of nights with at least one hour of high activity and a balanced Analysis of Variance, and time of night by mean number of calls per hour of night and a Chi-square goodness of fit test. Bat activity was similar among habitats and hours ($p > 0.05$). These results, coupled with the preliminary telemetry data, indicate bats are traveling to the refuge and foraging throughout the night on all areas of the refuge. Our management recommendation includes increasing availability of potential roosts throughout the refuge including large-diameter trees and bat boxes.

Open-source Software for Large-scale, High-throughput 3D Video Tracking of Bats
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Three-dimensional video tracking is a powerful tool for studying bat behavior in a variety of contexts such as roost exit counts, predator-prey and social interactions, and encounters with wind turbines. This technique usually requires specialized training and expensive equipment. Here, we present the current progress of a powerful open-source software platform that allows large-scale and high-throughput three-dimensional (3D) video tracking with minimal training. We discuss hardware solutions, comparing thermal and near-infrared cameras. We also demonstrate camera synchronization methods including electronic impulses sent via dedicated cables *versus* acoustic signals broadcast to the camera audio channels. Finally, we demonstrate software tools that are in development for 2D tracking, camera calibration, and multi-object 3D tracking. Together, these tools will provide high-precision quantification of bat movements in a wide variety of contexts with minimal training and equipment.

Impact of Aspect on the Microclimate of Bat Boxes and Artificial Roost Selection of Indiana Bats
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Bat boxes are important conservation tools, providing roosting locations in altered or suboptimal habitats. Of the few designs tested, many findings suggest suboptimal temperatures for bats. In a pilot study, we analyzed the microclimate of a common bat box design from 23 August to 5 September, 2018 at an early-successional field site in Kentucky. Our objective was to develop a temperature profile for bat boxes in this habitat and to assess effects of aspect on box microclimate. We deployed boxes facing either east or north (n = 3 per orientation), and measured internal temperatures hourly. In both orientations mean daily temperatures varied by ~12ºC, and we observed no overheating (i.e., temperatures > 40ºC). Compared to north-facing boxes, east-facing boxes were 0.4ºC warmer on average, peaked in temperature later in the day, and retained slightly more heat at night. Building on these results, we have now deployed 40 rocket style bat boxes at sites in Indiana and Kentucky. A standard design is our control, while 2 designs are intended to increase minimum temperatures, and 2 other designs are intended to reduce maximum temperatures. We aim to profile the microclimate provided by each box in different landscape contexts and to assess the subsequent roost selection by Indiana bats (*Myotis sodalis*) in response to box design and environmental variables. Our results will provide insights into roost selection by Indiana bats, and will better inform resource managers as to the proper design, microclimate, and placement of artificial roosts.

Post-emergence Migration Patterns and Habitat Associations of Female Indiana Bats in Arkansas
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In Arkansas, hibernacula used by federally endangered Indiana bats (*Myotis sodalis*) are well-known; however, migration patterns and maternity colony site selection remains unclear. Vulnerability to disturbance during pup-rearing poses a significant risk to the species making it crucial to gain an understanding of their summer habitat use. Despite extensive survey efforts in Arkansas, little evidence about the existence of maternity colonies has been revealed. In 2006, one maternity colony was documented at the Dave Donaldson Black River Wildlife Management Area in Clay County, Arkansas. Additionally, in July 2015 a single post-lactating Indiana bat was captured in the Ozark-St. Francis National Forest – Big Piney Ranger District in Newton County, Arkansas. To better understand migration patterns and summer habitat use, we used radio telemetry to track female Indiana bats from hibernacula to maternity roost sites in Arkansas during 2018 and 2019. Preliminary data generated in 2018 provided insight of initial migration trajectories, but no maternity colonies were located. In 2019, we tracked one individual from Newton County to Lawrence County, Arkansas, which resulted in the location of one maternity colony comprising two primary and five alternate roost trees. Our results confirm that Indiana bats do form maternity colonies in Arkansas, in the Mississippi Alluvial Plain ecoregion, specifically in the Black River floodplain. We anticipate the discovery of additional maternity sites within the state of Arkansas during the remaining two years of our project.

Movement Ecology of Urban Resident Black Flying Foxes
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The black flying fox, *Pteropus alecto*, is a nomadic species found throughout northern and eastern coastal Australia. Habitat destruction and urbanization have decreased native winter flowering habitat causing nomadic populations to fission into residential colonies in urban areas. To better understand the ecology of resident flying foxes and the possible impacts their movements have on the transmission of disease, targeted studies are needed to examine the movement ecology of *P. alecto*. Our study aims to characterize the movement ecology of winter foraging in two urban resident colonies for later comparison with nomadic colonies at this same time of year. We hypothesize that limited food supply during winter causes resident populations to increasingly rely on lower quality, nearby urban food resources, rather than widely spread native floral resources. In July 2019, we attached GPS-GSM trackers to 6

bats in each of two resident colonies, one highly urbanized and another adjacent to more rural habitat. We recorded 1–16 (and counting) nights of tracking data per bat, allowing comparison of foraging habitats, movement patterns, and variation in nightly foraging activities. Movement ecology of resident individuals is particularly important to understand given the human-wildlife conflict in these urban camps. Furthermore, *P. alecto* is the reservoir host for Hendra virus; therefore, understanding the movement ecology of resident camps is important for understanding disease spillover. Results of our study will contribute to the development of better public communication and ecological interventions, in an effort to break the vicious cycle of human-wildlife conflict in this system.

***Sex Ratios of Big Brown Bats in Michigan over a 10-year Period**

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*** Brooke Daly** received the **White-nose Syndrome Research Award.**

For various reasons, many mammals have disproportionate sex ratios. In 1980, Kurta and Matson (American Midland Naturalist, 104:367–369) indicated that males dominated in a sample of 362 big brown bats (*Eptesicus fuscus*) examined for rabies in Michigan, between 1975 and 1978, and suggested that males live longer than females. The number of animals tested each year has greatly increased since that time, and we reexamined sex ratios in this species, based on more than 14,000 bats that were submitted between 2008 and 2018. The proportion of males (62%) did not differ among the 10 years and was statistically identical to the ratio indicated by Kurta and Matson. The sex ratio did not differ among animals beginning hibernation, in October and November (52% male); in mid-hibernation, from December through February (56%); and those ending hibernation, in March and April (55%), suggesting that the sexes survive hibernation equally well. However, the percentage of males examined during May and June, when most females are pregnant or lactating, was 70%, suggesting a negative effect on the survival of females connected with the rigors of reproduction. Sex ratio of juveniles taken in June or July, when most were non-volant, was equal to the ratio in early August, when all juveniles were flying, indicating that survival from birth to independence is similar between the sexes. Overall, 49% of juveniles were male, which did not differ from the expected 50%.

Labs without Borders: Methods for Extracting, Amplifying, and Sequencing in the Field

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Genomic methods have revolutionized current understanding of the evolution and ecology of bats worldwide. At the same time, air travel restrictions and concerns about emerging diseases have made transporting bat tissues an increasingly expensive and fraught pursuit. To both overcome these restrictions and build capacity in high biodiversity countries, we implemented field-based molecular protocols. First, we sequenced the prokaryotic microbiome of multiple individuals in the field using a standard centrifuge, mini-PCR and mini-gel rigs, and a MinIon sequencer. Modifications to lab protocols included: 1) centrifugation steps robust at high- or mini-centrifuge speed, 2) extending proteinase-K incubation at ambient temperature and evaluating the elimination of ethanol in clean-up during extraction, 3) using lyophilized mastermix in amplification, and 4) eluting in molecular-grade water in library prep. The lack of a high-sensitivity method for quantifying DNA, however, limited the efficiency of multiplexing and reduced the life of the cell in sequencing. Second, we generated mtDNA barcodes using a cheaper, hybrid approach of extracting and amplifying in the field, with subsequent lab-based Sanger sequencing. We added a temperature control ceramic mug and Qubit fluorometer to the kit. By modifying standard procedures, and substituting some equipment with modestly priced consumer products (e.g., the mug), our protocols make critical steps in molecular genetics field-accessible, and open possibilities for future research on genomics, transcriptomics, and disease surveillance in bats.

Testing for Signatures of Dietary Switches in the 'Vision' Genes of Neotropical Bats

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Bats are well known for their highly evolved hearing and echolocation. In contrast, vision in bats has been largely overlooked. Recent molecular research has begun to readdress this balance and suggests that differing visual capabilities may relate to echolocation, diet, and roost preference across species. However, these inferences are largely based on studies of the three main visual opsins involved in color and dim-light vision. Therefore, little is known about the wider molecular adaptations of bats' visual systems and how these may relate to different dietary specializations. To study this, we used the model system of the Neotropical Noctilionoidea superfamily, which comprises ~200 species, and represents an extreme example of mammalian adaptive radiation. Noctilionoids have highly divergent sensory systems, contrasting feeding ecologies (e.g., insects, fruit, and blood), and diversity in the gross morphology of the eye suggests varying reliance on vision across the clade. In order to test for genetic evidence of this, we obtained eye transcriptomes of ~40 species and screened these for the presence of molecular adaptations (i.e., positive and diversifying selection) in key branches associated with changes in diet (e.g., from insect feeding to plant-visiting). Our results revealed that molecular adaptations of vision-related genes have occurred at several key points in noctilionoid evolution, and suggests specific parts of the visual system may be under selection in particular plant-visiting clades.

Estimation of Temporal Trends in Bat Abundance from Mortality Data Collected at Wind Turbines

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Bats experience mortality at wind turbines throughout the world, but the population level effects of this mortality have only been estimated for a single species. In this study, we leveraged a large dataset of standardized bat carcass searches at 699 turbines in southern Ontario, Canada, which were corrected for surveyor efficiency and scavenger removal. Using Bayesian hierarchical models, we tested the hypothesis that abundance of five species of bats has changed over time, controlling for the effects of mitigation at some operations. We explored whether spatial predictors including landscape features associated with bat habitat (such as wetlands, croplands and forested lands) predicted the number of mortalities for each species. We also directly tested the effects of mitigation (increasing turbine cut-in speed from 3.5 to 5.5 m/s) on mortality of each species. Our results suggest a 90–95% probability of rapid declines in the abundance of four bat species in our study area over seven years. The estimated declines were independent of the effects of mitigation, which significantly reduced bat mortality. We observed seasonal variation in spatial predictors of mortality at wind turbines, but woodlot cover consistently predicted late-summer mortality of hoary, red, and silver-haired bats, while mortality of big brown bats was highest at lower elevations. These landscape predictors of bat mortality can inform the siting of future wind energy operations. Nevertheless, our most important result is that bat abundance in the airspace appears to be declining rapidly, despite the effectiveness of mitigation in reducing bat mortality at turbines.

The Case of the Shrinking Bats: Signatures of Nutritional Stress Implicate Changing Prey Availability and Climate

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Many avian aerial insectivores in North America are in decline. These declines are attributed in part to reduced food availability, which could also affect insectivorous bats. To test the hypothesis that nutritional stress is impacting mammalian aerial insectivores, we analyzed 14 years of morphometric data from 3,759 individual little brown bats

(*Myotis lucifugus*) captured at 10 maternity colonies in Yukon, Canada. We explored temporal trends in bat size with linear mixed-effects models, using forearm long-bone length at maturity (FA) as a proxy for relative access to nutrition during development, and mass as a proxy for access to nutrition in the period preceding capture. Average adult female FA length declined by 0.04 mm/year ($p < 0.001$), and mass decreased by ~0.09 g/year ($p < 0.001$) when controlling for Julian Day. Average adult female mass declined most steeply during pregnancy (0.012 g/year) suggesting a potential decline in the frequency of reproduction. Mass also declined with increased amount and frequency of precipitation in the period preceding capture ($p < 0.001$). Taken together, our results reveal markers of nutritional stress in insectivorous bats and potential demographic consequences. Increasing precipitation may limit foraging opportunities for reproductive females, and further research should investigate potential declines in prey availability. A follow-up study at a larger geographic scale is in progress to clarify how widespread the observed trends might be across North America.

Phylogeographic Analysis Reveals Mito-nuclear Discordance in *Dasypterus intermedius*

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Northern yellow bats (*Dasypterus intermedius*) are tree-roosting bats in the family Vespertilionidae comprising two subspecies: *D. intermedius intermedius* and *D. intermedius floridanus* distributed in North and Central America. The two subspecies lineages are thought to be geographically separated but this has never been tested with a molecular approach. In this study, mitochondrial sequence data from 38 *D. intermedius* and nuclear microsatellite data from 92 *D. intermedius* (across 8 loci) from across their range were used to test the hypothesis that genetically defined groups will correspond geographically with the two morphologically-defined subspecies. Though high levels of divergence of the mitochondrial sequence (11.6%) resulted in clusters that corresponded to geographic origin, no genetic structure in the population based on nuclear markers was recovered. This study suggests that *D. intermedius* has a single continuous population with gene flow between the two subspecies and relatively high genetic diversity levels ($H_0 = 0.621$) possibly the result of isolation and secondary contact.

***Flexibility of Prey Size Selection in Sympatric Forest Bats (*Myotis*) Facilitates Dietary Overlap**

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*** Timothy J. Divoll** received the **Titley Scientific Award.**

Temperate insectivorous bats are generalist predators, taking a selectively opportunistic approach to foraging that allows them to exploit spatially or temporally patchy prey. *Myotis sodalis* and *M. septentrionalis* co-occur in forests across the midwestern USA, both aerially hawking and gleaning during prey pursuit. Both consume from 14 taxonomic orders, suggesting that prey selection is conserved in these sister *Myotis*. How do they avoid competition for food? We used DNA metabarcoding to compare prey richness and dietary overlap between 78 *M. sodalis* and 88 *M. septentrionalis* at a contiguous managed forest and riparian-wetland site in central Indiana during the 2014–2017 maternity seasons. We extend the status quo in molecular dietary analysis to redefine operational taxonomic units in terms of taxa-size classes to align our analyses with bat perceptions of prey. We found greater dietary overlap across species within sites (O_{jk} = 0.82–0.85) than within species across sites (O_{jk} = 0.71–0.77) and confirmed that both species eat what is most available—small moths, flies, and beetles (≤ 8–9 mm). However, both occasionally took larger prey (15–30 mm). *M. septentrionalis* took larger prey on average (9.9 v. 8.9 mm, $p < 0.001$) and *M. sodalis* consumed a greater richness (n = 547 v. 453 taxa). *M. sodalis* took small aquatic flies more often than *M. septentrionalis*. Subtle differences in prey frequency and sizes suggest that these sister *Myotis* may eat certain insect types at different rates and could use contrasting spatial strategies to find ephemeral or larger prey.

Systematic Review of the Roost-site Characteristics of North American Forest Bats: Implications for Conservation

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Continued declines in North American bat populations can be largely attributed to habitat loss, disease, and wind turbines. These declines can be partially mitigated through actions that boost reproductive success; therefore, management aimed at promoting availability of high-quality roosting habitat is an important conservation goal. Roost-site selection in bats has been well-studied for some species, particularly *Myotis sodalis* and *M. septentrionalis*, which have existing federal protections. If co-occurring species share similar roost-site preferences, then they may benefit from forest management practices targeting *M. sodalis* and *M. septentrionalis* conservation. We conducted a systematic review of the roost-site characteristics of 13 species inhabiting eastern temperate forests to: 1) synthesize existing knowledge across species; and 2) identify potential niche overlap in roost-site preferences among species. Of 95 included studies, 44 were focused on either *M. sodalis* or *M. septentrionalis*; in contrast, only six studies described roost trees used by *Lasiurus intermedius* or *L. seminolus.* We performed multivariate ordination techniques to group species based on the seven most-reported roost-site characteristics, including tree species, diameter at breast height (dbh), tree health, roost structure (e.g., in a cavity), tree height, canopy closure, and roost height. Species examined fell into three roosting guilds: 1) southern cavity specialists; 2) foliage roosting bats; and 3) dead tree generalists. Niche overlap with *M. sodalis* and *M. septentrionalis* was significant for four species, with species selecting roosts of similar dbh (26–40 cm), canopy closure (42–70%), and tree health, highlighting their potential as conservation umbrellas in forest management.

Ecosystem Disservices: Have We Overlooked Beneficial Insects in Ecosystem Service Valuations?

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Interest in ecosystem services provided by bats has resulted in a focus on pest insects. However, pest insects are only a fraction of bats' diets. A comprehensive understanding of bats' economic and societal impact will benefit from incorporating all insect taxa consumed. Here, I examine the full suite of insects eaten by bats in the context of the insects' relationship with humans by compiling next generation sequencing data from published papers. As possible, I classified each insect taxa as pest, beneficial, or neutral, and assigned each a functional role such as pollinator, predator, or disease vector. This analysis could reveal consumption of pest insects that have not yet been economically evaluated, or indicate that the benefits of consuming some insects may extend farther than previously thought. On the other hand, beneficial insects in the diet of bats suggest an ecosystem disservice. Regardless, this analysis will provide a broad assessment of the diet from the perspective of ecosystem services that will broaden our knowledge of these predator-prey interactions and their implications for human systems.

Testing the Protein-for-Water Hypothesis: Does Dehydration Cause an Increased Reliance on Protein Catabolism in *Eptesicus fuscus*?

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White-nose syndrome (WNS) augments water loss in hibernating bats, and dehydration plays a role in WNS-associated mortality. Some bats (e.g., *Eptesicus fuscus*), however, are resistant/tolerant of the disease and show no indications of dehydration following disease progression. While fat is the primary fuel for hibernation, the breakdown of protein yields five times more water than fat. Protein catabolism could, therefore, help WNS-resistant/tolerant bats reduce water requirements during hibernation. We hypothesized that a negative water balance influences the metabolic fuel mixture of *E. fuscus* during hibernation. To test this hypothesis, we hibernated bats in dry (~50% relative humidity) and humid (98% relative humidity) conditions at 8°C for 110 days (n = 10 per treatment) and used quantitative magnetic resonance, blood sampling, and infrared video monitoring to address our predictions. We predicted that if *E. fuscus* offset water loss under dehydrating conditions through increased protein catabolism, then compared to bats hibernating in humid conditions, they would: 1) have higher rates of protein (lean mass) loss and endogenous water production; 2) have an elevated plasma urea concentration, but a similar level of plasma osmolality; and 3) not differ in drinking frequency. We found no difference in rate of protein loss, nor

endogenous water production. However, bats hibernating in dry conditions drank 52% more frequently than bats in humid conditions. Our results demonstrate that, at least in an environment with adequate drinking water, hibernating *E. fuscus* do not rely on the protein catabolism to maintain water balance under dehydrating conditions, but rather modulate water losses behaviorally.

The Humerus Nature of the Femur

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Similar to the adaptive nature of the humerus for flight in bats, the proximal end of the femur shows adaptive diversity, a phenomenon hypothetically related to a combination of phylogenetic constraints and function (e.g., hanging, use of the uropatagium, quadrupedal locomotion, and flight). The spatial and functional relationships between the fulcrum (ball of the femur or femoral head), input levers (greater and lesser trochanters), and output lever (femoral shaft) require in-depth analysis in order to understand the myriad ways the hindlimbs are used in bat locomotion. We tested the hypothesis that adaptations of the femoral head and trochanters are related to both quadrupedal and flight locomotion. Preliminary results indicate that the proximal end of the femur is widely variable, showing functional divergence beyond phylogenetic constraint. We found that vespertilionid femur variation is driven by length variables, whereas phyllostomid variation is driven by angle variables, and molossids show limited variation in both. We conclude that femur variation is more related to flight rather than quadrupedal adaptations, or a combination of the two, similar to the humerus.

Preliminary Acoustic Bat Survey of the Boreal Peatlands of Central Ontario

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The boreal peatlands of central Ontario province are at or beyond the northern extent of the range of most of the eight bat species that occur in Ontario, half of which are listed as endangered species at risk. The region is underlain by granitic or gneissic bedrock, rich in potential mining resources that play an important role in the region's economy. Mining activity and other land use alternative habitats, potentially displacing native wildlife, including bats. Typical land cover at the northern extent of this ecoregion is peat shrublands, punctuated by scattered stands of coniferous and mixed forests, and dissected by small streams and rivers with densely forested riparian zones. Available habitats provide potential foraging and roosting, but not hibernation resources for bats. We conducted a preliminary acoustic bat survey of a proposed mining site in this region to characterize bat species diversity and activity in the area for an environmental impact assessment of proposed mining activity. We hypothesized that the site would be occupied primarily by long-distance migratory tree bats (*Lasiurus cinereus*, *L. borealis*, and *Lasionycteris noctivagans*), and possibly by larger-bodied, cold-tolerant cave bats, such as *Eptesicus fuscus*. We deployed two acoustic bat detectors along probable bat travel corridors (road and river) and recorded for ±20 nights. We will report on our preliminary findings and potential implications for proposed land use activities in the region.

Conserving Caves in the Caribbean for Critically Endangered Bats

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Bat species that depend on subterranean habitats and aggregate in large numbers are particularly vulnerable to threats that destroy or degrade roosts. However, caves are also focal habitats that are tractable targets for conservation. If executed effectively, cave conservation efforts can provide meaningful protections to safeguard species from extirpation. Here, we discuss recent efforts to identify and execute conservation measures to protect two caves identified as the last remaining roost sites for two critically endangered bat species in Jamaica—the Jamaican flower bat (*Phyllonycteris aphylla*) and Jamaican funnel-eared bat (*Natalus jamaicensis*). Jamaica is the most bio-endemic island in the Caribbean and an important contributor to biodiversity in the region. Primarily due to

the threat to its endemic species of bats, Jamaica is included in the International Union for the Conservation of Nature (IUCN) list of countries with the most at-risk mammals. Twenty-one species of bat are found on Jamaica; five of these species are endemic to the island, while another eight species are restricted to the Caribbean. Almost half (10/21) of the species found on Jamaica are obligate cave dwellers. Human population growth driving agricultural, industrial, and commercial expansion has resulted in intense competition for land, leading to the loss or fragmentation of many natural habitats and a reduction and loss of biodiversity. Bat Conservation International, the Jamaican Caves Organisation (JCO) and the National Environment and Planning Agency (NEPA) are collaboratively developing and executing cave conservation strategies to protect the remaining roosts of critically endangered bats in Jamaica.

Indiana Bat Presence in Sparta, IL before and after White-nose Syndrome Exposure

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The Indiana bat (*Myotis sodalis*) can be found throughout the state of Illinois. The Indiana bat has been federally listed as endangered since 1967. Due to the fact that the Indiana bat is federally endangered, the U.S. Fish and Wildlife Service (USFWS) requires surveys to occur before habitat modifications occur, which may impact the species. Surveys are conducted via mist netting per requirement of the USFWS. Surveying began in 2002 at Sparta Training Area through the Illinois Department of Military Affairs in accordance to the guidelines of the USFWS. The netting surveys resulted in no Indiana bats being captured in 2002. The Sparta Training Area was resurveyed in 2012 and resulted in Indiana bats being captured. In 2013, white-nose syndrome (WNS) was confirmed in the state of Illinois and is currently confirmed in all counties where bat hibernacula are located. The Sparta Training Area was resurveyed in 2014 where Indiana bats were captured after the exposure of WNS to the area. The full impact that WNS has on this particular population of Indiana bats has yet to be determined but surveying efforts will continue in July of 2019.

Integrative Taxonomy Reveals Cryptic Speciation in *Trachops cirrhosus* (Chiroptera, Phyllostomidae)

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Trachops Gray, 1847 is a monotypic carnivorous bat, with only *Trachops cirrhosus* (Spix, 1823) currently recognized. Three subspecies are broadly distributed across the Neotropics and some studies have raised the hypothesis of cryptic speciation in *Trachops*. Therefore, the main goal of this study was to investigate the diversity of *Trachops* along its distribution, integrating molecular, morphometric, and ecological niche analyses, to understand potential species boundaries in the genus. Results show that *Trachops* is composed of two species: *T. ehrhardti*, monotypic, and *T. cirrhosus*, with 2 subspecies (*T. c. cirrhosus* and *T. c. coffini*). Among all the genetic lineages, the southern Atlantic Forest (*T. ehrhardti*) was the most divergent, splitting from its sister (*T. cirrhosus*) about seven million years ago. Morphometric analyses also point to the existence of two forms of *Trachops*: large or small-sized, and although *Trachops ehrhardti* from the Atlantic Forest and *T. c. coffini* from Central America are similar in size, they are morphologically distinct. *Trachops c. cirrhosus* is larger, showing clinal size variation. Ecological niche overlap tests suggested that the similarity between niches may be acting to maintain similarities in size. Additionally, niche identity tests confirmed the uniqueness of the niches for each taxon. Integrating genetic, ecologic, and morphometric data allowed us to clearly delimit *T. ehrhardti* and *T. cirrhosus*. The current floristic differences between the southern and northern Atlantic Forest and all biotic and abiotic interactions involved may represent ecological barriers for the two species of *Trachops*.

Pit-tagging Species Impacted by White-nose Syndrome on Maternity Sites: Not So Simple

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Bats can be challenging to study; however, the development of new technology, such as the Passive Integrated Transponder (PIT tag) in the 80s, facilitated projects that required individual identifications. More recently, the appearance of white-nose syndrome (WNS) in North America raised questions, such as the potential carry-over effects of the winter disease during the summer time. While PIT tag data could provide valuable information about

the population dynamics of WNS-impacted species, few studies have been published yet. Our objective was to evaluate the seasonal and annual return rate of reproductive females at maternity sites with varying times since the arrival of WNS. On one site, we also captured bats during three consecutive years to evaluate pit tag loss. Between 2016 and 2019, we captured and pit tagged little brown (*Myotis lucifugus*) and northern long-eared bats (*M. septentrionalis*) on four maternity sites where WNS arrived recently (n = 2) and not recently (more than 5 years; n = 2). Manipulations included species identification, assessment of reproductive status and wing damage index, weighing, pit tagging, banding, biopsying, and *Pseudogymnoascus destructans* swabbing. Seasonal and annual return rate varied between 0%–71% and 0%–78%, respectively, with lower return rate on sites with recent WNS arrival. Average pit tag loss was 20% (n = 10). The impact of the manipulations seems to be higher on sites where WNS is recent and prevents us from evaluating population dynamic parameters. In-hand recapture was low (mean = 18%) compared to antenna detections (mean = 65%), which might be because bats remember and restrain themselves from leaving on capture nights.

Modeling Long-term Genetic Diversity of Little Brown Bat Populations after Infection by White-nose Syndrome

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The little brown bat, *Myotis lucifugus,* is one of many North American bat species showing large population declines due to white-nose syndrome (WNS), a fungal disease affecting hibernating bats. This disease has resulted in population declines of up to 99% in some colonies. However, long-term population viability studies have shown improved survival rates after WNS-related mortality events and suggest possible evolutionary rescue of *M. lucifugus* populations due to inherited WNS resistance sweeping to high frequency in affected populations. We created forward-in-time simulations based on *M. lucifugus* population parameters using the population modeling software simuPOP in order to examine the resulting change in genetic diversity of populations over time. The modeled populations were simulated to undergo population decline due to WNS mortality, followed by growth dependent on the frequency of resistant phenotypes, with parameter estimates from real WNS-infected *M. lucifugus* populations. We examined the effect of initial population size, threshold frequency of resistant phenotypes, varying growth rate after initial WNS-related mortality, and selection via evolutionary rescue. The effects of evolutionary rescue on genetic diversity at selected and unlinked neutral loci were tracked as changes in allele frequencies, heterozygosity, and effective population size in a variety of scenarios. Our results provide a forecast of the potential future impact of white-nose syndrome on genetic diversity in *M. lucifugus* populations.

Assessing the Conservation Status of North American Bats

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Assessing the conservation status of all North American bat species can be useful to mobilize support for bat conservation, and to identify priorities for conservation action. The North American Bat Conservation Alliance is assessing the status of North American bat species, using criteria similar to those recently applied by Partners in Flight to assess the status of all bird species in North and Central America or the Mexican federal government to assess all plant and animal species in Mexico. The assessment considers several criteria: population size, distribution, population trend, intrinsic vulnerability, and threats (as an indication of anticipated future population trend). Each criterion is assigned a numeric value from 1 to 5, based on a combination of quantitative data and expert judgement. Intermediate scores are assigned when information is lacking, allowing assessment of both well-known and poorly known species. The combined score gives an index of conservation concern, with higher scores representing greater concern. For threats, additional information is tracked on the specific threats affecting each species. A workshop is planned for the two days immediately prior to NASBR, using expert elicitation approaches to apply these criteria to assess the status of all species occurring in the USA and Canada. A subsequent workshop will be held in Mexico to assess the remaining species. This presentation will describe in detail the criteria and their rationale, and will summarize the outcomes of the first workshop.

The Role of Skin Temperature in the Resistance of *Myotis leibii* to White-nose Syndrome

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White-nose Syndrome (WNS) was first observed at 6 caves in central New York during 2007–08. WNS is caused by a cutaneous infection with the fungus *Pseudogymnoascus destructans* (*Pd*) during hibernation. This fungus has since spread to bat hibernation sites located in 33 U.S. states and 7 Canadian provinces. WNS leads to over-winter mortality rates as high as 98% for 4 of the 6 bats that hibernate in the northeast: *Myotis lucifugus*, *M. sodalis*, *M. septentrionalis*, and *Perimyotis subflavus*. The Eastern small-footed bat (*Myotis leibii*) may be more resistant to cutaneous infection with *Pd*, however, since the number of *M. leibii* hibernating at 42 sites has declined by only 12% since the appearance of WNS. We conducted a 3-year study on *M. leibii* hibernating in New York to test this hypothesis. The mean torpor bout duration of hibernating *M. leibii* was 25.4 $\pm$ 3.0 d, with a mean skin Temperature (Tskin) during torpor of 15.7 $\pm$ 1.1ºC. The mean Tskin maintained during torpor ranged from 12.0–18.8ºC between individuals, with 71% of the *M. leibii* observed maintaining a Tskin > 16.0ºC during torpor. Little brown bats (*M. lucifugus*) hibernating in the same mine during this period, however, maintained a mean Tskin during torpor of 11.5 $\pm$ 1.0ºC. The growth of *Pd* is inhibited at temperatures > 16.0ºC. Our findings thus indicate that *M. leibii* is more resistant to *Pd* growth on their skin during torpor, and thus WNS, due to a relatively higher Tskin maintained during torpor.

Intraspecific Variability in the Wing Morphology of Migratory Silver-haired Bats

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Differential migration—intraspecific variation in migratory distance among individuals—is very common across taxa, including some bat species. Within differentially migrating populations of some species (e.g., some birds and insects), longer-distance migrants differ morphologically from shorter-distance migrants and/or sedentary individuals, often in ways that optimize flight efficiency. Recent stable isotope evidence suggests that silver-haired bats (*Lasionycteris noctivagans)* are differential migrants and we used stable hydrogen isotope techniques to investigate morphological correlates of variation in migratory distance in this species. We hypothesized that longer distance migrants would be better adapted to optimize flight efficiency than shorter distance migrants. We predicted that migrants with stable hydrogen isotope fur (δ^2H_{fur}) values indicative of more northern locations of summer residency would have higher wing aspect ratios, lower wing loading, and more pointed wing tips than individuals originating from a lower latitude of summer residency. We collected measurements of wing morphology and samples for δ^2H_{fur} analysis from 81 bats captured during spring migration in New Mexico. There was no relationship between δ^2H_{fur} and any of the predicted flight metrics, but a principal component analysis indicated that bats whose δ^2H_{fur} indicated they spent the summer at higher latitude or elevation locations were larger than those from lower latitudes or elevations. These findings suggest a previously undescribed cline in *L. noctivagans* size that aligns with Bergmann's Rule and has important implications for the energy budgets of larger summer residents at northern latitudes that may be engaging in cross-continental migration.

Major Threats, Challenges, and Solutions to Global Bat Conservation

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Many of the threats that bats face (e.g., habitat loss, bushmeat hunting, climate change) reflect the conservation challenges of our era. However, compared to other mammals and birds, we know significantly less about the population status of most bat species, which makes prioritizing and planning conservation actions challenging. Over a third of bat species assessed by the International Union for Conservation of Nature (IUCN) are considered threatened or data-deficient, and well over half of the species have unknown or decreasing population trends. That equals 988 species, or 80% of bats assessed by IUCN, needing conservation or research attention. Delivering conservation to bat species will require sustained efforts to assess population status and trends and address data deficiencies. Successful bat conservation must integrate research and conservation to identify stressors and their

solutions and to test the efficacy of actions to stabilize or increase populations. Global and regional networks that connect researchers, conservation practitioners, and local stakeholders to share knowledge, build capacity, and prioritize and coordinate research and conservation efforts, are vital to ensuring sustainable bat populations worldwide. We will present recent efforts toward focused conservation action on critically endangered bats to showcase how targeted conservation actions are key to saving species from extinction.

The Hibernation Phenotype: Interspecific and Regional Variation of Hibernation Physiology

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Hibernation is a common strategy used by temperate bat species to cope with periods of resource limitation. Despite the commonalities of hibernation across species, the specific strategies used by hibernating bats vary with respect to latitude and regional environmental conditions. Regional adaptations of torpid metabolic rate (TMR), evaporative water loss (EWL), and accumulated fat stores are often observed. For most bat species, however, there is little information on hibernation strategies, nor has there been focused study on the influence of environmental conditions on hibernation physiology and behavior. We tested the prediction that hibernation physiology varies among species and regions. Specifically, we predicted that bats in colder, drier habitats will have lower TMR and EWL to conserve energy and water during hibernation. To test this prediction, we used dataloggers to record hibernaculum microclimate and respirometry to measure TMR and EWL from ten western bat species. We observed species-specific variation in EWL but no differences in TMR. Bats that inhabit arid regions and use unstable microclimates during hibernation had lower EWL than bats from wetter habitats that use stable hibernacula. By measuring the suite of physiological characteristics, or "hibernation phenotypes", exhibited by hibernating bats, we can develop a new framework by which to categorize the conservation needs of hibernating bats. With the increasing threats of white-nose syndrome, wind energy production, and widespread habitat loss, understanding the habitat needs of hibernating bats within a conservation physiology framework will provide valuable information for future conservation efforts.

Human-caused Disturbance and the Effect of Nature-based Tourism on Bats

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Nature-based tourism is a growing industry worldwide, with over 8 billion visitors annually to protected areas. This industry generates financial resources for protected areas, wildlife conservation, and raises public awareness and appreciation of nature. However, tourism also places pressure on protected areas and wildlife as managers try to balance tourism with ecological conservation. Tourists and the disturbances caused by tourists can be perceived by animals as predators or predation risk. These perceived threats can affect fundamental life history processes and behaviors, ultimately decreasing the overall fitness of the animals. The nocturnal habits and unique life history traits of bats make it difficult to compare the impacts of tourism between this unique group of mammals and other taxa. The literature analyzing these impacts on bats and their habitats is very limited, leaving bats in a perilous condition without a baseline to draw proper conservation initiatives. Here, we emphasize the need for research on areas addressing topics such as behavior, ecology, and physiology, which are fundamental to understanding the unknown consequences of the growing tourism industry on bats.

Warming Up Without Dinner: Hibernating Bats without Foraging Opportunities Desynchronize from Sunset despite Warm-climate

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For hibernating bats, arousals from torpor account for up to 90% of energy budget. A previous study of bats from moderate climate found hibernating bats synchronized arousals with sunset to allow foraging opportunities on warmer nights ("Warming up for dinner" Hope and Jones 2012). In another study, bats hibernating in cold-climate with no opportunity for winter foraging, aroused randomly ("Staying cold through dinner" Czenze et al. 2013). We conducted an experiment to test which factors could lead to synchronized nocturnal arousals. We collected 98 tricolored bats (*Perimyotis subflavus*) from Mississippi, placed them in environmental chambers at different

temperatures (5, 8, 11ºC), and recorded arousals from December 2018 to March 2019. We hypothesized: 1) if arousal synchrony is linked to possible winter foraging then arousals should be synchronized with nocturnal periods at warmer temperature; 2) if external cues (e.g., light, temperature cycle) are required for maintenance of circadian rhythm then arousal times should randomize over time; and 3) if endogenous factors (e.g., fat stores) drive arousal synchrony then arousal times should synchronize with nocturnal periods as fat stores decline through hibernation. We found partial support for each of our predictions. Synchrony of arousals was related to temperature (nocturnal arousals in colder temperatures), period of hibernation (nocturnal arousals in early hibernation), and body condition (synchronized arousals in lowest body weight bats late in hibernation). Combined, these results suggest the maintenance of synchronized arousals through hibernation is the result of both endogenous (energy stores) and exogenous factors (environmental conditions, external sensory cues).

Cataloguing Bat Ecological Interactions across the Globe: The Bat Eco-interactions Database
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Bat Eco-Interactions Database Project, Houston, USA

With over 1400 species worldwide, bats are critical components to many ecosystems as pollinators, seed dispersers, and insect predators. Scientific studies of their interactions with plants and arthropods are increasing and continue to reveal the critical roles bats play in nature and the benefits they provide to human economies. We created a platform, the Bat Eco-Interactions Database (formerly the Bat-Plant Interactions Database), to catalog all published accounts of bat interactions with plants and arthropods to facilitate scientific research, reduce duplication of effort, and share and visualize published data. For each interaction we include family, genus, and species of each interactor (bat, plant, or insect); type of interaction (pollination, visitation, consumption, dispersal, transport, roost, host); details of the location (country, habitat type, elevation, GPS); and citation. Search results can be visualized in tables or geographically and are available for download. The database is open sourced, free, and updated by its users at www.batplant.org. Currently over 8000 interactions are included from Latin America, Asia, and Africa and we are continuously adding regions and publications to the list. We invite students and researchers to become a part of this online community by submitting publications or adding data directly through the online portal.

A Pilot Study to Assess Using Pooled Guano from Summer Roosts for National *Pseudogymnoascus destructans* (*Pd*) Surveillance
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Surveillance of the fungus that causes white-nose syndrome in bats, *Pseudogymnoascus destructans* (*Pd*), primarily involves collecting skin swabs or environmental substrate at underground sites during winter hibernation. However, there are regions where hibernacula are unknown or inaccessible, particularly in the western United States. Results of preliminary field and laboratory experiments indicate that analyzing pooled guano collected at above-ground summer roosts may be a promising alternative surveillance strategy for early detection of *Pd*. We conducted pilot field studies at states along the leading edge of the pathogen distribution to provide proof-of-concept prior to incorporating this strategy into national surveillance efforts. Sites that were within 200 km of the nearest *Pd* detection and that contained *Myotis* species were targeted. Fresh guano was to be collected over a four-week period starting in mid-May, shortly after bats started arriving after hibernation. No *Pd* was detected at the 15 roosts sampled in 2018, but several factors could have increased the probability for false negatives, including delayed sample collection due to difficulty identifying and accessing summer roosts that met site selection criteria, site substitution with roosts of non-target species, improper execution of collection protocol, and temporarily lost shipments. In 2019, 40 sites were targeted with stricter selection criteria and improved guidance on protocols. Results from these samples will be presented and benefits and limitations of this sample type will be discussed in the context of the national *Pd* surveillance project.

NABat on the Northern Prairie: Year 1 of State-wide Acoustic Monitoring in North Dakota
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North Dakota is in a precarious position in regards to white-nose syndrome (WNS) and its impacts on bats in the region. With the presence of the disease in three of the four neighboring states/provinces, plus the documentation of a WNS^{+} *Myotis lucifugus* in central North Dakota (ND) in June 2019, more information is needed about the status of

bat populations in the state. In Summer 2019, we launched the first statewide acoustic monitoring program for bats in ND, following the GRTS methodology of the North American Bat Monitoring Program (NABat). The goal of the project was to collect the first of many years of data in a long-term acoustic monitoring effort to assess relative changes in bat populations over time. Acoustic data were collected at 58 sites across the state from June to August 2019, with a minimum data collection of four nights per site. Echolocation call sequences were classified to species using Sonobat 4.4.1; all data and associated classifications were submitted to the NABat database. Data will: 1) be used to examine patterns of species presence/absence across the state and assess agreement with known distributions, 2) serve as a comparison point for data collected in future summers at the same sites, and 3) be compared to the results of ad hoc acoustic sampling done in a non-standardized manner across ND from 2009–2018.

Monitoring Bats to Assess White-nose Syndrome Impacts in Great Lakes National Parks

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Over the past decade, the combined threats of wind energy, climate change, and the fungal disease white-nose syndrome have prompted greater interest in bat research and conservation, including on public lands. The National Park Service began coordinated region-wide bat acoustic monitoring in Great Lakes parks in 2015. We present data collected in the summers of 2016–2018 at nine parks located in Indiana, Michigan, Wisconsin, and Minnesota. We conducted passive acoustic sampling at over 200 sites per year, with an average of 9 nights per deployment. This resulted in over 275,000 bat echolocation call files recorded per year and detection of at least six species per park. Bat activity (call files per deployment night) decreased in 2017 and 2018 compared to 2016. As a group, hibernating species showed greater declines than migratory species. Since hibernating species are more susceptible to white-nose syndrome, our results suggest that the disease was impacting Great Lakes populations during this three-year period. Continued monitoring will help parks track the status of their bat populations and provide data to better inform management decisions.

Searching for a Silver Lining: Requesting Data for Silver-haired Bats

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To assess whether silver-haired bats exhibit regional or partial migrations, I am requesting that colleagues from across North America, particularly from latitudes within the northern United States and Canada, share data with me. The data I need include acoustic recordings during spring and fall migrations, winter acoustic recordings, and capture records during peak migration (spring and fall) and winter. Using acoustic data, I will compare the timing of spring and fall migration between silver-haired and hoary bats (long-distance migrants) and little brown bats (regional migrants). If the migration timing of silver-haired bats is similar to one or the other, it would suggest these bats use one migratory strategy versus the other. Additionally, I will analyze my own winter acoustic data to determine if and where silver-haired bats are active in the winter months. Finally, I aim to compile tissue samples from across the range of silver-haired bats to explore the landscape genetics and relatedness of populations. It is my goal to collect data from North American bat researchers, across the range of silver-haired bats, to complete this large-scale project.

Seasonal Variation in Male Urinary Estradiol and Transfer to Female Conspecifics in *Eptesicus fuscus*

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Current research suggests that unconjugated steroids excreted in the urine of male mice alter the reproductive behavior and physiology of female conspecifics. These observations support the notion that steroids can act as pheromones in mammals. Using tritium (^{3}H)-labelled estradiol (E_2) as a radioactive tracer, we have shown that female big brown bats (*Eptesicus fuscus*) readily absorb exogenous ^{3}H-E_2 applied via cutaneous and intranasal exposure, with radioactivity measured throughout neural, peripheral, and reproductive tissues 1 hour after exposure. Additional experiments with ^{3}H-E_2 have shown the reliable transfer of estradiol from male *E. fuscus* to cohabitating female conspecifics during the Autumn mating season. Here we explore seasonal variation in estradiol transfer between male and female *E. fuscus* at three relevant time points: Autumn (mating season), Spring (female ovulation, ovum fertilization, and implantation), and Summer (maternity colony formation, parturition, and maternal care). We

found substantial seasonal variation in the amount of ^3H-E_2 transferred from males to a variety of female tissues, including the frontal cortex, heart, liver, uterus, and blood serum, with a number of other tissues approaching statistically significant differences among seasons. We present data demonstrating the presence of unconjugated and bioactive estradiol in male urine across the mating cycle, with the peak concentration occurring during reproductively relevant times. We concluded that estradiol is a likely vector for steroid transfer between individuals. Seasonal variation in estradiol transfer could influence sexual behavior and reproductive physiology of female bats during critical reproductive periods, as transferred steroids were found in both neural and reproductive tissues.

Foraging Behavior and Habitat-use of Female Rafinesque's Big-eared Bats on a Fragmented Landscape in Rural Arkansas

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Studies have been conducted on the foraging behavior and habitat-use of Rafinesque's big-eared bats (*Corynorhinus rafinesquii*; CORA) in different habitats types; however not much is known about their behavior on a highly-fragmented, agricultural landscape. Bottom-land hardwood forests are the main habitat type for CORA located in the Mississippi Alluvial Plain but are rapidly being converted for alternative land-use practices. The purpose of this study was to compare foraging behavior and habitat-use between lactating and post-lactating females from a barn colony during the months of July and August (2018 and 2019). The study site was a family-owned farm in Jackson County, Arkansas. In total, 24 lactating females and 13 post-lactating females were transmittered and radio-tracked. Semi-fixed, simultaneous triangulation was the method used to collect spatial data. LOAS calculated the coordinates of their locations during triangulation, and BIOTAS estimated home ranges and core foraging areas. To assess habitat-use, coarse-scale habitat assessments and land-usage maps were created in ArcGIS, and R was used for all statistical analysis. Lactating bats used the barn to roost while post-lactating bats were found more often in roost trees. A total of 15 roost trees were located between the two years. Also, lactating bats were more stationary while foraging and post-lactating were sporadic, suggesting differences in foraging behavior based on reproductive status. Many core foraging areas for both lactating and post-lactating bats occurred over agricultural fields, thus implying that our study species could play a role in controlling pests within the research site and similar habitat types.

***Host and Environment Interact to Drive Colony Persistence of *Myotis lucifugus* Impacted by White-nose Syndrome**

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*** Alexander T. Grimaudo** received the ***Bat Research News*** **Award.**

Following the invasion of *Pseudogymnoascus destructans* into North America, white-nose syndrome (WNS) caused widespread population declines and extirpations of the little brown bat (*Myotis lucifugus*). However, some remnant colonies of *M. lucifugus* have stabilized and are now persisting despite infection prevalence remaining high. Identifying the mechanisms of persistence in these colonies is essential to the conservation of bat populations impacted by white-nose syndrome. In this study, we conducted a translocation experiment with *M. lucifugus* collected from persisting colonies to explore the relative role of the host and the hibernacula environment in driving persistence. Our data suggest that traits favorable to host survival have been positively selected for by WNS, but that environmental characteristics within hibernacula interact strongly with these traits to determine disease outcome. In the warmest and wettest site, mortality during the WNS epidemic was 100%, but in the persisting little brown bats used in this experiment, we observed only 20% mortality within the same site. However, mortality was significantly higher in this site compared to a cold and wet site, where mortality was <1%. Ultimately, our results show that the coevolutionary dynamics between hosts and pathogens following pathogen invasion can be dependent on the host's environment.

Population and Habitat Assessment of Bats in Southwest Nova Scotia Post White-nose Syndrome

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White-nose syndrome (WNS) was discovered in Nova Scotia in 2011, resulting in a >95% reduction of the resident bat populations. Prior to the onset of WNS, Kejimkujik National Park (KNP), in southwest Nova Scotia, had

apparently healthy populations of *Perimyotis subflavus, Myotis lucifugus,* and *Myotis septentrionalis*. We examined the status of these populations and their respective roosting habitats in a post WNS scenario. We used mist nets to catch bats along rivers and forest trails in KNP from June to mid-August. We did not catch or detect any *M. septentrionalis* and they are likely absent from KNP. The captures/unit effort show a large reduction when compared to previous efforts made during the summers of 2003–2004 and 2007–2008. We radio-tagged certain individuals and tracked them to their roosts. *P. subflavus* exhibited high roost site fidelity, roosting in clumps of *Usnea tricodea* on spruce trees in the same spatially distinct areas as prior studies. Any *M. lucifugus* found roosting within KNP were alone, and exclusively in hardwood snags. Although maternity roosts exist in buildings within 1 km of the park boundary, we did not find any natural maternity roosts within the park. These results imply a need to further examine the severity of WNS impacts in Atlantic Canada. Understanding the population decline and subsequent recovery of bats can give insights on where to focus management efforts here, and in areas with similar climates.

Population Genetics of the Honduran White Bat in Costa Rica

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Gene flow is the main factor in the maintenance and increment of biodiversity, which can be influenced by geography likewise dispersion, connectivity between populations, and habitat fragmentation. *Ectophylla alba* is a specialist species classified as "Near Threatened", apparently feeds just on fruits of *Ficus colubrinae,* and is affected by the habitat fragmentation in its natural distribution. We used 10 microsatellite loci to evaluate the population genetic structure of the Honduran white bat (*Ectophylla alba*) in 6 localities of Costa Rica. Our results indicate medium levels of population genetic structure among sampled populations. We observed low to medium genetic diversity across most loci. Total heterozygosity for all populations was medium to low (mean HE = 0.659, mean HO = 0.672). The AMOVA showed that most of the genetic variation was within populations and was due to differences among populations, mainly due the geographic distance among them. The absence of the significant correlation between genetic and geographic distances indicated little isolation by geographic distance. Average relatedness within colony members was close to zero, did not differ significantly between the different colony types, and kinship is unlikely to be a major grouping mechanism in this species with no evolutionary evident kinship selection. The results of this study are a framework for future studies, they can also be used for the right management and conservation of this species.

Genomic Shifts Behind Dietary Diversification in Phyllostomid Bats and Genomic Signatures of Parallel Evolution in Nectar-feeders

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The New World Leaf-Nosed bats (Phyllostomids) exhibit a diverse spectrum of feeding habits and innovations in their nutrient acquisition and foraging mechanism; however, the genomic signatures associated with distinct diets are unknown. We conducted a genomic comparative analysis to study the evolutionary dynamics related to dietary diversification and specialization. We sequenced, assembled, and annotated the genomes of the Phyllostomid species: *Macrotus waterhousii* (insect-feeder), *Artibeus jamaicensis* (fruit-feeder), and the nectar-pollen feeders *Leptonycteris yerbabuenae, Leptonycteris nivalis* and *Musonycteris harrisonii*. Previously sequenced *Desmodus rotundus* was also incorporated into the analysis. Phylogenomic analysis displays differences in gene family expansion, contraction, and pseudogenization events, whereas the vampire and nectar-feeders exhibit many rapidly evolving genes. Independent of diet, genes involved in iron metabolism and food intake experienced multiple expansions. We also identified many losses and pseudogenizations in sensory genes (photoreceptors, taste and olfactory receptors) that may be relevant for feeding strategies. Moreover, we found adaptation signatures associated with specialized diets: the vampire exhibited traits associated with the complex mechanisms needed to maintain a blood diet (such as coagulation mechanisms), whereas the nectarivore lineage had a group of 14 positively selected genes involved in sugar, lipid, and iron metabolism. Interestingly, we detected for the genes *Acetoacetyl-CoA*, *Acid-*

alpha glucosidase, and *alpha-ketoglutarate,* signals of adaptative selection exclusively for the nectar-feeders Phyllostomids and Pteropodids fruit bats. Finally, we identified eight genes with signatures of parallel evolution in this group of nectar-fruit bats. These genes may explain how these animals avoid the adverse effects of diets with high glucose content.

Sex- and Age-specific Rates of Survival for Two Northern Populations of Little Brown Bats
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Peripheral populations near the limit of a species' range often exhibit lower vital rates than central populations. Understanding how these vital rates change over time is essential for managing these potentially vulnerable populations. We used seven years (2011–2017) of mark-recapture data for 4932 individual little brown bats (*Myotis lucifugus*) from two northern populations, to test the hypothesis that demographic characteristics, such as sex and age, along with seasonal environmental factors, affect variation in annual survival of little brown bats. We used Cormack-Jolly-Seber models to account for permanent emigration from the populations and included summer and winter weather parameters as predictor variables. At both hibernacula, annual survival varied over time with both age and sex of bats, but not with either summer or winter climatic variables. At 'Abyss' males had higher average annual survival rates (0.75 ± 0.035, standard error) than females (0.61 ± 0.04). Survival of young-of-the-year (YOY) was higher for males (0.23 ± 0.01) than for females (0.13 ± 0.01) but was lower than adult survival. At 'St. George' adult male survival (0.67 ± 0.07) was not different from that of adult females (0.65 ± 0.07), but higher than survival for both YOY males (0.47 ± 0.13) and YOY females (0.44 ± 0.13). In general, estimates of annual survival for these populations were lower than published estimates for insectivorous bat populations at lower latitudes. Through this long-term monitoring program, we identify females and YOY as vulnerable demographics in these populations and suggest targeted efforts to protect these groups.

Bat Fly-associated Fungi: Current Developments and a Call for Global Collaborations
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Bats serve as hosts to ectoparasitic blood-sucking bat flies, which in turn can carry Laboulbeniales fungi. This is an exciting tripartite system because it is a natural experiment replicated in two different hemispheres. Here, we summarize our main findings thus far. Molecular phylogenetic inference of the large subunit ribosomal DNA and application of species delimitation methods reveal that at least one taxon of *Arthrorhynchus*, restricted to Eastern Hemisphere bat flies, is a species complex, segregated by host genus. We are also looking at associations between parasitism and abiotic factors. We used MERRAclim variables and performed statistics to explain the distribution of *Arthrorhynchus* on bat flies across Europe. *Arthrorhynchus* occurrence and prevalence was higher in habitats with low annual mean temperature and humidity, suggesting that climatic elements can shape fungal distribution. *Gloeandromyces* fungi are associated with streblid bat flies in the Neotropics. Fieldwork in Panama and study of Latin American bat flies preserved in EtOH resulted in the description of several species and morphotypes (*formae*) of *Gloeandromyces*. Similar to *Arthrorhynchus*, we found host specialization in *Gloeandromyces* taxa as a contributor to diversity—whether ephemeral or incipient. One of the most important questions in this system concerns the effect of habitat on parasitism of bat flies by Laboulbeniales fungi. We hypothesize that habitat disturbance causes parasite prevalences to increase, in line with the "dilution effect." This can only be resolved based on large, non-biased datasets and so we call for global collaborations with bat scientists and organizations.

Weather-dependent Home Range Expansion by *Nycticeius humeralis* in an Urban Environment
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Despite the negative connotation of urban sprawl for bat populations, fragmented green spaces such as parks, cemeteries, and golf courses have the potential to provide necessary resources for bats. For example, water sources in these areas can include lakes, ponds, streams, and drainage ditches. Such water resources, however, can be ephemeral when subject to prolonged periods of high temperatures and low precipitation. Yet, recent studies reveal that bat species are potentially able to adapt by using unconventional, anthropogenic-based resources, such as

residential swimming pools. Thus, for those bats utilizing urban green spaces, we hypothesized that they would expand or shift their home ranges to access swimming pools as an alternative water source in the surrounding neighborhoods. To explore this hypothesis, we conducted a telemetry study tracking resident evening bats (*Nycticeius humeralis*) caught in a local park system across their summer activity period from 2017–2019 in Fort Worth, Texas, USA. Our results supported the proposed hypothesis, demonstrating that bats expanded their home ranges from the park system into the surrounding neighborhoods when average nightly temperatures exceeded ~30°C and total weekly precipitation was <1 inch. Furthermore, we observed that the home ranges increased over 4 times in size under these conditions. Thus, our study indicates that urban neighborhoods surrounding green spaces can provide important alternative resources for bats, and if managed appropriately can contribute to and encourage healthy, stable bat populations.

Ancestral Generalization was a Gateway to Rapid Dietary Divergence in Neotropical Leaf-nosed Bats

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As a prime example of adaptive radiation, Neotropical leaf-nosed bats (Phyllostomidae) are a frequent subject of macroevolutionary studies. Many of these studies focus on mechanical aspects of skull morphology relating to feeding, leaving the evolution of sensory structures understudied. We used diceCT scans of 79 specimens, representing 42 species of phyllostomids and two species of outgroups, to analyze relationships between the relative volumes of three sensory structures (olfactory bulb, orbits and cochleae) and diet. Those trends were then compared with inferred ancestral sensory states. We hypothesized frugivory and nectarivory are associated with enlarged olfactory bulbs and orbits, while animalivory is associated with enlarged cochleae. We predicted that the signature sensory profile of modern plant-eating bats emerged in the ancestral phyllostomid, but not in outgroups. We also expected shifts in the rate of evolution of sensory structure volume for olfactory and orbit size in the stenodermatine ancestor coinciding with a known shift in speciation rate. We found that frugivory is associated with larger olfactory bulbs and orbits, while nectarivory is associated with relatively smaller cochleae. The phyllostomids, regardless of diet, have similar relative proportions of sensory structures and collectively differ from outgroups. The phyllostomid ancestor had larger olfactory bulbs and orbits, but no difference in cochlea volume relative to its common ancestor with outgroups. This sensory blueprint reflects the consumption of plant matter and persists across modern phyllostomids. The enlarged olfactory bulbs and orbits of the ancestor, necessary for generalizing away from insectivory, allowed for specialization into new and diverse niches.

Bat Use of Upland Ponds within the Hardwood Forest Ecosystem of Southern Indiana

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The watershed systems of the Morgan-Monroe and Yellowwood State Forests (MMYSF) of southern Indiana are largely composed of ephemeral streams. The Indiana Department of Natural Resources (DNR) created man-made ponds within the state forests for the benefit of game species. The DNR would like to determine how these ponds are used by bat species living within state forest boundaries. During the summer months of 2018 and 2019, acoustic surveys were conducted at 27 ponds within the MMYSF boundaries to determine bat activity levels for the season. Mid forest vegetation surveys were conducted at each pond to determine vegetation density, which may limit bat accessibility to ponds based on body size morphology. These activity and vegetation density levels provided the preliminary results to show a negative correlation between high vegetation levels and bat activity. From these preliminary results, a small experiment was conducted in the summer 2019 on a subsample of five ponds with low bat activity. The subcanopy vegetation was removed to determine if lower vegetation clutter will increase overall bat activity levels. Preliminary results suggest that lower vegetation density does not increase overall bat activity.

Smart Curtailment in North America: Recent Results, Ongoing Research, and Future Challenges
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"Smart curtailment" is an approach to reducing bat fatalities at wind energy facilities that uses near real-time information to predict when bats will be active in an area and curtails turbines only when bats are known or suspected to be present and at risk. One approach to smart curtailment is referred to as Turbine Integrated Mortality Reduction (TIMR), which uses real-time bat acoustic and wind speed data to make curtailment decisions. A recent study conducted in Wisconsin used the TIMR smart curtailment approach to make curtailment decisions at control turbines (n = 10) versus treatment turbines (n = 10). The TIMR approach significantly reduced fatality estimates inside search plots for treatment turbines relative to control turbines for pooled species data (–84.5%) and for each of five species observed at the study site. Our group estimated that the TIMR approach would have reduced curtailment time by about 48% relative to turbines operated under a standard curtailment rule used in North America (curtailment up to 6.9 m/s). The TIMR approach to smart curtailment will be discussed and the first TIMR study as well as two other TIMR studies, one ongoing and one planned, will be described. These studies are designed to improve our understanding of smart curtailment approaches in different North American ecoregions and address uncertainties associated with the first TIMR study. Some of the future challenges confronting bat ecologists seeking to understand and implement smart curtailment approaches at wind energy facilities in North America will be presented.

Evidence of Morphological Divergence in the Minor Red Bat (*Lasiurus minor*) from Mainland Red Bats
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The *Lasiurus* species complex has presented a taxonomic challenge with morphologically indistinct species, vast and sometimes overlapping distributions, and a lack of adequate sample size in small isolated regions with rare endemic species. The Minor Red Bat, *Lasiurus minor,* is currently known from Bahamas, Hispaniola, and Puerto Rico, and was originally described from two individuals. A continuing lack of specimens has prevented quantitative analysis of divergence from other recognized Red Bat species. A recent discovery of several hundred *L. minor* remains deposited by owls in a cave in Haiti provided sufficient data for the first quantitative analysis with nearby mainland species (*L. borealis* and *L. seminolus*). Skull remains from 60 *L. minor* individuals were compared to mainland species with data collected from existing literature. Results from four linear measurements revealed some morphological distinction from males and female mainland species. The condylobasilar breadth was significantly smaller in *L. minor* than mainland Red Bats, while the post-orbital constriction was significantly larger. The breadth between the anterior of the upper first premolar and posterior of the upper third molar alveoli was broader in *L. seminolus* than in *L. minor*, while only being larger in the female sampling of *L. borealis*. The length of the palate in *L. minor* was also larger than the male *L. seminolus*, yet smaller than the female *L. borealis*. These unique morphological characteristics support the taxonomic independence of the Minor Red Bat from mainland species and opens new possibilities to help the conservation assessment of this elusive Caribbean bat.

Regional Migrations of Threatened Bat Species
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Aerial and terrestrial landscapes are becoming increasingly fragmented, potentially jeopardizing the traditional migration routes of bats. Mortality of *Myotis lucifugus* and *Eptesicus fuscus* from interactions with wind turbines is higher in Ontario than other areas in North America, and turbine-related mortalities of these species may be concentrated during these species' travel from summer maternity roosts to fall swarming sites. However, the paths they take on these journeys are unknown, limiting potential risk analyses. We used the Motus Wildlife Tracking System to track the movement of bats from maternity roosts to swarming sites in southwestern Ontario. We captured 108 bats (78 *M. lucifugus* and 30 *E. fuscus*) at 6 maternity roosts between July 18–August 29, 2018 and attached coded Motus nanotags (NTQB-1, Lotek Inc.). We found that some *M. lucifugus* traveled at least 175 km from their maternity roost in early September. Some individuals traveled at least 20 km/hr and 125 km/night. In contrast, *E. fuscus* were not detected farther than 40 km from their roosts. Based on speed and travel distance, it is likely that *M.*

lucifugus are taking direct routes to swarming sites. These routes overlap with multiple wind farms in southwestern Ontario, suggesting that the risk of turbine encounters/mortality may be highest for *M. lucifugus* during migration. Conversely, the shorter distances travelled by *E. fuscus* may result in no increased risk of turbine encounters during migration.

Ecological Traps and Thermal Refugia Determine White-nose Syndrome Impacts and Persistence

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The introduction of novel pathogens to naive host populations is a key threat to global biodiversity. The environment is a critical modifier of disease impacts, and environmental refugia where hosts but not pathogens can survive may help maintain species in the presence of virulent pathogens. However, host preference for habitats or niches where disease impacts are high may result in ecological traps that alter host population dynamics. Here, we quantify the relationship between temperature and the invasive fungus that causes white-nose syndrome in *Myotis lucifugus* to determine whether disease can shift the thermal niche of hosts. We used field mark-recapture data and Bayesian approaches with prior information from laboratory culture experiments to assess the relationship between temperature, fungal growth, and bat survival over the timespan of white-nose syndrome invasion. We found that fungal growth rates were higher on bats that roosted in relatively warm microsites, and correspondingly, bats roosting at warm temperatures were less likely to survive the winter. At the regional scale, average bat roosting temperatures declined 1ºC from pre- to post-invasion, because colder hibernacula served as thermal refugia from disease impacts. However, despite extremely strong selection pressure, the majority of bats continued to roost at warm temperatures that decreased bat survival. Our results suggest that source-sink dynamics are pervasive in ecology of white-nose syndrome, and that population stability will be determined by the relative availability of thermal refugia and thermal sinks or traps.

Cryptic Connections and Spatial Segregation Drive Infection Patterns in Bats

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Understanding host interactions that lead to pathogen transmission is fundamental to predicting and controlling epidemics. While the majority of transmission often occurs within social groups, the contribution of connections that bridge groups and species to pathogen dynamics is poorly understood. These cryptic connections, which are often indirect or infrequent, provide transmission routes between disconnected individuals, and may play a key role in large-scale outbreaks that span multiple populations or species. We quantified the importance of cryptic connections and space use in disease dynamics by simultaneously characterizing social networks and tracing transmission dynamics of surrogate pathogen epidemics through eight communities of hibernating bats. We then compared these data to the invasion of the fungal pathogen that causes white-nose syndrome (WNS). We found that cryptic connections increased links between individuals and species by an order of magnitude. Individuals were connected, on average, to less than two percent of the population through direct contact, and only six percent through shared groups. However, tracing surrogate pathogen dynamics showed that each individual was connected to nearly fifteen percent of the population and revealed widespread transmission between solitarily roosting individuals and extensive among-species contacts. The importance of both direct and indirect connections in pathogen transmission were reduced by within hibernacula spatial segregation not clustering behavior. Connections estimated from surrogate pathogen epidemics, which include cryptic connections, explained four times as much variation in transmission of the fungus causing WNS as connections based solely on direct transmission.

Bats and Lasers: Estimating Colony Size in Roosting Bats Using Ground LiDAR and Quantitative 3D Modeling

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Accurate estimates of population size and assessment of long-term trends in endangered species are critical elements of implementing a recovery program. Conservation managers and biologists use these data to make listing decisions, develop recovery plans and criteria, and inform specific consultations. Precise colony estimation remains difficult for wildlife like bats that are highly mobile, live in large groups, and are active at night. Although an increasing number of tools are available for estimating colony sizes based on emergence counts, existing survey methods for roost assessment have notable limitations—they can be invasive, inaccurate, labor-intensive, cost-prohibitive, and have low repeatability. Here we report on the development and application of an alternative method to estimate the size of cave-roosting bat colonies using Ground Based LiDAR Scanning (GBLS) technology. The associated Subtractive Volume Estimation (SVE) analytical method based on GBLS compares scans of the roost with and without the bats and derives an accurate estimate of their numbers. We scanned one mixed-species hibernaculum in Missouri that is a significant roost for the endangered Indiana bat and one, medium-sized, summer roost of the Brazilian free-tailed bat in Texas. Colony estimates derived from GBLS/SVE compare favorably to estimates derived from emergence counts and have the added benefit of providing new information about the arrangement of bats and utilization of the roost. The resulting tool provides a promising and effective alternative to historic methods for deriving colony size estimates and has potential for broader application in other model systems like birds, butterflies, and even historic preservation.

Eastern Small-footed Myotis Roosting Habitat on the Niagara Escarpment

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Rocky habitats are abundant in Ontario, primarily in the form of granite rock barrens and limestone cliffs and talus of the Niagara Escarpment. Despite this, there have been few records of eastern small-footed myotis (*Myotis leibii*) in the province, and only one known active maternity colony, located in a building. In 2017, we carried out a study to improve our understanding of both the distribution and roosting habits of this species on the Niagara Escarpment in Ontario. Mist netting was undertaken directly in open or semi-open talus habitats, or on forest trails near open talus between late May and September 2017. We tracked six eastern small-footed myotis, including one lactating female, to roosts found primarily in crevices in cliffs adjacent to the capture locations. One juvenile male was also confirmed to roost in the crevice of a large talus boulder in August. We also conducted 37.5 hours of ground-based visual searches of accessible rock habitats at each study site and nearby roadside rock-cuts. Visual searches were ineffective at identifying roosts for any species of bat. Our results confirm that cliff crevices of the Niagara Escarpment provide roosting habitat for adult and juvenile Eastern Small-footed Myotis, including maternity roosting habitat. They also suggest that visual searches are not an effective way to identify roosts of Eastern Small-footed Myotis within the cliff and talus habitats of the Niagara Escarpment.

Little Brown Bats Responding to and Rebounding from White-nose Syndrome

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White-nose syndrome (WNS) has now been impacting hibernating bat populations in the northeastern United States for over a decade. Little brown bats (*Myotis lucifugus*) are one of the hardest hit species, but the population has recently shown signs of stabilization. Using a mark-recapture design, we seek to determine the status and future of the little brown bat population in the region. In addition, we are examining the impacts of WNS on the life history of little brown bats. From 2016–2019, over 2,500 bats were captured at maternity colonies in New Hampshire, Vermont, and Massachusetts, approximately 20% of which were recaptures. All were banded while a subset of bats at two colonies were also PIT tagged. PIT tag and band recapture data show individuals surviving WNS and reproducing over multiple years as well as bats banded as juveniles surviving and returning to their natal colonies. In addition, emergence counts conducted in the field and from infrared video suggest stable to increasing colony sizes.

Wing-damage, fungal prevalence (of the causative agent of WNS, *Pseudogymnoascus destructans*), and reproductive data suggest that the effects of WNS linger into the early summer, impacting the rate and timing of reproduction with potential consequences for juvenile survival. Comparisons to pre-WNS data from New Hampshire suggest possible shifts in life history strategies, with little brown bats beginning to reproduce at an earlier age. The results of this study will ultimately be used to inform and develop conservation strategies to promote reproduction, survival, and recovery of little brown bats.

Kootenay Community Bat Project: A Community-based Program Supporting Regional Bat Conservation in British Columbia, Canada

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The Kootenay Community Bat Project (KCBP) is a 15-year, community-based bat conservation program located in the Kootenay region of southeastern British Columbia, Canada. KCBP goals include: engaging with and supporting landowners to promote the conservation and enhancement of roost sites, increasing education and awareness around bats, their habitat and threats, and establishing permanent roost monitoring sites to gather baseline population size information. Roosts were identified through direct landowner reports (phone, email), indirect reports (neighbours, pest control), or suspected roost site investigations by KCBP biologists. KCBP developed a 'Bat Ambassador' program training community members in facilitating various types of bat workshops and educators to deliver school programs. In 2005, the "Annual Backyard Bat Count" was initiated as an attempt to document bat populations over time using citizen-science and evolved into the BC Annual Bat Count in 2012. Eight bat species were detected in roost structures, of which the *Myotis* genus was detected most often. Over 700 roost sites were identified, of which maternity roosts were detected most frequently. In general, bat roosts were detected most often in human-occupied buildings, particularly in the upper portions of the structures (roof, attic, chimney). KCBP has offered hundreds of education and outreach events including community presentations, school programs, public mist netting nights, bat house building workshops, and targeted outreach to pest control professionals, roofers, builders, and realtors. In 2019, between 2–4 counts were conducted at >25 sites throughout the Kootenay region by engaged citizens. Future directions and lessons learned from this long-standing project will be shared.

Winter Foraging Activity of Two Cave-hibernating Bat Species in Tennessee

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During winter in the southeastern United States, individuals of cave hibernating bat species susceptible to white-nose syndrome (WNS) will often arouse from torpor. During arousals, some individuals may leave hibernacula to forage on the landscape. We deployed VHF radio transmitters on individuals of two bat species (*Myotis grisescens* [n = 8] and *M. leibii* [n = 2]) captured outside cave hibernacula during winter and used aerial radio telemetry to explore their foraging activity. Bats were tracked from release at the hibernacula until their transmitter signal was lost or they remained stationary for $\geq$15 mins. To understand which landscape features influence foraging area selection, we mapped foraging points in ArcGIS and compared them to random points using Welch's t-tests. *Myotis leibii* were tracked 1.20 $\pm$ 0.32 km and *M. grisescens* 4.14 $\pm$ 0.58 km from hibernacula. Both species selected to forage along streams ($p \leq 0.01$), with all foraging points located within 0.57 km of water features. *Myotis leibii* also selected to forage along roads ($p < 0.01$). Management for these important landscape features, particularly streams, may benefit *M. leibii* and *M. grisescens* populations, especially during winter when prey resources are low and bats are stressed by the rigors of hibernation and WNS. Similar data collection is recommended for other bat species affected by WNS that have seen high over-winter mortality.

Winter Torpor and Arousal Activity of Four Cave-hibernating Bat Species in the Southeastern United States

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In the southeastern United States, bats susceptible to white-nose syndrome (WNS) frequently arouse from torpor during winter and are often active outside hibernacula. We investigated the torpor and arousal activity of four WNS

affected species, two with relatively low (*Myotis grisescens* and *M. leibii*) and two with relatively high (*M. sodalis* and *Perimyotis subflavus*) WNS susceptibility. We deployed temperature-sensitive radio transmitters on bats captured outside cave hibernacula during winter to monitor torpor and arousal profiles (n = 21) and recorded activity of others at cave entrances by implanting them with passive integrated transponder (PIT) tags (n = 1,349). *Myotis leibii* had a higher torpor skin temperature (18.57 $\pm$ 0.20°C) than *M. grisescens* (13.72 $\pm$ 0.60°C) and *P. subflavus* (14.62 ± 0.49°C*;* $p < 0.048$). *Myotis leibii* also had a higher arousal skin temperature (32.29 $\pm$ 0.67°C) than *M. grisescens* (29.01 $\pm$ 0.64°C) and *M. sodalis* (28.59 ± 0.38°C; $p \leq 0.016$). *Myotis leibii* had the highest activity frequency throughout the hibernation period (November–February), with 74.22 + 10.62% of tagged individuals detected at cave entrances each month compared to <30% of tagged individuals from other focal species. Of the 531 PIT tagged bats active during winter, only 12.60% (n = 67), the majority of which were *M. leibii*, were detected at a cave entrance more than once/night. For this species, the time between detections in the same night was 0.87 $\pm$ 0.09 hrs. Understanding these differences in torpor and arousal activity will help inform WNS management strategies.

***Agave* Flower Visitation by Pallid Bats in the Big Bend Region of Texas**

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Pallid bats, *Antrozous pallidus,* though primarily gleaning predators, are known to consume nectar of cardón cacti, *Pachycereus pringlei*, and act as effective pollinators of this species in the Sonoran Desert. It is unknown whether a similar nectar feeding behavior may be occurring in the Chihuahuan Desert of southwest Texas, where several researchers have captured pallid bats covered in pollen. We collected pollen samples from pallid bats in Brewster County, Texas each month between April and August 2018. A total of 77 pallid bats were captured. Clear tape was used to collect pollen density samples from 67 pallid bats and fuchsin gel cubes were used to collect samples for pollen identification from 60 pallid bats. Of the 67 bats sampled with tape, 56 had substantial pollen densities on their wings. Pollen-covered pallid bats were captured in every month sampled; however, mean pollen densities in June were significantly lower than pollen densities in April and July. The pollen collected in all samples was identified as *Agave* pollen. Two *Agave* species occur in this region of Texas, *Agave havardiana* and *Agave lechuguilla*. A linear discriminant analysis (LDA) was used to distinguish pollen of *A. havardiana* and *A. lechuguilla* using measurements from reference collection pollen. The LDA classified 701 of 723 of the pollen grains as *A. lechuguilla* based on posterior probabilities of >0.5. Additional evidence from infrared video footage collected in August of 2018, indicates that pallid bats are becoming covered in *A. lechuguilla* pollen as a result of nectarivory.

Hidden in Plain Sight: Using Geometric Morphometrics on CT Scanned Bat Specimens from Open Access Repositories

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Bats (Order Chiroptera) are a diverse group of mammals of which over 1300 species have been described. Traditional methods of measurement involve the use of dry skulls, a procedure that substantially increases the variance in measurements across users. Recent advances in Computerized Tomography (CT) technology have provided us with the ability to analyze wet museum specimens and thus better understand the internal structures of bats. This study is an ongoing project that highlights the use of geometric morphometrics on high resolution micro CT scanned specimens that have been previously deposited in open access repositories such as Morphosource. By describing craniofacial landmarks and semi-landmarks, inferences can be made about the size and skull shape of bats and predictions can be made about diet. Moreover, the precision involved with high resolution micro CT scanned data makes these measurements replicable and reproducible. The landmarks and semi-landmarks will be placed using the geomorph package in R and analyzed with Procrustes superimposition methods. Furthermore, this can be used as a template to study other species of mammals that have been collected and deposited in open access repositories.

Are Statistical Models Useful for Predicting Energy Budgets of Hibernating Bats?
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Regulating energy expenditure during hibernation is critical for survival in temperate bats. Multiple models have been proposed to estimate fat and mass loss during hibernation based on biophysical models and a classical understanding of hibernation dynamics. These models have provided invaluable insights into hibernation biology, but are impossible to parameterize for all but the best-studied species. Here, we aim to determine if data on skin temperatures, which are easily collected in wild populations, can be used to estimate body mass and fat loss using statistical models instead of biophysical models. We performed a captive hibernation study using 98 wild-caught tri-colored bats, *Perimyotis subflavus*. We attached temperature dataloggers to bats and maintained them in temperature and humidity controlled environmental chambers for 87 days. We measured body mass and body composition at the start and end of hibernation. We transformed skin temperature data using nonlinear multipliers and calculated the area under the curve for each bat with the goal of maximizing the amount of variation in body and fat mass lost over the hibernation period that can be accounted for by simple regression models. Based on body mass alone, our best model accounts for ~40% of variation observed. We are finalizing body composition data, which will provide higher resolution than simple body mass and should increase our descriptive power. This modelling approach represents the first such statistical model, and we hope such techniques can ultimately be more widely applied than biophysical models and thus prove useful for management and conservation questions.

Flexible Foraging Behavior in the Hawaiian Hoary Bat
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The foraging ecology of the Hawaiian hoary bat, an endangered species, has been poorly characterized and lack of information is hampering efforts to develop effective recovery plans. We used long-term acoustic monitoring to determine habitat preferences and radio telemetry to determine core use areas (CUA) through a kernel analysis at 50% and 95%. We used the Generalized Random Tesselation Stratified survey design to select acoustic sampling sites across nine habitat types covering a ~30,000 ha study area. Calls were recorded for three nights in each habitat and rotated five times (round) every other month for five months for a total of 223 deployments. We applied generalized linear mixed effects models with the package glmmPQL to account for over-dispersed count data and used a negative binomial distribution with a log link. Bat activity (bat calls per minute) was highest in gulches, low-intensity developed habitats, and grasslands and lowest in forested habitats; this contrasts to data from Hawai‘i Island suggesting bats are tightly associated with mature forest habitat. We also outfitted 16 bats with radio transmitters to characterize their foraging ranges. Mean CUA was 3,700 ha on Maui; this contrasts with 25.5 ha on the Hawai‘i Island. Our data suggest the bat prefers foraging in different habitats on Maui than bats on Hawai‘i Island and at 50% kernel has a mean CUA of over 100 times the size of the mean CUA for bats on Hawai‘i Island. Our data suggest foraging flexibility in the species and have substantial implications for management decisions.

Can UV Lights Be Used to Create Foraging Patches for Bats in the Wake of White-nose Syndrome?
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Bats with higher fat stores are more likely to survive the winter when infected with *Pseudogymnoascus destructans (Pd)*, the fungal pathogen that causes white-nose syndrome (WNS). We explore the use of ultraviolet (UV) lights to create foraging patches of night-flying insects for bats during the pre-hibernation fattening period. We selected the Upper Peninsula of Michigan for this study because of the presence of remnant populations of *Myotis lucifugus* persisting several years after invasion of *Pd* and mortality from WNS. UV lights were deployed at 5 mine sites used as hibernaculum, lights at each sited were turned on every other night, to determine whether insect prey were attracted and bats foraging rates were higher at lights. We quantified bat foraging activity using bat detectors and infrared cameras, and insect biomass using light and malaise traps. Results will inform novel management approaches focused on helping bats survive the impacts of WNS.

Infection Patterns of *Pseudogymnoascus destructans* in Male and Female Bats
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Understanding the role of infectious diseases in shaping animal populations is crucial as increased anthropogenic movement supports new pathogen invasions, as exemplified by the introduction of the fungal pathogen *Pseudogymnoascus destructans* (*Pd*) that causes white-nose syndrome (WNS). The negative effects of WNS are evident among cave-dwelling bats as mortality occurs during the winter hibernation period, when host physiological functions become disrupted by fungal growth. We hypothesized that *Pd* infection might vary between male and female bats given their different patterns of contact and arousal behavior. We sampled bats at 25 hibernacula across the northeast and midwest to quantify infection prevalence and intensity (i.e., fungal loads), and used generalized linear mixed models to assess differential patterns of infection by sex. We found that females were significantly more likely to be infected and had higher fungal loads than males. Previous research has found that female bats have 22% shorter torpor arousal bouts compared to males, which could limit their opportunity to remain euthermic long enough to inhibit infection. Although male bats may have more frequent contacts during mating, our results suggest that differences in torpor ecology are likely more important than sex-based differences in contacts. Female bats may suffer higher direct mortality as a result of higher fungal infections, and there is potential for WNS to have cascading effects on bat reproduction. These effects could reduce overall recruitment, resulting in Allee effects on bat populations, thus extending the effects of WNS beyond the hibernation season.

Bat Responses to Nocturnal Insect Light-traps in Eastern Iowa
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There are nine species of insectivorous bats (Chiroptera: Vespertilionidae) recorded for Iowa that consume both human-disease vectors and agricultural pests. These bats are crucial components to healthy forest ecosystems and human economies. This project sought to determine whether using insect light-traps to attract insects would in turn serve to attract bats. This could enhance opportunities to capture bats for research. Our Null hypotheses are no differences in bat community structure (measured as both species diversity and abundance) at light-trap sites versus control sites. To evaluate the impact of light-traps on bat activity, SM3Bat detectors (Wildlife Acoustics, Inc.) were deployed at multiple locations within Dubuque County, Iowa. At each location, likely bat travel corridors associated with water sources were identified. Bat detectors were deployed at each site at least 100-meters apart; one associated with an operating light-trap while the other was associated with a non-operating light-trap. Data files were analyzed by Kaleidoscope Pro software, which provides species-specific identification for bat calls with sufficient data. Preliminary results suggest that total bat calls per night at sites with insect light-traps is greater than at sites without light-traps. More specifically, *Myotis lucifugus*, which was the most abundant species as measured by bat calls, were the main drivers of the overall results as they appeared to respond more strongly than other species at sites where light-traps were deployed when compared to sites without light-traps. Initial data analysis implies that light-traps do have an impact on bat activity and community structure.

Predator-prey Kinematics of a Specialized Population of Swainson's Hawks and Brazilian Free-tailed Bats
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Predators and prey often exhibit coupled dynamics, especially during pursuit and evasion. These interactions require the coordination of complex sensorimotor control on rapid timescales, with a high potential cost for prey. Many predators and prey have co-evolved over time, resulting in an evolutionary arms race that can influence morphology and behavior. In this study, we investigate the pursuit and evasion strategies, respectively, of Swainson's hawks (*Buteo swainsoni*) and Brazilian free-tailed bats (*Tadarida brasiliensis*). Bats are not typical prey of Swainson's hawks, but a small population of these birds have specialized to prey upon the seasonal population of free-tailed bats outside of one cave in central New Mexico. We recorded, with stereo video, the pursuit and evasion of hawks and bats during flight, and reconstructed 3D trajectories of individuals. From the trajectories, we quantified flight behavior of predators including path, speed, attack angle, and acceleration; for the prey, we quantified escape success, escape trajectory, flight speed, acceleration, escape angle, and reaction distance. We found mixed strategies

for pursuit among hawks, and no stereotypical evasion strategies among individual bats. Our results suggest that the behavior of these populations has not likely co-evolved.

Patterns in High-altitude Bat Movement over Texas Revealed by Radar
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Movements of insectivorous bats foraging in open space and at high altitudes are very poorly understood. Advances in technology such as radar and telemetry have provided some clues. For example, Brazilian free-tailed bats (*Tadarida brasiliensis*) fly over 3 km above ground level (AGL) after leaving their cave roosts, but we do not know if they maintain those altitudes while foraging, or if they forage in proximity to other bats. Some movement patterns may depend on factors related to insects, such as their location, abundance and diversity, whereas other patterns may depend on factors related to bats themselves such as phenology of juvenile flights and density of foraging bats. These patterns vary within and among nights and seasons. We used an aerostat carrying bat detectors aloft to ground-truth a vertical radar installed in an area with many nearby colonies of *T. brasiliensis* in southern Texas, where large numbers of bats forage over agricultural fields. We then analyzed data from three seasons in 2018 and compared them to data from a nearby weather radar. We characterized bats' behaviors in several ways, including finding that bat activity peaked in most seasons at approximately 200 m above ground level though bats were active to at least 1600 m from April-November. We report distributional patterns of bat activity between 50–3000 m above ground level. Understanding these foraging movement patterns is crucial for bat conservation efforts, because flights within range of large maternal colonies occur at altitudes matching threats from growing wind energy facilities.

***Observing Social Behaviors of *Eptesicus fuscus* within the Roost**
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Previous research has demonstrated that big brown bats, *Eptesicus fuscus*, exhibit moderate repeatability in measures of activity and exploration, indicating consistent individual differences in behavior (i.e., personality). Such differences could serve as the basis of dominant and submissive relationships among individuals within a social group, although this idea has not been tested. The goal of this project was to conduct a preliminary assessment for the presence of dominant/submissive relationships in a captive colony of big brown bats. Specifically, we analyzed the positions of animals within their roosts (bat boxes) during three 30-minute periods within a night across a six-week period. Recordings were scored in Noldus Observer to determine the position of each animal within the group huddle (top, middle, bottom, away from group). Data were analyzed to determine if individuals differed in their distribution of positions within the group over the study period; we also examined the relationship between an individual's distribution of positions and their activity and exploration scores, which were collected as part of another study. Overall, this research provides a first glimpse into the relatively unstudied topic of the behavior of big brown bats within the roost.
*** Derek T. Krueger** received the **Batgoods Award.**

Gray Bat: Recovery Progress and Future Innovation
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Following the listing of the gray bat (*Myotis grisescens*) as endangered in 1976, the U.S. Fish and Wildlife Service (Service) developed the Gray Bat Recovery Plan to guide recovery actions throughout the species' range. Extensive efforts have been undertaken to achieve recovery criteria that have resulted in significant conservation of gray bats including permanent protection of 90% of Priority 1 hibernacula. A landmark conservation accomplishment was the protection of Coach and James Caves in Kentucky. Because of the cumulative benefits of implemented actions, populations of gray bat have increased in many areas and the overall range-wide status is considered stable. Specifically, surveys have documented marked increases in population at some of the most significant caves in Kentucky, Arkansas, Tennessee, and Missouri. Despite achievements in recovery, vulnerability to more recent and emerging threats, such as white-nose syndrome and wind energy development, could still be hampering recovery

and are being assessed. Evaluation of success according to the criteria established in the Recovery Plan has proven challenging in some cases based on historic monitoring strategies. For instance, documentation of stable or increasing populations at Priority 1 maternity caves for at least 5 years (Recovery Criterion 2) has not been met due to the number of caves, access issues, and lack of appropriate survey methods. To address the discrepancy between needs and available tools, the Service and its partners are undertaking targeted efforts in research and data management that will bridge the gap and inform future recovery of the gray bat.

***Partial Migration in Mexican Free-tailed Bats: Ecology and Bioenergetics of Winter Residents**

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*** Emma L. Kunkel** received the **Bat Conservation International Award.**

Migration is characteristic of individuals and the sum of individual migratory behaviors creates population-level patterns. When costs and benefits of migration differ across individuals some animals forego migration, resulting in partial migration systems. Within a partial migration system, we investigated characteristics and energetic strategies of non-migrants. Mexican free-tailed bats are partially migratory, with most individuals migrating south for winter while remnant populations remain at summering grounds. We hypothesized differing costs and benefits of migration between sexes would create a sex bias in winter residents, specifically predicting more males would overwinter. We hypothesized overwintering individuals would balance foraging activity and torpor use to maximize energy intake while reducing energetic costs. We predicted nighttime temperature (T_a) would correlate with bat activity, foraging intensity would be reduced through winter, and bats would enter torpor more frequently on colder nights with multi-day bouts during longer periods of low T_a. We worked at a Texas roost from September 2018–May 2019. To examine seasonal shifts in sex ratio, we captured >1000 bats and recorded their sex. To delineate shifts in foraging intensity, we collected blood from 174 foraging bats and assayed for plasma triglyceride concentration. To investigate torpor use, we measured skin temperature with temperature-sensitive radio transmitters attached to 30 bats in February 2019. There was a strong male sex bias in winter residents, resident bats regularly used torpor, and triglyceride concentrations indicated foraging on warmer nights. Winter residents balance nightly torpor and active foraging throughout winter, highlighting the extreme energetic flexibility of this sub-tropical mammal.

Effect of Hurricane Maria on Ectoparasites of Bats on Puerto Rico

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Environmental or reproductive stress potentially can lead to changes in the number and kind of ectoparasites that dwell on a mammal. Hurricane Maria, in 2017, was the most devastating storm ever to hit the Caribbean island of Puerto Rico, causing massive defoliation, destruction of woody vegetation, and disruption of natural communities. Although, cave-dwelling bats can successfully outride a serious storm by remaining in their subterranean haunts, a reduction in available food afterwards often impacts survival and reproduction. We predicted that the resulting stress, post-Maria, would result in poorer physical condition by these mammals and, ultimately, in an increase in the number of their ectoparasites. We also predicted that this effect would be more pronounced in nectarivorous/frugivorous bats and less so in insectivorous species. Fourteen months after the hurricane, we examined the assemblages living on two nectar-feeding bats (*Monophyllus redmani* and *Erophylla sezekorni*) and two insectivorous species (*Pteronotus quadridens* and *Mormoops blainvillei*) and made comparisons to data obtained before Maria. Although many bats died after the storm and reproductive patterns were affected, the data did not support our predictions. Prevalence did not change significantly, except that we actually documented a reduction for *M. redmani*. Similarly, intensity was unchanged for three species but decreased in *M. redmani*. Diversity of parasites (Simpson's Index) decreased on *P. quadridens*, increased on *E. sezekorni*, and stayed the same for the other two bats.

Using Whole-Room Sanitation Technology to Treat Infected Hibernacula with Ultraviolet Light

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The research and management community has made significant advances in developing management strategies for white-nose syndrome (WNS). Several control agents have been shown to inhibit *Pseudogymnoascus destructans* growth; however, for most potential treatments logistical constraints challenge cost-effective treatment of entire colonies/sites and little is known about possible environmental impacts. Recently, low-dose ultraviolet (UV) radiation has joined the suite of potential treatments, but to date large-scale implementation methods have not been developed. We tested the use of whole-room UV sanitization as a feasible and ecologically safe method of reducing *P. destructans* loads from hibernaculum substrates by deploying a portable robotic console to disperse low dose UV-C light in portions of two WNS-infected mines. Prior to UV deployment, we mounted contact plates of lab-grown *P. destructans* at multiple angles along the wall and ceiling surface, and swabbed presumed bat roost areas for subsequent culture of both *P. destructans* and the resident microbial community. After UV treatment, we assessed viability of *P. destructans* among contact plates and compared presence and viability of all cultured microbes before and after treatment. We also measured sound and temperature changes in the immediate vicinity of the robotic console to consider potential impacts on hibernating bats and other cave dwelling organisms. We report on the preliminary findings of this pilot work.

The Effects of Forest Management Practices on Habitat Use by the Evening Bat

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Bats in eastern deciduous forests are declining in numbers due to habitat loss, disturbance, and disease. To promote the conservation of insectivorous bats, it is important to assess the effects of forest management practices on bat habitat use. Additionally, forest management practices may affect the sexes differently due to their unique requirements over the reproductive cycle. We therefore assessed the effects of a wide range of landscape characteristics on sex-specific foraging habitat use by the evening bat (*Nycticeius humeralis*), a forest-dwelling species, in Arkansas from June–August 2013 and 2014. We used a maximum-entropy (MaxEnt) machine-learning approach to determine the effects of 18 landscape variables (eight land-use land-cover classes, three stand types, two topography measures, normalized difference vegetation index, and four management variables) on sex-specific foraging habitat use and to further predict sex-specific areas of habitat suitability for *N. humeralis*. Our results demonstrate that female *N. humeralis* show preference for foraging near stands treated by prescribed fire, while males show preference for reforested stands. Interestingly, the area of predicted suitable habitat for male *N. humeralis* was approximately four times larger than for female *N. humeralis*, demonstrating that male *N. humeralis* expressed more flexibility in their foraging habitat use. Because our study was conducted during the period of lactation and post-lactation, male *N. humeralis* may have been excluded from foraging in the less-cluttered burned sites by females, who were likely more energetically constrained.

The Environmental Reservoir Mediates Species Connections during Hibernation

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White-nose syndrome (WNS) has decimated bat populations across North America at an unprecedented rate. While pathogen transmission is pivotal in disease outbreaks and primarily occurs within social groups, environmental reservoirs can connect otherwise disconnected species and groups, exacerbating disease impacts. We examined

transmission dynamics related to white-nose syndrome, between bat species and the environmental reservoir using a surrogate pathogen. We employed an ultraviolet-fluorescent (UVF) dust, to determine the extent of pathogen spread between species and how the environmental reservoir influences this relationship. We found that the extent of the environmental reservoir differentially influenced the connectedness between different species. Our results suggest that control measures that target the environmental reservoir have potential to reduce the impact of WNS in multiple bat species.

Development and Testing of an Anti-*Pseudogymnoascus destructans* (*Pd*) Probiotic Cocktail Applied at Maternity Roosts to Reduce White-nose Syndrome-caused Mortality

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Using bacteria sourced from healthy bats in British Columbia (BC), Canada, we have derived a prophylaxis (probiotic) for prevention of white-nose syndrome (WNS). This prophylaxis contains multiple bacteria, isolated from bat wings and naturally found in some soils. These bacteria reduce the growth/germination of *Pseudogymnoascus destructans* (*Pd*). Our goal is to delay or prevent winter *Pd* growth on bats by preemptive exposure to probiotic in late summer at maternity roosts, increasing overwinter survival from WNS. This is a 'made in the west' solution because while WNS kills bats during hibernation, few locations for hibernacula are known in western North America. Instead, however, significant numbers of summer maternity locations for building-roosting bats are known and continuing to be discovered through efforts such as BC Community Bat Program, Alberta Community Bat Program, Canada's BatWatch.ca, etc. Our goal is not to treat WNS but to be proactive, reducing the ability of *Pd* to take hold on bats' wings. We present results from our successful fall 2018 'proof-of-concept' and final spring 2019 captive trails, using Yuma myotis (*Myotis yumanensis*). We will provide updates on August 2019 field implementation in Metro-Vancouver, an area likely to see *Pd* imminently given its proximity to Washington WNS detections. At these field sites we have established baseline behavioral and microbiological data, including tagging of maternity colonies of Yuma and Little Brown Myotis for long-term tracking. Probiotic inoculations are passive using clay powder dusted onto roosting substrates; the applicator is cheap, easy to deploy, and easily scaled up for widespread implementation.

Are Bats Seeking Out Clean Water? A Perspective from the Namib Desert

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Water abundance, flow, and quality are key elements affecting species distributions in arid environments, yet how exactly they interact to structure specific wildlife communities is often unclear. We examined relationships between bodies of water and bat communities in the northern Namib Desert in Namibia, and explored whether these flying mammals may serve as new bioindicators of water quality. We predicted that water quality would be poorer (i.e., higher indices of electrical conductivity and ion concentrations) during the dry season and at artificial pools, and that bat species richness and activity would consequently be lower at these sites. We conducted extensive fieldwork at the terminus hot, dry season from November 2016 to January 2017 and at the conclusion of the subsequent wet season from March to May 2017, collecting water samples and acoustic recordings of bat activity at both natural springs and artificial pools. Bat species richness and overall activity increased during the wet season. Variations in water quality, however, were predicted by neither seasonality nor water body type. Although individual artificial pools harbored a greater number of bat species and activity, more than 35% of the species we detected were only recorded over natural springs. Particular species of bats rather than the entire community as a whole may still be useful water quality indicators, but other factors (e.g., roost and prey availability) require further investigation as they also likely affect distributions of Namib Desert bats.

Differences in Coding Sequence of DNA Repair Genes between Bats and Humans

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The average human life span continues to increase as does the incidence of age-related diseases. For example, cancer is currently the second leading cause of death globally. Taken together, these observations indicate a critical

need for novel cancer prevention and treatment strategies. Despite the clear association between age and incidence of cancer in humans, elephants and bats are also long-lived animals, but rarely develop cancer. Elephants have been shown to be resistant to cancer due to the presence of multiple copies of the TP53 tumor suppressor gene. This protein provides elephants with a very robust response to DNA damage that may be present in malignant cells as it triggers cell death. The TP53 gene, other genes involved in DNA repair pathways, and those involved in telomere maintenance have been found to be under positive selection in bats and may explain why bats have exceptional longevity coupled with a reduced incidence of cancer; however, a direct comparison of nucleotide sequence in the coding regions among bat species and humans is lacking. We hypothesize there are nucleotide and amino acid differences among bat species and humans for genes involved in DNA damage response. We have isolated RNA from wing punch samples of *Myotis velifer* and *Tadarida brasiliensis*, converted samples to cDNA, and then obtained DNA sequence from select genes involved in these pathways. A comparison of bat DNA sequence with human DNA sequence for these genes will be discussed.

Occupancy and Activity of Bat Species in Yellowstone National Park

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Cavernicolous bats are expected to decline in the Rocky Mountain region as white-nose syndrome continues to spread, making it important to collect acoustic recordings of bat activity for continental monitoring and research. However, it is often unclear how land stewards will apply this information toward bat conservation efforts. Our goal was to compare occupancy models for 12 bat species to models of activity rates in Yellowstone National Park. To do so, we deployed SM4BAT acoustic detectors at 32 locations in 2018 and 2019, each within 5-km^2 quadrants within 10-km^2 grid-cells prioritized by the North American Bat Monitoring Program. We also drove 12 road transects within these grid-cells and compared data collected from stationary detectors to data from mobile transects using species accumulation curves. Mobile transect routes were driven twice each year, and stationary detectors remained in the field for approximately one month. We created a suite of single-species occupancy models, including detection probability and landscape-scale habitat parameters, and ranked competing models using Akaike information criterion corrected for small sample sizes (AICc). Estimates of species occupancy ranged from 4% for *Euderma maculatum* to 97% for *Myotis lucifugus*. Estimates of detection probability ranged from 30% for *Myotis californicus* and *Antrozous pallidus* to 91% for *Myotis lucifugus*. Compared to null models, occupancy models that included landscape parameters performed poorly. Conversely, models of species-specific activity rates were improved by inclusion of these variables. These data suggest that activity was more sensitive than occupancy in our study area and will likely reveal population disturbances before changes in occupancy estimates will.

Detection of Tarnished Plantbugs, Apple Maggots, and Codling Moths in Bats' Diet in Michigan Apple Orchards

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Michigan is ranked third for apple production in the United States. Insectivorous bats provide a key ecosystem service for some agriculture systems and may provide one for southern Michigan apple orchards by consuming apple pest insects. My thesis evaluates if big brown bats (*Eptesicus fuscus),* silver-haired bats *(Lasionycteris noctivagans),* eastern red bats *(Lasiurus borealis),* and hoary bats *(Lasiurus cinereus)* consume three economically-important apple pests: tarnished plantbug (*Lygus lineolaris*), apple maggot (*Rhagoletis pomonella*), and codling moth (*Cydia pomonella*). The objective provides farmers with sustainable and inexpensive alternatives to pesticides. I will capture bats and collect fecal samples from 4 organic and 4 conventional orchards in southern Michigan. Target insects will be collected from pheromone traps during surveys to measure relative abundance. Molecular data may not be available, but I will be extracting DNA from the fecal samples and amplifying the DNA using polymerase chain reaction (PCR). DNA will be analyzed for target insect presence or absence using the genetic technique restriction fragment length polymorphism (RFLP). Positive samples will be categorized by bat species and orchard type followed by comparing them to the total number of samples, across bat species, and between conventional and organic orchards as well as to samples collected each night. Results analyzed by the conference will include relative bat and insect abundance. I predict my results will show bats are eating these pest insects, especially during peak emergences. My predictive conclusion is bats can provide farmers with an alternative pest control method they can implement within their current practices.

Summer and Autumn Roosting Ecology of *Myotis septentrionalis* in Pennsylvania
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Knowledge of the roosting ecology and behavior of several bat species is largely based on summer studies. Although less studied, autumn is an important time for temperate bats to migrate and prepare for hibernation. Furthermore, some species traditionally considered "cave bats" are recently discovered to also hibernate outside of caves, possibly in structures similar to their autumn roosts, demonstrating the need to better understand autumn habits. Our goal was to study summer and autumn day-roosts of *Myotis septentrionalis* and to determine the timing of autumn migration. To do so, we tagged male and female northern myotis belonging to a remnant population in central Pennsylvania with traditional radio transmitters and coded NanoTags. We tracked tagged bats to their roosts each day and collected a suite of habitat measurements at each tree. We also constructed seven automated telemetry stations within the study area to help determine when bats migrate. We used multinomial regression and an information theoretic approach to compare biologically informed models predicting differences between male, female, and available (unused) trees during summer and autumn. At the time of abstract submission, we radio-tracked 22 bats to 66 day-roosts. During summer, females were most likely to use snags of larger diameter located in stands with higher basal areas of live and dead trees than males. Males also selected smaller trees than those available. Autumn data will be presented. These data illustrate the importance of snag availability for remnant bat populations and will provide an important baseline for comparisons with autumn roosts.

The Luxury Effect Beyond Cities: Bats Respond to Socioeconomic Variation across Landscapes
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The luxury effect describes the positive relationship between affluence and organismal diversity or activity in urban ecosystems. Previously, the luxury effect has been found in two bat species within a city, the red (*Lasiurus borealis*) and the evening (*Nycticeius humeralis*) bat. We were interested in determining if the luxury effect scaled beyond a single city and across multiple bat species. We examined landscape scale bat activity patterns from seven bat species to test for the luxury effect, and bat activity and land cover associations. We used mobile transect data from the North American Bat Monitoring Program in North Carolina from 43 sites collected from 2015 to 2018. Land cover data were from the 2016 National Land Cover Database and income data from the 2016 American Community Survey 5-year estimates. We constructed generalized linear mixed models to identify bat-land cover and bat-income relationships. Across landscapes, activity of red bats and evening bats was positively correlated to income independent of land cover, a result consistent with the previous single-city study. We found a negative relationship between hoary bat (*Lasiurus cinereus*) activity and income. All species had specific land cover associations. We conclude that the luxury effect is an ecological pattern that can be found at a broad spatial scale across different landscapes. We suggest the need for multi-scale ecology studies to identify the mechanism(s) underlying the luxury effect and that the luxury effect could cause inequity in ecosystem services.

Responses of Temperate Bats to Silvicultural Treatments—A Qualitative Synthesis
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Most bat species depend on forests for roosting, foraging, and drinking during part or all of their life cycles. Many of the world's forests are managed using a variety of silvicultural treatments and over the past 40 years, researchers have studied the responses of bats to these treatments. I conducted a qualitative synthesis of the literature on stand level responses of temperate insectivorous bats to silvicultural treatments to determine what treatments may be most compatible with conservation of temperate insectivorous bats and to guide future research. Eighty-eight studies from Canada, the United States, Europe, Australia, and New Zealand met review criteria. Based on the proportion of negative responses to treatments, bat foraging and commuting habitat use was less affected by silvicultural treatments than roost habitat use. Mid-rotation treatments such as thinning and prescribed fire, which reduce clutter while retaining overstory structure, appeared to have fewer negative effects and more neutral and positive effects than treatments that remove all or part of the overstory and eventually result in thick second growth forests. Based

on caveats identified in the studies included in this synthesis, I suggest that future studies: 1) strive to account for treatment effects on detection probability of bats when using acoustic detectors, 2) examine responses of bats to silvicultural treatments outside the maternity season, 3) examine demographic and physiological responses to silvicultural treatments in addition to changes in habitat use, and 4) use stand level data to model forest management effects across the landscape.

Effects of Omnidirectional Microphone Placement and Survey Period on Bat Echolocation Call Quality and Detection Probabilities

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Many factors, including microphone type, affect the quality of acoustic calls recorded by bat detectors and detection probabilities of individual species. Because omnidirectional microphones tend to have a shorter range and record more noise than directional microphones, it has been suggested that these microphones be set farther from reflecting surfaces. Our objective was to determine the effects of microphone height (1.5 m, 5 m, and 9 m), distance from forest edge (1 m, 3 m, and 5 m), and survey timing on the number of bat files recorded, quality of recorded files, the proportion of identifiable files, and the probability of detecting individual species. We deployed 3x3 arrays of two types of bat detectors with omnidirectional microphones at two sites in Kentucky during two survey periods. We found little evidence for effects of microphone height or distance from forest edge on call quality or detection probabilities of any species. In contrast, survey period significantly affected the number of files, the proportion of high-quality files, the proportion of identifiable files, and the probability of detecting individual species and the length of the recording session significantly affected the probability of detecting some species. Thus, it appears that biologists have some latitude when placing detectors with omnidirectional microphones on the landscape but timing of surveys should be considered when designing and analyzing bat acoustic survey and monitoring studies.

Effects of Forest Fire on the Bat Community in Waterton Lakes National Park

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The Kenow Wildfire occurred in Waterton Lakes National Park (WLNP) in southwestern Alberta, Canada in September 2017. The wildfire, started by lightning, burned 38% of WLNP and resulted in a predominantly ‘very high’ burn severity throughout the park. As the wildfire occurred at the end of summer after bats had dispersed to their wintering grounds, there was likely no direct mortality. Therefore, any changes to bat diversity and relative abundance can be attributed to the wildfire’s impact on the environment. Past studies have suggested that bats respond positively to fires, by increasing the roosting and foraging opportunities for most species. From 2015–2017 bat acoustic surveys were conducted by Parks Canada staff in WLNP from late June to early August. Acoustic monitoring was continued after the Kenow Wildfire (2018–2019), providing the opportunity to compare bat diversity from before the fire to levels after the natural disturbance. During the summer of 2019 (June–August), bats were also captured using mist nets, and body and reproductive conditions were assessed. Capture data from 2019 was compared to data from trapping surveys in 2011 and 2012. Little Brown Myotis reproductive females were also radio-tagged and tracked to their maternity roosts in 2019. Preliminary results of capture data show a strong preference for anthropogenic roosting structures and decreased species diversity compared to 2011 and 2012. The analysis of acoustic results is in progress; however, given the lower than expected species diversity, I predict this to also be reflected in the acoustic results.

Effects of Open Aerospace Habitat on Aerial Insectivorous Bat Communities in Lamanai, Belize

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Neotropical bats stratify vertical aerospace due to adaptations associated with diet, foraging strategy, echolocation, and size. Aerial insectivores, in particular, forage in open, non-cluttered spaces high in the aerosphere. Due to their use of open aerospace, these bats are not expected to decline with habitat disturbance and deforestation. However, sensitivities to habitat changes may vary from species to species. Passive acoustic monitoring was used to assess community structure of aerial insectivorous bats from three open aerospace habitats in Lamanai, Belize. Recordings were taken over a lagoon (natural habitat), over an unused airstrip (cleared forest), and above a lodge with a flood

light (disturbed forest with anthropogenic light). Nine total nights of recordings were analysed with 20,195 bat calls identified. Richness was found to be unaffected by habitat type, however, community composition differed on both a family and genus level across all three sites. Activity decreased over cleared forest but increased with disturbance and anthropogenic light. Bats in Mormoopidae family were more sensitive to habitat disturbance, while Vespertilionidae became the dominant family in sites with anthropogenic light. Understanding the changes to community structure in Neotropical aerial insectivorous bats allows us to better include them in conservation projects and studies in the future.

Functions of In-flight Social Calls of *Eptesicus fuscus* and *Nycticeius humeralis*

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Bats produce social calls while in flight, and the behavioral context of in-flight social calling in bats is not well understood. We have identified in-flight social call types produced by the big brown (*Eptesicus fuscus*) bat and the evening (*Nycticeius humeralis*) bat. Social calls produced by these species contain species-specific signatures and are produced during different behavioral contexts. *Eptesicus fuscus* complex social calls frequently appear with foraging buzzes suggesting a competition function. Upsweeps and downsweeps of *E. fuscus* and *N. humeralis* occur most often when there are multiple species of bats present suggesting a group cohesion function. In this study we conducted playbacks in Greensboro, North Carolina, USA to identify the functions of common social calls produced by these species. We compared changes in bat activity between social call playbacks, echolocation call playbacks, and silent control trials. We predicted that *E. fuscus* complex social calls would have a negative effect on total bat echolocation calls, whereas upsweeps and downsweeps would increase total bat echolocation calls. We found no effect of complex or downsweep playback calls on subsequent bat activity; however, we found that playback of *E. fuscus* upsweep social calls decreased total echolocation calls. Therefore, our results suggest the call does not facilitate group cohesion. Our study is ongoing with additional social call types that will be presented. There are rich social behaviors that can be studied from the response of free flying bats to social calls through controlled playback experiments.

Does Metabolic Rate Predict Activity and Cooperative Behavior in Common Vampire Bats?

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Individual variation in sociality could be linked to metabolism and energy expenditure due to energetic costs and benefits associated with cooperative investments. Individual differences in social behaviors, like allogrooming, might be driven merely by individual differences in activity level, a trait associated with high metabolic rates. I hypothesize that social or cooperative individuals are more active than those individuals who do not engage in social interactions as often. Resting metabolic rate (RMR) of 22 bats was estimated from oxygen consumption data, measured using open-flow respirometry, and correlated with an individual's average activity level and amount of social behavior. Activity level, quantified by the amount of movement within an enclosed arena, and social behavior were evaluated using video footage of each bat while isolated and while housed with conspecifics, respectively, after a fasting period to encourage food sharing. Preliminary data on RMR among the bats show high intra-individual variation. Metabolic rates of these individual bats will be linked to further research on individual differences in vampire bat sociality and in the underlying neuroendocrine mechanisms. Variation in metabolic rates could largely determine which individuals are most central in a social network.

Dietary Patterns of Big Brown Bats in a Diverse Landscape

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Over the past decade, advances in high-throughput sequencing of DNA extracted from bat guano have allowed researchers to gain new insight into the foraging ecology of bats. Recent work has provided new perspectives on basic biological questions, including inter-/intraspecific competition and seasonal differences in prey selection, as well as applied topics such as the potential importance of bat predation for insect pest management. Here we expand on this emerging knowledge base with an analysis of big brown bat (*Eptesicus fuscus*) guano collected from six maternity colonies across a diverse New Jersey, USA landscape over a 26-week period in 2017. Using metabarcoding of 419 samples (~10 guano pellets per sample), we identified 2,815 amplicon sequence variants (ASVs), corresponding with 552 species from 151 arthropod families. The most common taxa included Lepidoptera (moths), Coleoptera (beetles), and Diptera (flies), as well as the primarily aquatic Megaloptera, Ephemeroptera, and Trichoptera. Prey included many agricultural (e.g., brown marmorated stink bug, tarnished plant bug) and human (e.g., mosquitos) pests. Prey diversity differed seasonally and among colonies, largely driven by landscape-level characteristics and time of year.

Befriending Bats: Using Citizen Science for Acoustic Data Collection in an Urban Park

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Involving citizens in the collection of scientific data is an effective method of engaging people to learn more about local wildlife, while also adding to the database of scientific studies. Projects such as Neighbourhood Bat Watch have allowed for citizens to submit bat sightings online, while few others have implemented on-the-ground data collection. The Native Bat Conservation Program at the Toronto Zoo partnered with Friends of Cedarbrook Park to conduct walking transects and collect acoustic monitoring data on bat species in a suburban park in Toronto, Ontario, Canada. Volunteers were initially taken on one evening bat walk through Cedarbrook Park to learn about the species of bats found in Ontario, while also being trained to use a PeerSonic acoustic recorder and record bat observations on a datasheet. Volunteers are completing this 4-km walking transect on a biweekly basis throughout the summer, which will result in a total of nine nights of data collection. *Eptesicus fuscus* is the most commonly observed species in the area, followed by *Lasionycteris noctivagans* and *Lasiurus cinereus*. On each night of data collection, members of the community were invited to join the walk, now lead solely by volunteers. Devoted volunteers also began undertaking data analysis on their own based on visual observations during each night. The success of this project was dependent on the commitment of the Friends of Cedarbrook Park volunteers to continue collecting data on a regular basis, allowing for more information of bat activity in the city.

Modeling and Mapping Western Bat Hibernaculum Suitability Before and After *Pseudogymnoascus destructans* (*Pd*) Exposure

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As the fungal pathogen *Pseudogymnoascus destructans* (*Pd*) and resultant white-nose syndrome (WNS) continues to advance into western North America, it will infect new bat populations, species, and hibernacula. Western North America's extensive public lands host the continent's highest bat diversity, so it is critical that western land managers have the information they need to anticipate and address the conservation needs of WNS-susceptible species. We estimate suitability of potential winter hibernaculum sites continuously across five bat species' ranges in the West, then predict future changes in suitability with *Pd* exposure by integrating spatially explicit pre- and

post-exposure estimates of winter survival capacity with high-resolution landscape data. We estimate winter survival capacity from a mechanistic survivorship model based on host bioenergetics, *Pd* characteristics, and climate conditions. Leveraging the Google Earth Engine platform for spatial data processing, we use boosted regression trees to relate these estimates, along with key landscape attributes, to bat occurrence data in a hybrid correlative-mechanistic approach. Winter survival capacity, topography, land cover, and access to caves and mines are important predictors of winter hibernaculum selection, but their relative importance varies among species. *Pd* exposure is generally expected to decrease winter survival capacity and in turn reduce hibernaculum suitability, often in areas currently estimated to be most suitable. We aim to help managers anticipate which species are most susceptible to declines, and where to implement effective conservation strategies for western bats. We conclude by discussing the implications of interacting impacts of *Pd* and climate change on hibernaculum selection and survival.

Insect Perspective on High Altitude Bats

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Many bats are known to fly at high altitudes. Not all high-flying bats feed aloft, but over a dozen species belonging to four bat families are now documented to do so. These bats share features of morphology, flight dynamics, echolocation, and feeding strategies that are common to open-airspace foragers, but they may also face challenges unique to high altitude environments. While the ecology of high-altitude flight has received little attention from bat ecologists, insects aloft have received extensive study. Here we posit that studies of nocturnal, high-flying insects can inform us on the challenges faced by bats at high altitudes, and on opportunities presented to the bats. Layered structure, waves, and circulatory motions are dominant features of the night sky. Temperature, wind speed, relative humidity, and air pressure vary at different altitudes but not necessarily as smooth gradients. Temperature and humidity may increase with altitude, and bats and insects at altitudes of several 100 m above the ground may be flying in air temperatures as much as 10ºC above surface temperatures. Insects form layers at altitudes with higher temperatures and favorable winds, and insects actively seek these habitats, which may result in patches of resources that influence the social and foraging behavior of bats. In mountainous and hilly terrain, the rapid ascents at night of insects are assisted by thermally assisted winds that are deflected upslope. Bats may use the same winds for their own purpose.

The Influence of Microclimate Manipulation on Hibernation Physiology and White-nose Syndrome

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Microclimate conditions affect hibernation physiology and the dynamics of white-nose syndrome (WNS). Other studies have investigated the effect of temperature, few have considered humidity, and no study has considered the combined effects of both. To test the influence of temperature and humidity on hibernation and WNS, we conducted a captive inoculation study with bats housed across a range of temperature (5–11°C) and potential evaporative water loss (pEWL; 0.5–1.6 hPa). We collected 70 *Perimyotis subflavus* from Mississippi, inoculated them with *Pseudogymnoascus destructans,* and maintained them in environmental chambers for ~3 months. We used quantitative magnetic resonance to measure body composition, and quantified fungal load (qPCR), UV fluorescence (wing photos), and histology. Our design allowed examination of independent effects of temperature and humidity. We found higher temperatures and pEWL increased arousal frequency, but temperature also independently increased energy expenditure through other mechanisms. We did not observe behavioral symptoms of WNS. Wing photos revealed little UV fluorescence, fungal loads remained low, and few bats were observed with diagnostic histopathology characters of WNS after 82–86 days of hibernation, longer than the predicted duration of Mississippi winter. Lack of WNS severity is consistent with previous captive studies that suggest symptoms of WNS increase rapidly late in hibernation (>90 days). Our experimental results suggest dynamics and outcomes of WNS may be different in regions where winters are shorter. This finding emphasizes the importance of continued research and monitoring in these regions to understand the implications of WNS across a growing geographic range.

Modeling Bat Species Co-occurrence in Dubuque County, Iowa
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Insectivorous bats are important mammals for agricultural pest control. Native bats are threatened by habitat loss and fragmentation, disease, wind turbines, and climate change. Nine species of bat are known for eastern Iowa including the Federally Endangered *Myotis sodalis* and Federally Threatened *M. septentrionalis*. We sought to evaluate bat co-occurrence in eastern Iowa as they adapt to increasing threats and are potentially restricted into smaller desirable habitats. Co-occurrence data can give insight into interspecific interactions and inform management and conservation strategies for Iowa's bats. Acoustic data were obtained from 22 sites within Dubuque County (Iowa) during summer 2018. From these data, 18,399 calls were identified through Kaleidoscope with all nine native bat species detected. To assess co-occurrence, we ran ten single-season two-species occupancy models in Program PRESENCE for five species (*Eptesicus fuscus*, *Lasiurus borealis*, *M. lucifugus*, *M. sodalis*, and *Perimyotis subflavus*). Four species (*Lasionycteris noctivagans*, *Lasiurus cinereus*, *M. septentrionalis*, and *Nycticeius humeralis*) were detected too rarely or frequently for reliable modeling. A *Phi* value equal to 1 suggests that the two species occupancy patterns are independent, a value greater than 1 suggests stronger co-occurrence that is not independent, and a value less than 1 suggests avoidance. While most models yielded *Phi* values very close to 1, a few suggested potential co-occurrence or avoidance between species pairs. Notably, a strong co-occurrence of *M. lucifugus* and *M. sodalis* (*Phi* = 1.57) may reflect challenges in distinguishing between the two species' vocalizations and not reflect the presence of *M. sodalis* in the area.

The Advancing Front of White-nose Syndrome: Using Bat Dispersal Models to Explain Disease Spread
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The emergence of a new pathogen can cause disastrous declines in otherwise healthy species, a fact illustrated all too clearly by white-nose syndrome. Relating physical landscape structures to pathogen incidence has the potential to estimate the risk of disease spread on a broad geographical scale and identify specific paths in a landscape that a pathogen can take. White-nose syndrome presents a clear test case for the use of predictive disease spread models. This work combines metapopulation modeling with SIS disease spread modeling to provide insight into ways that landscape structure and the spatial position of hibernating colonies impedes or promotes the spread of white-nose syndrome. Multiple models of bat dispersal between hibernacula among *Myotis lucifugus*, *Eptesicus fuscus*, and *Myotis sodalis* in the eastern United States are constructed and an overlaying SIS model applied. Differing models adjust the effect of spatial distance, topographic features, and cross-species interactions. The generated disease trajectories between known hibernacula are compared to the observed spread of white-nose syndrome. The greatest similarity to the historical spread of white-nose syndrome is found in dispersal models modulating exchange of bats between hibernacula by intervening topographical slope and allowing limited cross-species interaction. Results from these models can allow for predictive trajectories of white-nose syndrome in as of yet unaffected areas. This project seeks to identify features of populations and regions that are at greater risk of spreading white-nose syndrome and to inform decision-making by managers.

Comparative Analysis of DNA Damage Response Gene Regulation in Bats and Humans
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Genome maintenance and prevention of DNA damage contribute to increased longevity and cancer resistance. Bats are exceptionally long-lived and cancer resistant, relative to humans. Furthermore, bats have been shown to have genome-level differences in several genes involved in the DNA damage response (DDR) and tumor suppression compared to humans. However, the physiological consequence of these differences in bats is not currently known. In order to test the hypothesis that the observed genome-level differences in bats contribute to enhanced DDR, we will identify and analyze gene regulatory sequences of genes with established roles in DDR. We have evidence to suggest that several of our candidate genes are coordinately deregulated in the context of cancer in humans. This supports the hypothesis that these genes are regulated by the same, or similar, upstream factors in humans. Transcriptional start sites (TSS) for our genes of interest will be determined, and candidate gene regulatory regions will be generated by PCR amplification of 1500–2000 bp upstream of the TSS. Candidate promoter sequences will

be tested for their ability to drive gene expression in two bat cells lines. Those sequences capable of driving gene expression will be considered promoters, and analyzed further. Transcription factor binding site analyses will be performed on sequenced regulatory regions using promoter analysis software, and the promoters derived from bats will be compared to their human counterparts using DNA analysis software. We predict that differential expression between bats and humans arises from sequence differences in the promoter region of each gene.

Development of Auditory Sensitivity in the Big Brown Bat

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Bats have excellent hearing, which they use for orientation, alerting functions, communication, and prey detection. We studied development of auditory sensitivity in the big brown bat (*Eptesicus fuscus*). The opening of the outer ear canal in both ears occurred until postnatal day (PND) 7 in 23 of 30 pups; the earliest time when both ears were open was PND 4, and the last time was PND 11. We then documented progressive development of hearing sensitivity using auditory brainstem response (ABR) recordings. The ABR is a synchronous neural response evoked by acoustic stimulation and represents the summed activity of neurons in the auditory pathway between the cochlea and upper brainstem. Recording ABRs is a relatively non-invasive procedure, with measurements conducted in awake or lightly anaesthetized animals and repeated in the same individual to track hearing onset and development. We measured hearing thresholds in 22 *E. fuscus* every three days between PND 10 and PND 31. Nursing pups were returned to their mothers between recordings. Further measurements were taken in some bats at PND 60, PND 90, and after one year. There was a dramatic shift in auditory thresholds across development for frequencies between 4 and 100 kHz. Prior to PND 13–16 when pups were still non-volant, most bats were unable to hear frequencies above 48 kHz; however, sensitivity to higher ultrasonic frequencies increased with age. Notably, this change occurred near the time when young bats start learning to fly and echolocate.

Home Range and Habitat of Northern Long-eared and Tri-colored Bats during Fall Swarm

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Fall swarm is an essential period in the annual life-cycle of bats. Foraging during this period is under-studied in comparison to the summer maternity season. We completed a study to describe landscape-use during fall swarm and create a resource for managers tasked with decisions about the future viability of northern long-eared (*Myotis septentrionalis*) and tri-colored (*Perimyotis subflavus*) bats on their conservation or management lands. In 2018, we conducted a ground-based foraging study during autumn on these two species in the Boston Mountain ecoregion of northeastern Oklahoma. Four northern long-eared and 13 tri-colored bats were radio-tagged and synchronized azimuths were gathered from five stations for five nights. Mean home range of northern long-eared bats was 196.0 ± 83.7 ha, and mean location distance (n = 84) from the swarm site was 1,337.8 ± 192.3 m. Mean home range for the tri-colored bat was 91.6 ± 11.8 ha, and mean location distance (n = 103) from the swarm site was 609.0 ± 76.6 m. Field surveys provided finer-scale habitat data than available from the National Land Cover Dataset; compositional analysis and linear regression showed that both species use breaks in the forested landscape, such as trails, to a greater degree than those habitats are available on the landscape. Both species used second-order and larger streams more than first-order streams, wetlands, ponds, or lakes.

Spring and Summer Energetics of *Myotis lucifugus* Recovering from White-nose Syndrome

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White-nose syndrome (WNS) causes hibernating bats to arouse too often in winter and use fat reserves too quickly. Therefore, bats that survive likely emerge in spring in poor body condition making it difficult for females to support reproduction. Despite the importance of reproduction, little is known about active season energy balance and reproduction of WNS survivors. We studied thermoregulatory energetics of reproductive female little brown bats (*Myotis lucifugus*) at the WNS invasion front in central Canada to test two hypotheses: 1) Carry over effects of the disease are influencing the torpor behaviors of the surviving females in the spring; and 2) Torpor expression by individuals is negatively correlated with severity of WNS-associated wing scarring. We captured bats from a

maternity colony in northwestern Ontario and assessed wing damage using the Reichard index. We attached temperature-sensitive radio transmitters during pregnancy (June 2017, $n = 13$) and lactation (July 2017, $n = 13$). We then used a datalogging receiver to record 122 bat-days of skin temperature data. Consistent with our hypothesis WNS surviving females are changing their torpor patterns, however not until later in the active season. This pattern only occurs in bats who had evidence of WNS damage. Torpor saves energy but delays offspring growth so our study will shed light on implications of WNS for reproduction by survivors. This is critical for understanding the potential of survival traits to evolve in endangered bat populations and aid population recover.

A Formal Technique for Monitoring Abundance of Bats on Talus Slopes

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Recent emerging threats to bat populations highlight a need for improved monitoring datasets. About 40% of bat species in North America are associated with rock-formations in at least part of their range, and status of many of these is poorly understood. We tested the efficacy monitoring one such species, the eastern small-footed bat, using visual surveys on talus slopes in Virginia. Bats were surveyed in random plots of varying size by teams of 2 to 3 observers. We assessed performance of the method at 6 sites, by comparing effects of observer, site, plot identity, season (pregnancy or lactation), and year on the number of bats counted per plot, with zero-inflated mixed-effects models. We also examined differences in outcomes for expert versus novice observers, and used trials with radio-tagged bats to quantify how often (and why) observers missed bats. Bat abundance varied significantly among plots and sites, but was similar among observers, years and between seasons. Novices tended to search more crevices and found slightly fewer bats than experts. Observers missed 36% of (4 of 11) bats; half were because bats were impossible to see, and half were visible but simply overlooked. Overall, visual surveys were surprisingly effective for quantifying eastern small-footed bats on talus slopes. Using multiple observers likely mitigated against observer bias. Visual surveys should be considered for use with other species of talus-roosting bats, especially in regions such as western North America where other forms of data are often lacking.

***Using Prepared Nectarivorous Bat Specimens for Pollination Studies: An Example with Bat-pollinated *Burmeistera* (Campanulaceae) from Ecuador**

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*** Juan I. Moreira-Hernández** received the **Basically Bats Wildlife Conservation Society Award.**

Specimens from biological collections are invaluable for bat ecology and evolution studies. In nature, nectarivorous bats often carry copious pollen from multiple plant species on their fur, making bat-pollinated flowers prone to receive heterogeneous pollen loads. We used prepared nectarivorous bat specimens (*Anoura geoffroyi*) to evaluate how heterospecific pollen deposition (HPD) affects reproduction of two sympatric species of bat-pollinated *Burmeistera* (Campanulaceae) from Ecuador. We created pollen mixtures that differed in the ratio of heterospecific:conspecific flowers used to make them (1:3; 2:2, and 3:1), applied them to flowers using the bat specimens, and quantified abortion rates, seed number, and seed mass of the resulting fruits. For *B. borjensis*, greater amounts of HPD decreased seed production and seed mass whereas no significant effect was detected in *B. ceratocarpa*. *Burmeistera borjensis* aborted more fruits than *B. ceratocarpa* (44.1% vs. 18.8%), however, fruit abortion rates were not affected by HPD in either species. We found differential effects of HPD on the reproduction of our study species: increasing HPD reduced seed production and seed mass of *B. borjensis* but not in *B. ceratocarpa*. Because prior work showed that interspecific pollen transfer by bats in nature is much higher from *B. borjensis* to *B. ceratocarpa* than in the opposite direction, we suggest that tolerance to HPD helps *B. ceratocarpa* to successfully coexist with its congener while sharing their bat pollinators. Our study demonstrates a novel use of nectarivorous bat specimens for pollination studies and suggests that tolerance to HPD might be common among bat-pollinated plants.

Evolution of the Major Histocompatibility Complex Class-I in New World Bats
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Host-Pathogen interactions have led to an endless evolutionary race, in which pathogens exert a strong selective pressure over the host, which consequently has developed mechanisms of defense known as the immune response. This response is divided in two types: a fast and non-specific innate response and a slower but highly specific adaptive response. One of the most important molecules of the adaptive response is the Major Histocompatibility Complex (MHC), a multigenic family that recognizes and binds the pathogen peptide and present it to T cells that triggers the immune response. MHC genes are under strong balancing selection and are considered as the most polymorphic loci in vertebrates. The order Chiroptera is one of the most interesting groups to study immune evolution, as it has been suggested that bats possess a unique and extremely polymorphic immune system due to its role as natural reservoirs of viruses. By performing whole RNA sequencing and *de novo assembly* of liver transcripts in five species of microbats, each one classified into a different family, we made a qualitative analysis of the MHC class I transcripts, responsible for the recognition of virus. We assembled the complete peptide binding region encoded by exon 2 and 3, both exons were under positive selection. A unique insertion of 5 amino acids was detected in some exon 2 sequences among the five species. This insertion may allow the recognition of longer peptides, that along with the maintenance of ancestral MHC-I loci might favor the effectiveness of defense against viruses.

Recovery of Little Brown Myotis (*Myotis lucifugus*) Surviving and Thriving after White-nose Syndrome
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Since 2006, white-nose syndrome (WNS) has caused precipitous declines of some bats in North America. But the effects are not consistent over the area from which WNS has been reported. WNS was first reported in southern Ontario in 2010 and significant mortality observed in 2012. For five years from 2014 to 2018 we monitored a population of *Myotis lucifugus* at a roost in southern Ontario. We observed stable growth, returns of adults and recruitment of subadults into the adult breeding population. We radio-tracked bats to nine other roosts within a 2-km radius and documented variable use of roost types. We characterized fidelity to roosts and movement patterns among roosts. We used passive implanted transmitter tags to quantify the association of individuals to the roost at various life stages through the year. In spring, some bats showed infection by WNS, but these symptoms disappeared later in the summer. This population appears to be doing well and could be a source for recovery. Three other species of bats use the roost as well. The roost functions in several manners including as a migratory stopover area, a maternal roost, a nocturnal resting area between foraging bouts, and possibly as a male swarming area. Three species of *Myotis* used the roost, all in different manners. *Myotis lucifugus* routinely moved among roosts and it appeared as though the presence of a network of roosts was important to this population.

***Kinematic Comparison of the Recovery Maneuvers between Two Bat Species**
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*** Alexander T. Morris** received the **Avinet Award.**

Bats show outstanding agility and control of their flight. Even so, collisions are commonplace, as they often fly in close proximity to one another and must navigate their surroundings through turbulent conditions. They minimize the impact of these collisions through compliant elements in their wing structure and dynamic actuation of many degrees of freedom to quickly recover stable flight. Here, we compare the recovery response of both *Rousettus aegyptiacus* and *Carollia perspicillata.* Previous studies indicate that wing mass moments of inertia scale linearly with body mass. Consequently, we hypothesized that both of our study species would employ similar passive dynamics to respond to and recover from perturbation. To test this, we trained five *R. aegyptiacus* and four *C. perspicillata* to fly through a small window bisecting a corridor (1.5 x 6.0 x 2.0m). On test trials, an air jet scaled to

2.5x each bat's body weight struck one wing after bats passed the window. We analyzed the 3D kinematics using multi-camera recording of 15 landmarks on each bat, and compared responses between species. We found that the perturbation induces less body rotation in *R. aegyptiacus*. These results reject our hypothesis, and indicate that factors other than wing moment of inertia play a role in stabilizing flight. In natural conditions, *R. aegyptiacus* typically fly greater distances in more turbulent conditions than *C. perspicillata*, which may have exerted selective evolutionary forces for highly effective reactions to environmental perturbations. Further research can help reveal the underlying stabilizing mechanisms used by *R. aegyptiacus*.

The Long Stems Characteristic of Bat-pollinated Flowers Greatly Reduce Bat Search Times while Foraging
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Botanists have long noted that flowers adapted to bat pollination tend to be particularly well-exposed, with long stems that position them away from other foliage. The selective advantage of this trait, however, has remained obscure. We captured nectar-feeding bats (*Anoura geoffroyi*) in cloud forests of the Colombian Andes and held them in flight cages to test the effects of floral exposure on foraging behavior. Ten bats were held for 3 days each, and in a series of trials we timed how long it took to locate a flower (of *Burmeistera succulenta*) affixed to one of six poles placed in the cage. Bats were exposed to four treatments: long or short floral stems, in either simple or complex backgrounds. Complex backgrounds included arrays of leaves around each pole, while simple had none. Flowers were randomly shifted after each trial so that bats did not simply learn location. In simple backgrounds, bats showed no difference in search times for long vs. short stems, while in complex backgrounds, bats took nearly twice as long to locate short-stemmed flowers. This suggests that increased flower exposure allows bat echolocation to better distinguish floral echoes from background clutter echoes. This, in turn, would favor the evolution of long stems to ensure that flowers are discovered by bats and thus can successfully reproduce.

Behavioral Responses of Hibernating *Eptesicus fuscus* to Variable Humidity
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During winter, when food is limited and ambient temperature is cold, many mammals hibernate, reducing body temperature and metabolic rate via bouts of torpor. Hibernators spend most of their energy during hibernation on costly arousals from torpor and white-nose syndrome (WNS) exacerbates energetic demand by increasing arousal frequency. Bat species vary in WNS susceptibility and *Eptesicus fuscus* appears resistant, although underlying resistance mechanisms are unknown. Evaporative water loss (EWL) and dehydration can increase arousals in hibernators and WNS also increases EWL, which suggests mechanisms affecting water balance could be involved in WNS resistance. We tested the hypothesis that *E. fuscus* relies on behavioral flexibility to maintain water balance in conditions of varying humidity. We predicted that hibernating bats in a dry environment would drink more frequently during arousals, and exhibit more huddling behavior during torpor, compared to bats in a humid environment. We housed groups of individually marked hibernating *E. fuscus* in one of two temperature- and humidity-controlled incubators set at 8°C and either 98% or ~50% relative humidity (110 days; n = 10 per treatment). Infrared cameras continuously monitored bats from above to quantify arousals and huddle size, and from the side to quantify drinking behavior. As predicted, bats in the dry incubator showed higher drinking frequency during arousals, and remained in a single, more compact huddle during torpor. Our results suggest that behavioral flexibility plays a role in reduced WNS susceptibility for *E. fuscus* and have implications for understanding WNS susceptibility in other bat species.

The Influence of Sensory and Biomechanical Modules on the Evolution of Neotropical Leaf-nosed Bats

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Sensory and mechanical structures share space in the head but have different spatial, geometric and mechanical requirements. We evaluated the co-evolution of mechanical and sensory structures and their association with the explosive radiation of Neotropical Leaf-nosed bats. We sampled all families within the noctilionoid tree (Phyllostomidae, Noctilionidae, Mormoopidae, Furipteridae, and Thyropteridae) and the major dietary niches within Phyllostomidae, for a total sample size of 42 individuals from 35 species. External landmarks were used to capture the shape of five areas of the cranium that reflect structural robusticity and contribute to bite-force performance (the cranial base, external vault, palate, face, and the zygomatic-glenoid region). Internal landmarks were placed on structures that house sensory systems (the olfactory bulb, petrous part of the temporal bone, internal vault, and orbit). We found support for nine separate anatomical modules in all cases: phyllostomids as a group, other noctilionoids as a group, and in each dietary class (frugivores, non-phyllostomid insectivores, phyllostomid generalists, and nectarivores). Each biomechanical and sensory module is unique, and their relative strengths and inter-module correlations are unique within noctilionoids, phyllostomids, and within each dietary class. We found that integration among modules tends to be lower in phyllostomids than other noctilionoids. We also found that the rates of evolution of the modules differed from one other and across dietary classes. While the number of modules is conserved across noctilionoids, the re-organization of biomechanical and sensory modules appears to have played a key role in the evolution of phyllostomid bats.

The Grumpy, Lazy Bat Hypothesis: Does White-nose Syndrome Select for a Behavioral Change in *Myotis lucifugus*?

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Wildlife populations can experience rapid phenotypic evolution if human impacts cause major mortality. White-nose syndrome (WNS), an invasive fungal disease, is devastating North American bat populations in one of the fastest declines ever observed for mammals. Traits favoring WNS survival could, therefore, be under selection in remnant populations. Animal personality traits, like sociability and explorative tendency, can affect pathogen transmission and may affect energy balance, which in turn may influence WNS survival. We tested the hypothesis that WNS selects for reduced activity and sociability in bats because reduced values for these traits reduces energy expenditure and/or risk of pathogen exposure. We conducted this study in central Manitoba, Canada where mortality from WNS was first confirmed in 2017. During the pre-hibernation period (August) in both 2014 (pre-WNS) and 2018 (post-WNS), we captured *Myotis lucifugus* and used Y-maze (n = 90 bats) and hole-board tests (n = 77 bats) to assess sociability, activity, and exploration of individuals. In contrast to our hypothesis, we found that post-WNS bats were more sociable than pre-WNS bats. However, as we predicted, post-WNS bats were less explorative than pre-WNS bats, which may reduce their risk of acquiring the WNS pathogen. While we cannot rule out behavioral plasticity as an explanation for our results, personality traits are repeatable in bats and heritable in other taxa, which suggests these differences could reflect an evolutionary change. Our results have implications for the social evolution of bats and for the design of management strategies that aim to facilitate bat population recoveries.

Winter Activity Patterns of Non-cave Hibernating Tri-colored Bats

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Cave and mine hibernating tri-colored bats (*Perimyotis subflavus*) have experienced precipitous declines from white-nose syndrome (WNS). However, tri-colored bats use tree cavities, bridges, culverts, and foliage during winter throughout parts of their range. Our objective was to determine environmental and biological factors that predict activity patterns of non-cave hibernating tri-colored bats during winter and relate them to WNS susceptibility. From November to March 2017–2019 we used temperature-sensitive transmitters to document activity patterns of tri-colored bats in south-central South Carolina, an area devoid of caves or mines. In addition to three bridge roosts, we tracked individuals to 24 tree roosts. We found that the probability of activity increased with ambient temperature and bats maintained a non-random arousal pattern with a high probability of arousal near dusk throughout winter. One-third of all recorded bat days contained an arousal overlapping nighttime. Of these nighttime arousal events, 71% involved activity away from the roost and 38% resulted in a roost switch. When bats aroused, the probability of activity away from the roost was greater in bridge roosts than tree roosts, increased with body mass, and increased with the previous day's mean vapor pressure deficit. We also found that season best predicted a switch between day roosts, with the greatest probability of switching occurring in early and late winter. Our results suggest non-cave hibernating tri-colored bats assess ambient conditions before arousing and might exploit ideal conditions for foraging opportunities. Therefore, non-cave hibernating tri-colored bats might be less susceptible to WNS than cave and mine populations.

Interspecific Variation in the Heat Tolerance and Evaporative Cooling Capacity of Bats with Differing Roosting Habits

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The majority of physiological research on small mammals has focused on coping with cold. However, given the predictions of climate change models, understanding how small organisms cope with heat is important. Using respirometry in the manner employed for arid zone birds, we estimated heat tolerance and evaporative cooling capacity of insectivorous bats. We predicted that the ability to cope with higher ambient temperatures (T_a) would reflect the nature of roost sites, with species using external roosts (hoary bats) having more tolerance and cooling capacity than bats using cavity roosts (little brown and silver-haired bats). Our data were collected in summer 2018 in Cypress Hills Provincial Park, Saskatchewan, Canada. Gas exchange measurements were conducted the day after capture using open flow-through respirometry at a range of T_as (~30–48°C in 2°C increments). Maximum T_a was reached before bats became hyperthermic ($T_{a,\ HT}$) and was significantly higher in hoary (46.5 ± 2.1°C) compared to little brown bats (44.1 ± 1.6°C). The $T_{a,\ HT}$ of silver-haired bats (45.3 ± 1.5°C) did not significantly differ from the other species. Our findings are consistent with predictions as the species that used exposed roosts had the highest heat tolerance.

Landscape and Microclimatic Drivers of Roost Selection in *Rousettus aegyptiacus* Across Southern Nigeria

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The Egyptian fruit bat (*Rousettus aegyptiacus*) is an obligate cave roosting species in Nigeria. The species is ecologically and economically important in southern Nigeria, where it is threatened by habitat loss (due to agriculture) and intense hunting, where offtakes can reach 4000 bats per hunting effort at a single cave per day. Despite having disjoint distribution due to cave-dependence and limited cave availability, knowledge of roost selection is poorly understood. Cave microclimatic condition, landscape effects, and human disturbance are known to influence roost selection in other cave dwelling bats. Therefore, unraveling the influence of cave microclimate, landscape effects, and human disturbance on bat abundance is critical to understanding roost selection in *R. aegyptiacus*. We assessed bat abundance at cave roosts by conducting emergence counts across localities in southern Nigeria. We measured cave microclimate and dimensions, vegetation structure at cave entrances, and recorded presence of water. Using high-resolution landcover data, we calculated proportion of major land use/landcover types: forest, farmland and bare rock at multiple spatial scales. To understand the drivers of roost selection, we will

model the relationship between *R. aegyptiacus* abundance, and cave microclimatic conditions, surrounding vegetation and landscape factors. The results will aid understanding of roost selection by an intensely hunted obligate cave roosting species in both native habitats and human modified landscape. The results will inform cave prioritization for the species conservation.

Seasonal Changes in Diets of Tropical Bats Revealed by Multi-tissue Stable Isotope Analysis

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Seasonal changes in temperature and precipitation in the tropics drive many biological processes. When food resources become scarce, animals may move to areas with greater resource abundance, reduce metabolic activity (i.e., use torpor), or switch to other available (though perhaps less efficient) resources. Stable isotope analysis of animal tissues can be used to track temporal variation in diet of individuals and/or populations by repetitive sampling of a single tissue type. However, the sampling of multiple tissues with different periods of dietary integration can be used to reconstruct past diets within individuals. In this study we sampled multiple tissues from individuals of Neotropical and Paleotropical bat species representing different trophic guilds and foraging ranges. Examining variation in stable nitrogen isotope ($\delta^{15}N$) values among tissue types allowed us to monitor changes in dietary niche breadth. We found more variance in tissue $\delta^{15}N$ among individuals with larger assumed foraging ranges than those of smaller foraging ranges. Additionally, we found a significant effect of period of capture on the pattern of $\delta^{15}N$ in different tissues across several species. Frugivorous bats had similar patterns of shifts in $\delta^{15}N$ throughout the year, whereas insectivores were more variable. There were no significant differences in isotopic niche breadth inferred from different tissues. Using multi-tissue stable isotope analysis is a beneficial way to assess individual and population level variation in diet and may be a valuable technique as it requires fewer sampling periods than other techniques to assess year-round diet in bats.

European Free-tailed Bats Use Wind Regimes to Fly High and Fast

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Bats use some of the fastest known vertebrate flight speeds and can forage thousands of meters above the ground, but it is unknown how they manage these high-energy behaviors. We tracked the three-dimensional movement of European free-tailed bats (*Tadarida teniotis*) in northeastern Portugal and developed high-resolution wind models to test if bats use the underlying landscape and wind regime to generate high speeds and achieve high flight altitudes. Bats flew at speeds of 5.63 ± 3.66 m/s (maximum 41.24 m/s or 149 km/h) with airspeeds of 4.68 ± 3.79 m/s, (maximum of 37.52 m/s, 135 km/h). Bats largely follow the terrain at 182 ± 206 m above ground level (AGL), but appear to ride uplifting winds to travel hundreds of meters upwards in less than one minute to over 1600 m AGL. Predictive additive models using wind patterns alone are able to predict the location of these high-elevation ascents and explain 91.3% ± 11.1% of the deviance. This suggests that bats exploit the energy in vertical winds generated by the interaction between wind and topographic slope to minimize energetic expenditure, similar to diurnal birds, and likely follow a path of least resistance to high-elevation hunting grounds. Free-tailed bats generate some of the fastest powered flight speeds among vertebrates, forage at exceptional altitudes, and continue to challenge our understanding of flight in the wild.

Too Many Viruses

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Bats are natural reservoirs of a wide variety of viruses, but despite that many of these bat-borne viruses can cause diseases in other mammals, it seems that health and fitness of bats is not reduced or affected by an evident viral disease. These observations had led to the hypothesis that bats might possess a unique and extremely variable immune system, resulting from a co-evolutionary process between bats and viruses. The main objective of this work was to identify which families of viruses are being expressed in the liver of our species. RNA was extracted and sequenced with RNA-seq technology from liver samples of fifteen individuals classified in five distinct families from southern Mexico. Bioinformatics analysis revealed sequences of at least ten virus families of DNA and RNA type, with Flaviviridae, Herpesviridae, and Arenaviridae being the most frequent. Assembled contigs were homologous to functional viral transcripts or protein sequences, which are essential for retrovirus replication, suggesting that these viruses were replicating in the species at the moment of capture. Our results suggest that at least two species of bats have been under chronic liver inflammation produced by Hepatitis-C like virus, increasing the risk for developing liver cancer.

On the Diversification of Afrotropical Bats

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The radiations of Afrotropical bats remain poorly known, obscured by grossly inadequate genetic and geographic sampling. Our recent efforts to resolve these shortcomings with fairly dense sampling at least in Eastern and Southern Africa have resulted in preliminary phylogenetic and phylogeographic analyses of *Rhinolophus* (Rhinolophidae), *Hipposideros, Doryrhina,* and *Macronycteris* (Hipposideridae), *Nycteris* (Nycteridae), *Otomops* (Molossidae), *Miniopterus* (Miniopteridae), and *Scotophilus* and *Myotis* (Vespertilionidae). Each has included 'species delimitation' analyses to identify evolutionarily independent lineages using multiple independent loci (4–6 nuclear introns) and a range of priors with BPP. Our studies offer clarity on the phylogenetic positions of Afrotropical clades within genera that are distributed across the Paleotropics and beyond. Most genera show evidence of endemic radiations, deep divergences and cryptic, apparently unnamed clades. Recurring patterns of phylogeographic breaks help to identify geomorphic features that promoted historical disjunctions. Yet reliably naming the evolutionarily distinct lineages we have identified will require extensive integrative taxonomic efforts to identify congruent patterns in the differentiation of external, cranial, dental, and bacular morphologies, as well as documenting their vocalizations and ectoparasites. A profusion of 19th and early 20th names (sometimes based on fragmentary or poorly described material and many now considered synonyms) must each be evaluated before the cryptic lineages can be given dependable binomials. A recent appraisal that Africa is home to only 221 species of bats may underestimate its true diversity by 50%.

Winter Ecophysiology of North American Desert Southwest Bats

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To help predict potential impacts of white-nose syndrome (WNS) on currently unaffected populations, we launched a study focusing on the hibernation ecology and physiology of desert-adapted bats in Arizona. Our specific objectives are to: 1) describe the presence and abundance of various bat species in AZ hibernacula using visual inspection and photographic documentation, 2) describe the use of shallow and prolonged deep torpor using temperature transmitters, 3) determine total length of hibernation in a given winter using passive acoustic monitoring, 4) measure relative amount of winter energy expenditure (as decline in whole-body fat content) using an EchoMRI unit, and 5) describe winter activities outside of hibernacula that may be related to foraging behaviors, also using passive acoustic monitoring. In winter 2018/19, we completed multiple visual inspections with

photographic documentation of bats across three sites, attached temperature-sensitive transmitters to two individuals from two species (*Corynorhinus townsendii* and *Eptesicus fuscus*), collected acoustic data at the three sites from October through April, and estimated pre-hibernatory fat content in 15 individuals of 6 species and post-hibernatory fat content in 12 individuals of 4 species. Very small hibernating populations (maximum $n = 24$) and only solitarily roosting individuals were observed, with a single exception to the latter. Results from the first year of this study will be discussed, as well as methodological modifications we will implement during winter 2019/20.

Changes in Summer Bat Activity Following the Invasion of White-nose Syndrome in Nova Scotia
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Millions of bats in North American have been reported dead at overwintering sites as a result of a fungus, *Pseudogymnoascus destructans*, that causes white-nose syndrome (WNS). In Nova Scotia, Canada, the fungus was first detected in 2011 and resulted in an average decline of 93% at five hibernacula during 2012–2013. The impact of the disease away from hibernacula is not well-known and is an important link to understand how winter mortalities affect summer population activity and abundance. We compared acoustic data from the summers of 2005–2006 to resampling in 2018–2019 at the same habitats and sites. We predicted a dramatic decline in bat activity for non-migratory species and no significant change in migratory species activity. Acoustic monitoring was conducted along 88 forested rivers in southwest Nova Scotia covering an area of ~22,000 km^2. Each site was monitored for six nights between 2005–2006 and resurveyed during 2018–2019. We recorded >1,000 detector nights to compare changes in magnitude of bat and species activity from pre- to post-invasion of the fungus. Our results will be used to assess if the change in summer activity levels reflects the WNS-related decline observed at hibernacula to inform recovery potential of WNS-affected species.

Molecular Adaptations Underpin Dietary Diversification and Specialization in Neotropical Leaf-nosed Bats
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The molecular adaptations underpinning dietary specializations are poorly understood. Among mammals, the bat family Phyllostomidae (New World leaf-nosed bats) has undergone extreme diversification linked to diet, with different lineages specializing on fruit, nectar, insects, and blood. To determine whether these evolutionary transitions have involved molecular adaptation in different sets of loci and pathways underpinning metabolism and morphology, we performed genome-scale screens across 66 bat species. We find that genes under selection in branch leading to the ancestral phyllostomid encode proteins with diverse roles in carbohydrate, protein and lipid metabolism, consistent with adaptation for a generalized diet. At the same time, we detect surprisingly little subsequent selection in the branch leading to frugivores, but a second burst of molecular adaptation for carbohydrate metabolism in the nectar-feeding bats. Vampire bats, on the other hand, show strong selection for the excretion of waste products. Our findings open up new opportunities for studies of metabolism in bats and other mammals.

Predicting Foraging Strategies from Morphological Traits in *Myotis*
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The genus *Myotis* is found on every continent except Antarctica and comprises three primary ecomorphs with different foraging strategies (i.e., aerial hawking, gleaning, and trawling for aquatic prey). Despite striking morphological similarities within ecomorphs, recent molecular phylogenies have shown that these groups are not monophyletic. In this study, we investigated which morphological traits of *Myotis* bats show convergent evolution across lineages, and used morphological trait data to attempt to predict foraging strategies. We evaluated 15 traits hypothesized to be of significance for predicting foraging strategies in an analysis of over 300 specimens representing 54 species from 6 continents. No phylogenetic signal was found for any of the traits, with each trait displaying a low K value and lacking statistical significance, suggesting that similarities among different species in these traits is due to convergence rather than shared ancestry. Convergence analyses using the L1OU package revealed significant changes in the mean values for each trait at particular nodes of our tree, and detected a lower

number of regimes than shifts for each trait, which together are indicative of convergent evolution. A machine-learning analysis to predict feeding type resulted in an accuracy rate equal to or greater than 75%. The three most important traits for prediction of foraging strategy are ear length, tibia length, and foot length. Ear length may play a role in ability of bats to hear prey-generated sounds, and tibia and foot length may play a role in prey capture using the uropatagium and feet.

Establishing Provincial-scale Bat Monitoring in British Columbia in Advance of White-nose Syndrome
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White-nose syndrome has not yet been detected in British Columbia (BC), but it's devastating effects may be imminent. Wildlife Conservation Society Canada is aiding in disease surveillance, mitigation, and future recovery efforts in BC through two parallel projects: North American Bat Monitoring Program (NABat) and BatCaver. In collaboration with the BC government, we have catalogued baseline bat diversity and relative abundance in 51 grid cells. A network of trained biologists deployed two to four stationary acoustic recorders and conduct two driving transects in designated 10 x10 km grid cells between late May and early July each year. As of summer 2019, we have collected four years of baseline data, expanding the NABat sampling effort each year. Using paired data collected by stationary acoustic recorders and driving transects, we compare the effectiveness of both methods at estimating species distributions. Additionally, we examine whether a strategically collected passive dataset analyzed using an activity index metric can estimate relative abundance with lower variance than the driving transect method. Through our BatCaver program, cavers have also identified and described winter hibernation sites in Western Canada. Capitalizing on caver expertise and geographic knowledge since 2013, we have collected reports of bat sign in over 175 caves and mines, and deployed acoustic recorders paired with environmental dataloggers in known and suspected hibernation sites. We have identified microhabitat features and cave/mine characteristics that are most associated with the caves and mines used as hibernacula in Western Canada.

Female Vampire Bats Vary in their Cooperativeness towards Strangers
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Although cooperation is common across animals, plants, and fungi, individual differences in cooperativeness can make it difficult to predict if and to what extent two individuals might cooperate. Female vampire bats form stable, cooperative food-sharing relationships with both kin and non-kin, and these relationships develop at different rates due to individual variation in co-roosting and allogrooming behavior. Although it appears that some individuals may be more likely to cooperate than others, the cause of this remains largely unknown. To address this problem, we rigorously tested whether there is consistent inter-individual variation in cooperativeness among female vampire bats. We first measured individual rates of allogrooming and food-sharing using video footage of 70 female vampire bats captured from three different populations and tested in captivity. However, because cooperation depends on the identity of both the actor and receiver, we also determined individual variation in rates of allogrooming and food-sharing towards strangers that were introduced through forced association (n = 56). To test factors which might explain why bats differ in their propensity to cooperate, we measured kinship, age and/or age category, and urinary oxytocin, a hormone commonly associated with affiliative social behavior. We detected individuality in cooperativeness, and foresee that our findings will shed further light on the importance of individual variation in the evolution of cooperation. This work lays the foundation for future research that seeks to comprehensively quantify the causes of individuality in cooperativeness.

The National Response to White-nose Syndrome in 2019
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White-nose syndrome (WNS) has been a fixture in research and conservation efforts for North American bats since its discovery in 2007. The causative fungus, *Pseudogymnoascus destructans,* is now present in at least 37 states and 7 provinces in North America, where at least 12 species have been confirmed with the disease and 8 others

identified bearing *P. destructans* without disease. Framed by sister national plans in the United States and Canada, the community of scientists and stakeholders have propelled comprehensive preparation and response actions to address research and management needs for WNS. The U.S. Fish and Wildlife Service is the lead federal agency coordinating the response in the United States, and from 2008 to 2018 the agency has provided $34 million to researchers, conservation organizations, and state and federal agencies to address WNS. Our investigation of this disease is advancing our understanding of the life history and ecology of cave microbes, the dynamics of fungal infection and transmission, and bat hibernation physiology and ecology as we search for ways to control *P. destructans* and conserve native bats. In 2019, the Service offered funding opportunities for state-initiated management actions, priority research needs, development of treatments for WNS, and innovative ideas to reduce the impacts of WNS. The working groups of the WNS National Plan continue to advance national efforts including guidance for disease surveillance and diagnostics, decision frameworks for management, resources for monitoring bat populations, and outreach materials in support of national priorities.

Working Towards Reliable Range-wide Status and Trend Analyses using NABat Monitoring Data
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North American bats face unprecedented risks from continuing and emerging threats including white-nose syndrome, wind energy development, and habitat loss. Based on local monitoring efforts, many species of bats are thought to be experiencing unparalleled population declines. However, local observations at known roosting sites or high-quality habitat may not be indicative of species status and trends across larger spatial extents (e.g., across the entire range of a species). The North American Bat Monitoring Program (NABat) aims to provide reliable information on the status (e.g., distribution, activity, local abundance) and trends (changes in these measures) of all 47 species of bats shared by the United States, Canada, and Mexico. NABat seeks to improve the state of conservation science for bats by providing standardized protocols and facilitating cross-boundary agency coordination and sharing of limited resources. NABat will provide managers and policy makers with information they need to effectively manage bats, detect early warning signs of population declines, assess species vulnerability to potential threats, and measure recovery. Since implementation in 2015, acoustic and colony count data have now been collected in more than 40 states and 10 Canadian provinces. Some of these data are already being used to determine species distributions and population trends. I will present on the current state of the NABat program including efforts to compile acoustic and colony count monitoring data. I will highlight both ongoing and completed analyses and discuss how NABat plans to share this information with the broader scientific and conservation communities.

Acoustic Bat Survey of Santa Rosa Island
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The Channel Islands National Park encompasses five islands. Santa Rosa Island is the second largest of all the islands. It contains over 53,000 acres of sandy beaches, open grasslands, steep canyons, and is home to a variety of species that are endemic to the island. After 154 years of ranching and sport hunting, Santa Rosa Island is in the process of returning to wilderness. Because bats are an indicator species of ecosystem health, an understanding of how the island's bat populations change over time will shed light on the island's recovery. The island's rugged environment limits what people know about the bat populations. Currently, the *Myotis californicus* is the only species that has been physically vouchered on the island, though mammalogists expect up to eight species to inhabit the island. We describe the start of a long-term effort to use active detectors to find foraging bats, placing passive detectors strategically in foraging areas, and using machine learning to identify the species of bats our detectors record.

Paleogeographical Analysis of the Chiropteran Fossil Record
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Bats (Chiroptera) seem to have originated shortly after the Cretaceous-Paleogene boundary, as time-calibrated molecular and genomic phylogenies indicate (Teeling et al., 2005). They are known to have radiated fast during the early Eocene (Simmons, 2005) and today bats have reached a nearly global distribution being represented by more

than 1400 species. Paleogeographic patterns and timing of these distributions have been difficult to determine, due to the chronological gaps in the fossil record. In this study we compared the fossil record of bats, based upon three different sources. By using this database approach, we analyzed distributional patterns of all 18 families of bats by using state of the art GIS models, based on their fossil records. This study resulted in developing family level speciation and extinction frameworks from the first occurrence in the Paleocene to the Late Pleistocene.

Miniaturized Proximity Sensors Reveal Evidence for Maternal Guidance in Common Noctule Bats

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How do naïve juvenile bats learn where to roost and where to forage? The use of social information from informed adults is an often-discussed mechanism for the acquisition of knowledge on the whereabouts of such crucial resources during the early life of a bat. The maternity colonies of bats of the temperate zones where females communally rear their young create ideal conditions to answer this frequently asked question. However, studying social information transfer in wild bats is difficult with traditional tracking techniques due to the small body size of most species. We developed a novel 'next-generation' proximity sensor system (BATS) with animal-borne tags small enough to study medium sized bats and their offspring. By tracking the associations of juvenile-adult pairs, we found evidence for maternal guidance during switching roosts but not during foraging. The guided roost-switching behavior provides evidence for a form of maternal care that has long been assumed, but never documented. Brief and infrequent meetings of juveniles with other tagged bats during foraging were best explained by local enhancement. We did not find any evidence that mothers guide their young to foraging sites. Our study shows how recent technological advances in biologging provide researchers with means to answer longstanding questions in behavioral biology.

Torpor-assisted Migration: What's Good for the Lasiurine is Good for the Myotid

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Many animals undergo seasonal migrations, both long and short. Several temperate zone bats are either long distance or regional migrants, but both must contend with fuel acquisition and conservation for this energy-demanding endeavor. Recently it was found that long distance migrating silver-haired bats use torpor-assisted migration. To determine if the regional migrant Indiana bat also engages in this behavior, we used temperature sensitive radio transmitters to track female spring migrating individuals from hibernacula toward summer grounds and collected ambient temperature (T_a). We created an algorithm to determine when bats were in torpor, warming, normothermic, or cooling. We then used decision tree analysis to predict physiological state based on T_a and diel condition. T_a was significantly warmer when bats were normothermic than when they were in torpor or when they were cooling, but there was no significant difference between any other bat temperature (T_{sk}) and T_a combinations. The nighttime T_a threshold for physiological state was 9.8°C: there was an 87.7% chance bats were in torpor below this temperature. The daytime T_a threshold was 23°C: there was a 96.3% chance bats were in torpor below this temperature. We concluded that Indiana bats used torpor-assisted migration. During conducive weather, bats entered torpor during the day to conserve fuel, foraged before migrating, traveled and foraged throughout the night, and foraged before roosting. In inclement weather, bats warmed but did not emerge and then returned to torpor. Understanding how weather affects migrating bats can provide information about when bats are active on the springtime landscape.

Remarkable Variation in the Diet of *Noctilio leporinus* in Puerto Rico: The Fishing Bat Turns Carnivorous

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The bat *Noctilio leporinus* is common throughout the West Indies, where it is known to feed on fish and insects. Anecdotal observations in Cuba suggest that this bat could prey on other species of bats, at least when they are kept together in captivity. We set out to examine the diet of this species at three caves along the northwestern part of

Puerto Rico, namely: Amador Cave in Camuy, and Ventana and Matos Caves in Arecibo. Six guano traps were set under roosting sites of *N. leporinus* once a month. Traps were left overnight and fecal remains recovered were examined in the laboratory under a dissecting microscope. Our results indicate that, in addition to insects and fish, *N. leporinus* in northwestern Puerto Rico is preying on other species of bats. Three species of bats have been recovered under the roosts of *Noctilio*. It appears that this behavior is more common during the breeding season of fruit-eating bats, when *Noctilio* seems to prey opportunistically on the young of these other species.

Hurricane Mediated Extirpation of Bats from the West Indies

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Small islands within the Antillean arch are likely to represent an open system, where reinvasion may be the key ingredient to resilience of its bat fauna. We set out to do a long-term survey of Culebra Island. Culebra remains as the least studied island within the Puerto Rican bank, which in addition includes Vieques, St. Thomas, St. John, Virgin Gorda, Tortola, and Anegada. Three species of bats have been reported from Culebra. We monitored bat activity, both acoustically and with mist nets, over a total of 20 nights from February 2018 through August 2019. Our results suggest that the only species of bats remaining after hurricanes Irma and María that hit the Island in 2017 are *Noctilio leporinus* and *Molossus molossus*. The fruit-eating bat, *Artibeus jamaicensis*, appears to be extirpated from the Island, or its population is so greatly reduced that we could not find any evidence of its presence. Most of the fatalities caused by hurricanes among frugivorous bats on the Greater Antilles is due to starvation after the event, since typically caves provide adequate refuge during the hurricane. By and large, the Virgin Islands lack these refuges, a fact that combined with their smaller size may contribute to the periodic extirpation of local populations of bats. As the frequency and intensity of hurricanes increases, this could pose an important factor determining which species survive on these islands.

Urban Tree Roost Use by Evening Bats in Texas

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Bats spend a majority of time roosting and do so in various natural and anthropogenic structures. Our objective was to determine roost selection of evening bats (*Nycticeius humeralis*) on the Gulf Coast of Texas, a widely distributed species on the southern edge of its range. From June to July 2018 and 2019 we mist-netted and radio-tracked bats in a protected bottomland hardwood tract located near an urban area. We then compared roost trees with assumed non-occupied trees in the bottomland tract. Seven bats were tracked to five different tree roosts, all within a <1-km^2 area of an urban neighborhood. Colony size ranged from approximately 16 to 500+ bats. Bats selected for taller, larger live oak trees (*Quercus virginiana*; height: 27–31 m; dbh: 108–201 cm) with less surrounding canopy cover and understory vegetation (all $p < 0.0001$). Bats were utilizing protected areas for foraging yet roosting in urban neighborhoods. All bats stayed in roosts for the full life of the transmitter (5–21 days) and no roost switching occurred. The preservation of large trees in urban areas has created bat roosts and allowed a population of evening bats to thrive. These findings may help guide management to prevent decline of common bat species. Roosts could continue to be located and documented by the public with minimal training and lead to long-term monitoring of bat roosts, year-round, through citizen science. Park managers should aim to create more roosts by allowing the growth of large trees, while keeping understory clutter at a minimum.

Is Reduced Thermal Sensitivity in Distal Wing Muscles a Functional Adaptation to Bats' Unique Wing Morphology?

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Bat wings contain muscles whose fast, coordinated contractions are integral to the flight stroke. Muscle cooling slows contractile rates, however, and flight exposes bats to substantial convective and radiative heat losses. Since bat wings are poorly thermally insulated, a temperature gradient exists from the proximal core (warm) to the distal periphery (cool). During flights at ~22ºC, in *Carollia perspicillata* the distal extensor carpi radialis longus muscle (ECRL) operates at ~12ºC below core body temperature (T_b) while the proximal pectoralis muscle operates near T_b.

The ECRL is also less temperature sensitive than the pectoralis, i.e., it experiences a proportionately smaller decline in contractile rates after a given drop in temperature. This finding raises an important question: Is this high-to-low gradient in temperature sensitivity from proximal-to-distal in the bat wing a functional adaptation to the wing's local thermal environment, or the climate in which the bats live? To address this, we measured contractile rates in the ECRL and pectoralis muscles of *C. perspicillata* and *Eptesicus fuscus*, and in the ECRL muscle of *Tadarida brasiliensis* at a range of experimental temperatures (22–42ºC) to determine if muscle temperature sensitivity varies interspecifically. There was little difference in the thermal sensitivities of the ECRL or pectoralis muscles between species; however, the ECRL was less temperature sensitive than the pectoralis. These results suggest that the low temperature sensitivity of the ECRL muscle in bats may be due to local thermal challenges rather than as an adaptation to largescale environmental conditions.

Using Long-term Citizen Science Data to Assess Trends in Bat Populations in Northwest Ohio

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Citizen science efficiently gathers data and increases public knowledge of and interest in research, especially for unpopular species such as bats. We developed a citizen scientist program in 2011 to annually acoustically sample bats in three parks in the Oak Openings Region of northwestern Ohio, which is a major biodiversity hotspot and critical habitat for eight bat species. Volunteers walked trails in Oak Openings Preserve, Wildwood, and Secor parks. Each park was surveyed once a month from June to August. We found differences in bat activity and species richness across locations, species, and survey years. Oak Openings Preserve is the largest park with the widest range of habitats surrounded by agriculture and rural development and had the highest average bat activity (268 calls). Wildwood had the highest species richness as a result of having extensive forest cover and serving as a refuge for adjacent urban areas. Species richness decreased in Oak Openings Preserve and Secor between 2011 and 2018 (respectively from 8 to 7 and from 8 to 6), coinciding with the establishment of white-nose syndrome (WNS) in Ohio, with richness in Wildwood remaining steady. The total number of calls went down in all parks in the 2011 to 2018 period, suggesting an overall decline in bat activity over time, attributable to a combination of habitat impacts and WNS. Citizen science is a valuable tool for studying temporal trends, identifying favorable habitats, and creating a long-term data set for conservation of these vulnerable taxa.

Changes in Underground Roosting Patterns to Optimize Energy Conservation in Hibernating Bats

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Non-migratory bats in colder climates use hibernation to survive winter. By reducing metabolic rate (i.e., using torpor), bats can survive winter on stored fat reserves. During hibernation, bats arouse from torpor and may move within the hibernaculum, a process called "internal migration". We hypothesized that internal migration occurs to optimize hibernation energetics, in that bats move to select a microclimate to minimize energy expenditure both by moving to cooler areas of the hibernacula and avoiding areas with large fluctuations in temperature. By measuring the distance each tagged bat was roosting relative to the entrance of the mine as well as the temperature at 5 intervals along the mine shaft, we were able to assess the relationship between the two variables. Early in the hibernation season we observed that 62% of bats were roosting in the warmer, less energy efficient, deepest 50% of an abandoned mine hibernaculum. Late in the season there was a shift towards the cooler entrance area, thereby decreasing energy demands during the torpid period, with 78% of bats in the mine roosting within 50 m of the entrance. Although there was no significant effect of hibernation period (i.e., early vs late winter) on the number of bats in huddles, the largest huddles occurred close to the entrance at the end of hibernation season. To fully understand and manage bat populations it is important to understand that hibernation is a dynamic process with bats moving and interacting with one-another throughout the season.

White and Clear Wings in Bats

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White and clear wings are distinct features in about 30 species of tropical insectivorous bats (Mammalia: Chiroptera) belonging to three families (Emballonuridae, Molossidae and Vespertilionidae). Such wings may provide camouflage against the sky at dusk and dawn, when bats commute to and from the roost and are vulnerable to aerial predation from birds. We tested this hypothesis by comparing the contrast of black, white and transparent plastic models against the evening sky. Whitish wings indeed reduce the contrast compared to normally dark wings. They may also prevent overheating and therefore facilitate earlier evening emergence, thereby increasing the availability of crepuscular or diurnal insects for food. Whitish wings become maladaptive near artificial lights, where they are highly visible when illuminated against the dark sky. Pale but colored (not whitish) wings and reticulated patterns on translucent wings in some African and south Asian bats may be variations on the same theme, functional as camouflage against a lit background of vegetation and shades.

Using DNA Barcoding to Determine Community Structure of Bat Ectoparasites in Atlantic Canada

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Bats can be parasitized by a variety of ectoparasites, including mites, fleas, and flies. These ectoparasites may be a health concern for the bats as they may adversely affect body condition and therefore have fitness consequences. Many bat ectoparasites are host specific or limited to a group of closely related bat species while others such as *Cimex adjunctus,* the eastern bat bug, are generalist parasites. More research is needed to determine the diversity and number of ectoparasite species in North America and the hosts and ranges they inhabit. Ectoparasite diversity and community structure likely varies between bat species based on roosting strategies of the bats and parasite diet. Previously collected ectoparasites from throughout Atlantic Canada were identified using morphological characteristics and DNA barcoding for the mitochondrial COI gene. Specimens with a variety of collection dates going back 16 years were sent for sequencing at the Canadian Centre for DNA Barcoding. Specimens had a sequencing success rate of 85% with 60% of specimens receiving barcode status and were assigned barcode index numbers (BINs). The specimens were assigned to five operational taxonomic units (OTUs), one per morphological identified species except for *Macronyssus crosbyi* specimens, which were assigned to two OTUs. Nine haplotypes were identified for the 48 specimens of *Spinturnix americanus* and three haplotypes were identified for the four specimens of *Macronyssus crosbyi.* DNA barcoding is an effective method for confirming morphological species identifications for bat ectoparasites and for determining geographic population structure and divergence within species.

An Updated Synthesis on the Effectiveness of Operational Minimization to Reduce Bat Fatality at Wind Turbines

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Wind turbines are known to cause bat fatality, with estimates in the hundreds of thousands each year. Therefore, strategies designed to reduce or prevent fatality are important to avoid population level impacts to bat species. Operational minimization, also known as curtailment, has been scientifically proven to reduce bat fatalities at wind turbines. Specific curtailment techniques vary, but all seek to minimize bat mortality by limiting turbine blade rotation during periods of high bat fatality risk (e.g., low wind speeds). We plan to summarize publicly available curtailment studies to determine the overall effectiveness of operational minimization. In addition, we anticipate providing results based on specific curtailment strategies (e.g., wind cut-in speed) and efficacy by species. Summarizing the efficacy of curtailment strategies in a variety of circumstances will allow stakeholders to make more informed decisions on the most cost-effective approach to minimize the impact of wind energy on bats. This process will also help identify knowledge gaps and research opportunities to refine curtailment strategies. Furthermore, this synthesis will allow future work to compare curtailment to other minimization strategies, such as deterrents. A better understanding of the efficacy of fatality minimization techniques will allow conservation actions

to address specific project conditions, thereby maximizing energy production while minimizing the impact of wind energy on bats.

Personality Variation between Ground-roosting *Myotis leibii* and Raised-roosting *Myotis lucifugus*
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Behaviors that are repeatable across circumstances and time determine an individual animal's personality. Personality and behavioral variation are subject to selective pressures, including risks related to the use of different habitat types. We explored the ecological and evolutionary consequences of habitat selection by comparing the behavior of *Myotis leibii* and *Myotis lucifugus*, two closely related North American bats that display different ecological traits. *M. leibii* often roost in crevices on the ground, while *M. lucifugus* roost in crevices or cavities that are raised off the ground. We hypothesize that ground-roosting bats experience greater variety and risk of contact with potential predators. We predict that this behavior favors bolder personality and more exploratory and active traits, compared to raised-roosting bats. We examined inter- and intra-specific variation in behavior using a modified, 3-dimensional open-field test and quantified the frequency and duration of behaviors such as flying, landing, and crawling. Bats were continuously video-recorded in 1-hour nocturnal and diurnal trials. We created *a priori* mixed models using combinations of individual characteristics and life history traits to select the models that best describe each species. We found that *M. leibii* (n = 18) displayed more exploratory and bolder behaviors on the ground than *M. lucifugus* (n = 29), as well as higher overall activity during the trial. We also found that *M. leibii* displayed crawling behaviors and movements consistent with foraging while on the ground, which is remarkable for a Vespertilionid species. Future research should explore biomechanical adaptations associated with ground-foraging in *M. leibii*.

Bat Biogeography of Saint Kitts and Nevis
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Trade routes through the West Indies transformed St. Kitts into a sugar monoculture with a montane forest core. Since the decline of the sugar cane economy, which officially ended in 2005, the island has been transitioning to a tourist economy and much of the fallow sugar cane land is being converted to agriculture for local use. The tourist industry has increased the amount of infrastructure around the island, changing the landscape, anthropogenic noise, and light pollution on parts of the island. Given this massive land-use change, bat populations and habitat occupation are in flux. However, because Nevis did not rely on a sugar cane economy, yet shares strong biogeographical similarity with St. Kitts in all other ways, we expect the comparison between the two islands to reveal valuable information about land-use patterns and their effect on bat ecology. The last published mammal survey from St. Kitts dates to 2005, which corresponds with the official end of the sugar cane era. Our in-depth resurvey compares inevitable changes in the distribution of bats across these islands over the last fourteen years. We measured bat diversity and abundance using mist netting and roost surveys. The first acoustic monitoring on these islands was recorded and analyzed using an Eco Meter Touch 2 Pro and Kaleidoscope Pro software to provide additional species composition and abundance data. We compared our data with the 2005 data set in order to assess changes to population sizes and roost sites in relation to topographical and anthropological variables.

Seasonal Differences in Nocturnal Habitat Use by Northern Yellow Bats in Coastal South Carolina
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The southeastern Coastal Plain is projected to have one of the largest urban expansions in the United States. This region also marks the northeastern extent of the understudied northern yellow bat's range. The objective of this study was to understand seasonal differences in habitat use of this species to inform conservation and management. During February–March 2018 we placed Anabat Express acoustic detectors at 36 sites for 6–10 nights in Beaufort County, South Carolina. During May–August 2018 we placed detectors at the same and additional sites for a total of 64 sites. We placed detectors in upland forests, bottomland forests, fields, saltmarsh, and ponds, and characterized

habitat and forest structure within the surrounding 0.05 ha area. Additionally, we measured distance to saltmarsh, freshwater ponds, and residential areas. We developed *a priori* models based on forest structure and landscape covariates and used occupancy modeling to determine factors affecting habitat use in summer and winter. The top model for summer was forest structure, with higher probability of use at non-forested sites. The top model for winter was landscape resources, with higher probability of use closer to residential areas and farther from saltmarsh. Our results indicate that non-forested areas such as saltmarsh, fields, and ponds are important to this species in the summer when forests are cluttered. Alternatively, in winter when food resources may be scarce in some areas, landscape habitat may be a more important driver of use. These results will assist in development of management plans that account for changing habitat use throughout seasons.

Using NABat to Determine Factors Affecting Overall Bat Activity at Various Spatial Scales throughout South Carolina

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With many bats rapidly declining throughout the United States, there is a need to monitor bat populations and their response to land use change. Using the North American Bat Monitoring Program (NABat) guidelines, our goal was to monitor bat activity in South Carolina to aid in management decisions for bat conservation. During the summer of 2019 (15 May to 17 July), we conducted stationary and mobile surveys in 38 100-km^2 cells that were selected using the NABat sampling design for South Carolina. We conducted only stationary surveys in eight cells, only mobile surveys in 13 cells, and stationary and mobile surveys in 17 cells. We surveyed each mobile route on two nights during the designated survey week and set out stationary detectors for four consecutive nights during their designated survey weeks. We examined whether overall average activity varied by physiographic region and white-nose syndrome (WNS) presence and whether activity was related to forest structure. We expected overall activity in the Blue Ridge region to be lower than the other regions and expected activity at WNS confirmed sites to be lower than WNS negative or suspect areas. Also, we predicted average activity to be negatively related to basal area and tree density. However, overall activity did not differ by region nor by WNS presence ($p > 0.05$) and was not correlated with basal area or density. Physiographic region, WNS presence, and forest structure did not appear to significantly influence average bat activity in South Carolina during the summer of 2019.

Diphallia in *Corynorhinus townsendii*

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We describe the first reported case of diphallia in a bat, *Corynorhinus townsendii*, captured during fall swarming at a hibernaculum in northern Utah, USA. Upon examination, we determined that one phallus was functional, as evidenced by production of urine, while the secondary phallus appeared to be overgrown with skin. A review of the medical literature relevant to diphallia suggests that this is a case of pseudodiphallia with a bifid shaft. We hypothesize that this morphological deformity likely has a low impact on the survival of this individual but may act as a physical barrier to copulation. To our knowledge, this is the first reported case of diphallia in bats. This case appears to be that of an unusual member of the species *C. townsendii* that has undergone abnormal sexual development and grew an additional, physically distinct pene. While deformities such as those described are quite rare and could be difficult to observe from small mammals, we encourage other researchers to closely examine the genitals of captured animals to establish the frequency of such deformities in natural systems.

Recovery Plan for Québec's Non-migratory Bat Species: Main Objectives and Ongoing Actions

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White-nose syndrome arrived in the Québec province in 2010 infecting many cave-dwelling bat populations. Since then, it has spread in most areas of the province and important declines in populations of *Myotis* bats species has

been shown by inventories conducted in the province. In response to that, the province has implemented in 2014, in accordance with provincial regulations on endangered species, a bat recovery team. This team is composed of wildlife professionals from regional, provincial and federal ministries, or from local conservation organizations and consulting firms. In May 2019, the team published the Recovery Plan for Québec's Non-migratory Bat Species, which has as a long-term goal to ensure conditions for populations that are self-sufficient, ecologically functional, and mainly spread-out throughout the current air of distribution. To reach this goal, four objectives have been set concerning educating citizens, following the evolution of populations, developing and applying protection or mitigation measures, and knowledge acquisition. A recovery strategy containing thirteen measures and thirty-five actions is proposed. Some actions are already under implementation: education of bat extermination firms, emergence counts using bat watch, mining and wind farm mitigation measures, passively heated bat houses, monitoring bat activity using pit tagging, and habitat selection using Motus technology. Although most of these projects are on the way, preliminary results, success, and issues will be discussed. Involvement of the Québec bat recovery team has sparked, since its establishment, a lot of action and engagement. We believe these are good news to share!

Bats of the World: A New Taxonomic and Geographic Database

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The last comprehensive list of chiropteran species published in Mammal Species of the World in 2005 recognized 1,116 bat species. Although this represented a significant increase over previous tallies, known bat species diversity has continued to climb since that time, with ~1,400 valid species now recognized. Similarly, our understanding of the geographic ranges of many species has continued to change with new revisions and inventories. Researchers in diverse fields ranging from evolutionary biology to ecology and conservation need access to up-to-date information on bat species diversity, taxonomy, and geographic ranges to inform research and management decisions. Although definitive published volumes are desirable for many reasons, the modern digital age provides an alternative: a citable online database. With ongoing input from the Global Bat Taxonomy Working Group of the IUCN Bat Specialist Group, we have accordingly launched a new database at www.batnames.org that provides basic information on every valid bat species currently recognized. Long entries are available for many species and include name, authority, citation, common name, synonyms, type locality, distribution, map, threat status, comments, and references. Short entries (including name, authority, citation, and common name) are provided for taxa that we have not yet fully finished revising and updating. We hope to upgrade all of the short entries to long entries over the next year. Once all the original entries have been revised, the website will be updated biannually (April and October).

Body Mass of Pregnant *Eptesicus fuscus* is Diverging with Long-term Exposure to *Pseudogymnoascus destructans*

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Populations of several North American temperate bat species have experienced well-documented declines resulting from exposure to *Pseudogymnoascus destructans* (*Pd*), which causes white-nose syndrome. Effects on less susceptible species are not as well documented, but these bats could see cumulative damaging effects from annual *Pd* exposure, such as females with fewer energy stores to invest in reproduction. To examine if energy stores of persisting, less susceptible female bats is decreasing, we collected summer capture data of *Eptesicus fuscus* from New York and Indiana between 1994 and 2018. We used a linear mixed effects model to evaluate female mass as a function of year and site to quantify changes to body mass over time. We found no change in average mass across adult female captures between 1994 and 2018 ($p = 0.13$). Residuals were subject to an interaction between the number of years exposed to *Pd* and reproductive status (i.e., pregnant, lactating, post-lactating, and nonreproductive). *E. fuscus* mass diverged from the mean ($p < 0.001$), suggesting a growing variation in adult female energy stores with greater *Pd* exposure time. This was driven by increased variation in pregnant female mass ($p = 0.009$). Chronic *Pd* exposure on less susceptible species could have population level impacts due to the increased variation in pregnant female energy stores. Further investigation within the variation of these data, such as time and relative location of capture, is warranted to reveal the source of this striking variation.

Effects of Hurricane Maria on the Bat Community on the Caribbean Island of Dominica
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In the tropics, hurricanes are an occasional disturbance that can have severe impacts on the structure and composition of biotic communities. As climate change is predicted to increase the frequency and intensity of these storms, it is important to advance our understanding of species' responses to this disturbance to help us predict future impacts, and aid in conservation actions. In September 2017, Hurricane Maria, a category 5 storm, struck the small island (750 km^2) of Dominica, causing substantial damage to the vegetation across the island. This provided a unique opportunity to assess the hurricane's impact on bat community structure and composition in the Caribbean. I measured changes in diversity, abundance, reproductive rate, body condition, and habitat use using data I collected during mist netting surveys prior to Hurricane Maria (2016 and 2017), and after Maria (2018 and 2019). Nine species (750 individuals) were captured in the two years prior to the hurricane, with reproductive females documented for all species. Nine species (79 individuals) were captured post-hurricane in 2018 and six species (87 individuals) in 2019, with reproductive females documented for six species across the island in 2018 and 2019. A decline in the number of captures and percent of reproductively active females of several species indicates varying responses within foraging guilds. Preliminary results suggest a stronger sensitivity for frugivores, and a failure to reproduce post-hurricane. Analysis is on-going and further results will be presented.

Elucidating Patterns of Bat Species Occupancy across a Disturbed Landscape in California's Central Valley
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California's Central Valley, one of the most productive agricultural regions in the world, is home to 17 species of resident and migratory bats. The Central Valley ecoregion has been identified as a crisis ecoregion, with many species at risk due to anthropogenic habitat conversion and drought. In response to severe drought, California Department of Fish and Wildlife (CDFW) implemented the Terrestrial Species Stressor Monitoring (TSSM) project and collected baseline occupancy data for bats. We conducted surveys using SM3BAT acoustic detectors at 274 sites spanning the Central Valley in both the driest year on record (2016) and the wettest year on record (2017). The objectives of this analysis were to determine if human land use and drought influence bat occupancy at a landscape level. This data collection effort resulted in the largest bat acoustic survey of the Central Valley with over 3,300 events. Detections were autoclassified using Kaleidoscope software and manually vetted. We fit single-species occupancy models in a Bayesian framework. Migratory species (*Lasiurus cinereus, Lasiurus blossevillii,* and *Tadarida brasiliensis*) contracted their geographic range during the drought, while hibernating species did not (*Myotis lucifugus* and *Myotis californicus*). Further, arid-adapted species (*Parastrellus hesperus* and *Eumops perotis)* expanded from natural open areas into agricultural landscapes during the drought. Primary implications suggest that migratory species may more easily adapt to drought conditions, irrigated agricultural areas may act as drought refugia, and large-scale acoustic studies can serve as an alternative or supplement to capture for acoustically detectable species.

Defining Phenotypic Species Limits in Hoary Bats
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Defining population and species limits is fundamental in biogeography, community ecology, and evolutionary biology. Understanding these boundaries and the environmental factors that shape them can have strong implications also for conservation and taxonomy. Advances in machine learning and statistical cluster analysis to analyze phenotypic and environmental data can provide improved resolution for examining limits in groups that are difficult to sample genetically. Here, we look at hoary bats across the Americas to test the association of phenotypic limits with the environmental features that help maintain them. Sampling for 16 phenotypic cranial characters was performed on 173 individuals throughout the distribution of the three recognized species of Hoary Bat, including all island groups. Niche overlap analysis was performed on 1174 unique locality records throughout the distribution along with climatic data for 19 climatic variables plus elevation. Phenotypic analyses recovered the currently recognized species clusters (*Lasiurus cinereus, L. semotus,* and *L. villosissimus*). While we know *L. semotus* is genetically related to *L. cinereus*, phenotypically it clusters closer to Neotropical groups of Galápagos, Hispaniola,

and the mainland *L. villosissimus*, which also are differentiated from each other phenotypically. Niche overlap analyses showed group variation in niche breadth in a manner congruent with the phenotypic clusters. Our study exemplifies the importance of linking environmental and phenotypic information to shed light on species limits. This approach is especially useful for widely distributed species where cryptic groups can result from heterogeneous combinations of biotic, environmental, geographic, and topographic features of the places where they occur.

Ectoparasite Load Effect on Blood Cell Count in Rafinesque's Big-eared Bats
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In Arkansas, roosts for Rafinesque's big-eared bats (*Corynorhinus rafinesquii*) can be variable and consist of bottomland hardwood trees and man-made structures. Due to anthropogenic change a maternity colony in northeast Arkansas has persisted in an area of intensive agriculture, which was previously part of an expansive habitat of bottomland hardwoods. A maternity colony in a man-made structure is rare, and the ectoparasites on *C. rafinesquii* are understudied. Thus in July of 2018 and 2019, individuals (n = 41) were sampled from a storage barn and were found to be the hosts for ectoparasites in the family Cimicidae, which contains bat bugs (*Cimex adjunctus*) and bed bugs (*Cimex lectularis*). Ectoparasite loads were recorded and parasites were collected in 90% ethanol. In 2019, small samples of blood were taken from a subset of lactating and post-lactating individuals for blood smears. Neutrophils and lymphocytes were counted to compare neutrophil-lymphocyte ratios that were collected from a subset of individuals. Other immune cell counts were made with the stained slides. Finally, temperature-sensitive transmitters were fitted to a subset of bats (n = 10) to determine how torpor pattern affects ectoparasite load and immune cell ratios. Understanding physiological tradeoffs in this species is important due to their integral role in environmental services.

In-flight Social Calls of Insectivorous Bats: Species-specific Behaviors and Social Call Contexts
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A species' social environment acts as a selective pressure on its communication systems. Bats exhibit a broad diversity of social group size and complexity. Bats could be useful for studying the effects of sociality on communication, but their social calls are poorly understood. Passive acoustic monitoring occasionally captures in-flight social calls. Surrounding echolocation calls can provide information on which species produced the call and the behaviorally relevant context. We used passive acoustic monitoring in Greensboro, North Carolina, to test for species-specific differences in social calling behaviors and the contexts of call types. We identified seven distinct social call types. *Eptesicus fuscus*, *Nycticieus humeralis*, and *Tadarida brasiliensis* differed in production of social calls relative to activity and proportional usage of call types. Shared called types exhibited species-specific differences in call characteristics, indicating the potential for species recognition. Due to substantial temporal clustering, social calls were grouped into temporally independent call bouts. Time of night and bat activity were correlated with the probability of observing a bout. Bouts consisting of solely complex calls were more likely to occur in single species bat passes with foraging buzzes, suggesting these calls mediate foraging interactions with conspecifics. Bouts of solely downsweeps, solely upsweeps, and both downsweeps and upsweeps were more likely to be produced in multiple species bat passes, suggesting the calls may mediate interactions between unfamiliar individuals. Differences in rate of call production and the use of particular call types associated with different contexts suggest that bat species exhibit differences in in-flight social behavior.

Ways of Seeing: From a Bird's to a Bat's Eye View
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In a forested environment, trees provide the vertical scaffold for a larger community and a change to stand structure may affect how habitats are used by bat species. As it has been observed that sympatric bat species spatially partition resources based upon the structural characteristics of a habitat, clutter creation may affect the availability of habitat within an ecosystem for each bat species differently. In the absence of wildfire, blown-down trees become a primary source of new clutter and to investigate the effects we cut a single tree at six locations along a stream to

simulate clutter creation in structurally similar sites where it could be measured. We collected acoustic data at these sites before and after tree-felling as well as in open-canopy and closed-canopy forest stands June 2019 through August 2019. Using three-dimensional point clouds produced from photographs taken of the forest stands with an unmanned aerial vehicle (UAV), we segmented individual trees to quantify structural attributes of the forest stands and the amount of introduced clutter. These data will be used to examine how bat species may respond to changes in habitat availability.

Distribution and Prevalence of *Pseudogymnoascus destructans* at *Tadarida brasiliensis* Roosts in Central and South Texas

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In 2018, the southernmost detection of *Pseudogymnoascus destructans* (*Pd*) was detected on a Mexican free-tailed bat (*Tadarida brasiliensis*) in Central Texas. *T. brasiliensis* are not known to hibernate for extended bouts, and as a result are not expected to be highly susceptible to white-nose syndrome (WNS). However, because they migrate in large numbers, they may spread the disease further into the western United States and/or south into Mexico, Central and South America. Despite extensive statewide surveys for *Pd*, very little of the previous surveillance effort has focused on *T. brasiliensis*. Texas Parks and Wildlife Department conducted follow up surveys on the previous year's detection of *Pd* on *T. brasiliensis* to better understand the current prevalence of *Pd* in the Central and South Texas *T. brasiliensis* populations. To target the species, iNaturalist and the Texas Natural Diversity Database were queried to find winter roosts across the state. Roosting bats in twenty-three counties were swabbed and inspected for signs of WNS. Samples from six counties returned positive results for the fungus, including a new southernmost site. Through better understanding the current distribution and prevalence of *Pd* in the Central and South Texas, neighboring states and countries will be better informed for the arrival of *Pd* via this potential vector.

How Do Indiana Bat Populations Respond to Forest Management?

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Responsible forest management is a necessary part of wildlife recovery; however, we lack data on effects of management on heath and population sizes of endangered Indiana bats (*Myotis sodalis*). Missouri Department of Conservation established guidelines to minimize risk to Indiana bats while conducting forest management during the maternity season. From 2019–2026, we will use multiple methods to assess population size and individual health of Indiana bats in 6 conservation areas in northeastern Missouri, 3 with planned timber removal and 3 controls. We captured and attached radio transmitters to Indiana bats at 6 areas 23 May–26 July 2019, tracking bats both pre- and post-volancy and conducting simultaneous exit counts at known roosts to estimate colony sizes. We attached transmitters to 33 of 45 Indiana bats captured, located 39 roost trees, and counted 1–116 bats/area during simultaneous counts. We used Anabat Swifts with directional mics to record Indiana bat echolocation activity at 10 points/area for 5 nights pre- and post-volancy; we will use these data to generate estimates of occupancy and relative abundance for each area. At capture, we measured bats and collected blood, hair, and guano to allow future assessment of individual health via body condition, stress hormones, white blood cell counts, and parasite loads. This 8-year project offers a unique opportunity to test long-held assumptions about Indiana bats' responses to forest management and will inform future guidance on the creation and maintenance of suitable summer habitat capable of sustaining healthy populations of Indiana bats.

Testing Environmental Cleaning Agents to Reduce Contamination of Bat Hibernacula with *Pseudogymnoascus destructans*

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Pathogens with density-independent transmission can threaten the viability of host populations, as pathogen reproduction is not determined by host abundance. One such example is *Pseudogymnoascus destructans* (*Pd*), the fungus that causes white-nose syndrome (WNS), which has devastated bat populations across North America. *Pd* can persist in environmental reservoirs, resulting in density-independent *Pd* transmission and creating potential for host species' extinctions. Treatment of environmental reservoirs could therefore help reduce transmission of *Pd*, and thus, reduce bat population declines from WNS. We tested the efficacy of two environmental treatments for *Pd*: 1) ultraviolet-C radiation and 2) polyethylene glycol (PEG). We delineated circular plots on the walls and ceilings of three *Pd*-positive mines in Ontario, Alabama, and Arkansas (n = 120 plots per hibernaculum). Prior to hibernation onset, we applied one of four treatments to each plot: UV-C light (254 nm), 28% PEG-8000, 90% isopropyl alcohol (decontamination control), or no treatment (control). We then quantified how a one-time treatment application affected prevalence and load of *Pd* throughout the year, as well as non-target effects on the microbial community, by swabbing roosting substrates at four distinct time points. *Pd* prevalence and load were determined using real-time qPCR and the microbial community was characterized using 16S and ITS2 rRNA sequencing. Preliminary results suggest that responses to treatments were highly site-specific and there were no clear patterns across sites. Our results suggest that site-specific treatments and management responses may be important for reducing impacts of *Pd* on bat populations.

Non-random Association Patterns Reveal Overlapping Subgroup Structure: Evidence for Complex Social Behavior in Little Brown Myotis

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Group behavior is observed widely across the animal kingdom, yet factors influencing group behavior are typically poorly understood. To understand the proximate and ultimate causes and consequences of group formation, it is first necessary to characterize the organization of a group. Little brown myotis (*Myotis lucifugus*) are known to roost in groups that display complex patterns of interactions, described as fission-fusion societies in which groups split and merge through space and time. Here, we apply social network analysis to quantify associations among individuals and begin to test the bat sociality hypothesis, which proposes that bats form groups based on preference for association with specific individuals. We provide evidence of such preferences in association and found that the study population comprised multiple subgroups. Interestingly, subgroups showed high connectivity with other subgroups, supporting the presence of fission-fusion dynamics in these systems. We found only limited evidence that group organization was maintained across years, as there was some tendency for associations among individuals to persist across years. The patterns identified are consistent with the bat sociality hypothesis, but future study is needed to confirm that social preferences directly influence these patterns. Our study provides a basis to understand the group organization of a gregarious bat species and future studies should expand the geographic scope of the study, and investigate the intrinsic and extrinsic factors that influence the fission and fusion events that shape this group patterning, contributing to our broader understanding of complex social behavior in mammals.

Movement Patterns of Migratory Tree-roosting Bats During Autumn Migration

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Migration routes of long-distance migratory tree-roosting bats (*Lasiurus cinereus, L. borealis, and Lasionycteris noctivagans*) in North America are poorly understood. Large numbers of bat fatalities recorded at wind energy

facilities are contributing to likely population declines of these species. Most documented migratory bat fatalities at wind energy installations occur during autumn migration. There is some urgency to better understand migration patterns of these bats, because like many other jurisdictions, the Province of Saskatchewan plans to dramatically increase wind power generation capacity. We installed passive acoustic detectors in southern Saskatchewan during the migration period to measure migratory bat activity. We placed one set of detectors in a three-by-three grid pattern across the study area in locations with high wind energy potential and prominent landscape features. We installed a second set of detectors along 5-km transects perpendicular to four of the province's major rivers. We found higher levels of migratory bat activity in the eastern portion of the province. Activity was also generally higher in riparian areas and decreased with distance from rivers. This is consistent with access to resources such as roosting habitat and water being important in bat migration route selection. Sites located in riparian areas and the southeastern portion of the province contain more forested landscape than other sampling sites located in uplands and grassland ecoregions. Our results will inform siting decisions for future wind energy projects.

***Competitors Versus Filters: Drivers of Non-random Structure in Forest Interior Insectivorous Bat Assemblages along Elevational Gradients**

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*** Iroro Tanshi** received the **Karl F. Koopman Award.**

Non-random assemblage structure in species-rich bat assemblages may be driven independently or simultaneously by competition and environmental filtering leading to trait dissimilarity or similarity, respectively. Monotonic decline in bat species richness along forested Afrotropical elevational gradients is resource driven, yet the relative roles of competition and environmental filtering remain unclear. Ecomorphological traits, bite force and wing morphology, encode patterns of resource partitioning, but may also respond to environmental filtering, allowing examination of the relative role of competition and filtering. We hypothesize that if mean trait values change with elevation, then competition and environmental filtering simultaneously drive non-random structure of bat assemblages. We trapped bats using five harp traps set every 50 m along four 200-m long transects, at elevational strata ca. 250–400 m apart, along two forested elevational gradients in southeastern Nigeria. We measured vegetation structure within four 2-m^2 plots around each harp trap and collected insects using light traps at each transect. For captured bats, we recorded forearm length and body mass, and measured bite force using bite plates attached to a Kitzler force transducer and photographed wings of bats restrained to a gridded board. Wing morphology parameters were measured from photographs of bat wings. We developed regional null communities in trait space at each elevational stratum. We compared mean nearest neighbor distances between species in trait space of observed relative to artificial communities at each elevational stratum. The result of these analysis will uncover drivers of non-random bat assemblage structure along forested elevational gradients.

Bats of Vietnam: An Overview of Research and Conservation

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Vietnam owns highly diverse landscapes with various ecosystems within offshore archipelagoes, coastal realms, and continental regions. It contains different habitats, ranging from flatland with urbanized and agricultural sectors to mountainous and karstic areas with tropical forests. Prior to 1997, bats of Vietnam were poorly studied because the country lacked bat specialists. Since 1998, the author has investigated specifically the bat fauna of Vietnam with particular emphases on taxonomy, echolocation, and conservation. To determine the systematics, echolocation and conservation status of Vietnamese bats, a series of field surveys were conducted through a range of localities in the country. Although the known bat diversity of the country increased impressively over the past decades, many species have been threatened by illegal hunting, habitat loss, and other factors. Several action programs were implemented within selected areas for conservation of threatened species and habitats. The achievements from the surveys and conservation programs include records of species new to the country, discoveries of species to science, resolving the mystery of hipposiderid taxa, findings of special echolocation systems, effective conservation of threatened species, and capacity building. The country is recognized as a hotspot in Asia for bat research and conservation but its central and southern regions with offshore islands are almost unsurveyed. Both academic

research and practical conservation actions are required for understanding the bat fauna of Vietnam as well as saving threatened species and habitats in the future.

Persistence of *Myotis septentrionalis* in Suburban Forest Remnants

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Acoustic monitoring since 2015 indicated the presence of *Myotis septentrionalis* within Rouge National Urban Park (RNUP), a newly established urban national park covering almost 80 km^2, east of Toronto, Ontario, Canada. Captures in 2018 confirmed the presence of a breeding population of *M. septentrionalis* in one forest located in the south of the park and surrounded by suburbs. In this study we investigated the population, the bats' use of the forest, and their interaction with the surrounding human-made environment. We divided the forest into 500-m grid squares and conducted 10 consecutive nights of acoustic monitoring in each. We attempted to capture *M. septentrionalis* in a subset of grid squares and radio-tracked individuals to identify roosts and foraging movements. We also conducted acoustic monitoring throughout the rest of the park in forest patches larger than 10 ha. We identified acoustic activity of *M. septentrionalis* in all squares surveyed at our primary forest, but recorded negligible activity at other patches within RNUP. We conducted trapping surveys in six squares and captured *M. septentrionalis* in three. None of the tracked bats left the forest during tracking; their foraging activity centered around waterways, while roosts were in mature trees in the forest center. This reproductive population represents a significant record for this species in Ontario, where few observations exist. We conclude that this may be a remnant population, surviving in an isolated habitat patch. This observation demonstrates that *M. septentrionalis* can survive moderate disturbance in habitat fragments within highly urbanized landscapes.

Bat Box Design Affects Microclimate and Suitability as Bat Habitat

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Bat boxes are popular conservation tools, but we know little about how design affects internal microclimate and hot boxes could be ecological traps. We assessed microclimate in 20 box designs, modified by volume, insulation, shading, and airflow, measuring $T_{internal}$ via 12 dataloggers in each box, installed in close proximity and with bats excluded, in central Indiana (mid-May–mid-September 2018). For each design, we calculated proportion unsuitable (>40°C), instantaneous range of temperatures (availability), and daily variation (variability), and for each position, we calculated the bihourly difference from ambient (ΔT). We measured ambient air temperature (T_a), global radiation (G), and wind speed (u) onsite. In a standard design, $T_{internal}$ averaged 26.2°C, but varied from 12–52°C across all positions and days; the top was generally warmest, sometimes with lethal temperatures (≥45°C) in all 4 directions and ΔT >20°C. In the standard, mean availability ranged from 1.4–8.9°C and $T_{internal}$ varied by 3–34.5°C on single days. Other designs varied significantly from the standard and each other in terms of availability and variability. Changing box volume produced large differences; for example, a short box was 7°C more stable than a long box, but the long box offered greater availability (5.3 ± 0.2°C vs. 1.6 ± 0.1°C). Daily maximum T_a and G directly affected box temperatures, while daily maximum u had an inverse effect. Box design and weather affect box microclimate, which has important implications for the use of bat boxes as mitigation tools. We recommend examining seasonal design preferences by bat box dwellers.

White-nose Syndrome Fungus Triggers Similar Immune Response in Fibroblast Cell Culture as in Living Bats

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White-nose syndrome (WNS) has decreased populations of some temperate bat species to levels where conducting research on live bats must be curtailed, especially when destructive sampling is required. We reported previously a cell-culture method to assess immune function of bats using fibroblast cells isolated from wing punches, which exposes the cell cultures to the fungus responsible for WNS, *Pseudogymnoascus destructans* (*Pd*). Fibroblasts from WNS-susceptible species attempt to mount an immune response that is ineffective but likely costs the bat valuable energy. Conversely, fibroblast cells from WNS-resistant species do not show any immune response to *Pd*. However, a key question now is whether the responses to *Pd* of these cells in culture are the same as in the living bat. Because fibroblast cells *in vivo* secrete chemicals to activate the immune system when tissue is injured or infected, we

hypothesized that wing punches from bats after hibernating with *Pd* will show the same profile of gene activation as seen in the cell cultures. We have now developed/used quantitative real-time polymerase chain reaction (qRT-PCR) assays to test the activity of several immune genes that were upregulated in the cell-cultures (transcriptomics analysis). Generally, we found that wing tissue from tricolored bats (WNS-susceptible) late in hibernation showed increases in gene expression compared to pre-inoculation with *Pd*, but wing tissue from big brown bats (WNS-resistant) did not change (or decreased). These results, though preliminary, suggest that the cell-cultures may indeed be a good surrogate for using living bats in some kinds of WNS research.

Assessing Microplastic Contamination in Bats and Their Insect Prey

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Plastic pollution has been increasingly recognized as a serious environmental issue, with many potential ramifications to ecological and wildlife health. Microplastics are a type of plastic pollution, and are defined as a plastic particle that is between 1 nm and 5 mm in size. These particles have the potential to bioaccumulate across trophic levels, cause physical blockages in digestive tracts, and may become contaminated with organic environmental toxins or leach “plasticizing" chemical toxins that are present in the plastics themselves. Globally, bat populations have been in decline for decades from a variety of sources, such as human persecution, environmental contamination/degradation, and disease. As many bat species are slow to reproduce, these declines can be difficult to recover from, and the additional stress that microplastic pollution potentially adds may hamper their recovery. Bats may be exposed to microplastic contamination through their diet or drinking water; however, to date no studies have been conducted to assess the possibility of such contamination in bats. In order to do so, gastrointestinal tracts of bats as well as guano samples will be chemically digested using wet peroxide oxidation, and analyzed using microscopy and Fourier-transform infrared spectroscopy. Insect samples will be collected using Malaise traps and hand nets and analyzed in the same manner. Concurrent with that, guano samples will also be analyzed to identify DNA of prey items to compare with results from insect sampling, which will aid in identifying specific insect prey as a potential vector of microplastic exposure in bats.

Development of Wind Energy in Guatemala: A Negative Way to Report New Species for the Country

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Wind energy is one of the government strategies used to promote sustainable development using renewable resources in Central America. In Guatemala, there are no specific regulations for this kind of activity, and the magnitude of efforts made to determine the potential impacts varies considerably and depends greatly on each wind energy company. Almost all projects in operation and those in process of acceptance are located in the central region of the country, where Nearctic and Neotropical species converge. In this study, we describe the inconsistencies between pre-operation monitoring that described the bat diversity and post-operation monitoring, which described impacts of wind turbines on bats of a particular wind farm. In the pre-operation monitoring, 19.6% (19 species) of the bat species reported for the country were registered, whereas in the post-operational monitoring the percentage of species increased to 34% (33 species), plus four new species records. This increases the number of species reported for Guatemala to 101. It is virtually impossible to establish the impact of these findings at the population level, even more when the most affected species have been reported on very few occasions or their existence was previously unknown. These unexpected findings highlight the necessity of designing specific protocols to regulate wind energy in the future and to continue with the efforts to describe the bat diversity of the country.

Real-time Sequencing of *Pteropus hypomelanus* in Vietnam to Generate Genomic Resources and Build Scientific Capacity

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Historical collections in biodiversity hotspots represent some of the best repositories of scientific material, yet access to labs with the most up-to-date genomics equipment makes unlocking the full research potential of the

collections difficult. Bringing the lab to the museums solves this problem, while also serving to build scientific capacity for local scientists. *Pteropus* (Mammalia: Chiroptera: Pteropodidae) flying foxes are large fruit bats critical to the natural landscape of Vietnam serving as long-distance seed dispersers and pollinators. However, flying foxes have experienced population declines in the past few decades as foraging and roosting habitats continue to decline in quality as anthropogenic development increases. Of the three Vietnamese *Pteropus* species, *P. hypomelanus* is of greatest taxonomic interest due to its disjunct distribution, poorly known subspecies limits, and understudied genetic diversity. In Vietnam, *P. hypomelanus condorensis* is only found on Con Dao Island in the south, and its relationship to other *P. hypomelanus* remains unclear, despite its potentially high conservation value. Here, we used a portable DNA sequencer, the MinION (Oxford Nanopore), to sequence DNA from tissue samples of historical specimens of *P. hypomelanus* at IEBR-VAST in Hanoi, Vietnam. This method precluded the need to send samples to outside sequencing facilities. We reliably produced high quality genomic DNA without the need for excessive infrastructure or equipment and we developed protocols for bringing real-time sequencing to regional collaborators, dispelling some barriers of unequal access to genomics. At the same time, we were able to answer pressing questions about the genetic diversity of *P. hypomelanus condorensis*.

Morphological Variation and Origination of Chiropteran Wing Membranes

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Bat wings comprise several, novel membranous structures that are supported by elongated forelimb and digit bones. The achievement of powered flight in bats led to an unprecedented adaptive radiation and diversification in membrane structure, such that today bats employ diverse flight styles and account for over 20% of all mammalian species. Despite the importance of the evolution of the bat wing to the group's success, the mechanisms that drove the origination and subsequent diversification of the novel components of the wing remain largely unknown. Our research specifically investigates the evolutionary origination and diversification of two novel membranes of the bat wing: the plagiopatagium, which connects the 5th digit to the body and hind limb in all bat species, and the uropatagium, which connects the hind limbs in many species. We seek to determine when during development and from what tissue sources the membranes initially form, and when differences in membrane form arise among species. This is achieved by performing geometric morphometrics on embryonic specimens housed at the American Museum of Natural History (AMNH). Additionally, we establish a general cellular and molecular framework for plagiopatagia and uropatagia development in bats and establish how this framework differs among species with divergent membrane development. This is achieved by visualizing cellular processes, gene expression, and protein localization in developing embryos. We determined that divergence in wing morphologies occurs later in development via differential timing of cellular proliferation and variation in gene expression.

Drivers of Flying Fox Hunting in Southeast Asia

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Hunting of flying foxes, species of *Pteropus* and *Acerodon* (Pteropodidae), is widespread in Southeast Asia, and threatens 21 of the region's 30 species (IUCN 2019). The primary use of hunted bats reported in Red List assessments is for human consumption (20 species), but this simple explanation does not capture the diverse beliefs and motivations driving hunting behavior, hampering conservation intervention. The goal of our project is to develop, test and distribute a standardized, scientifically sound protocol to study hunting of flying foxes regionally and develop effective responses to conserve flying foxes. Our protocol is intended to both quantify the magnitude and extent of flying fox hunting and characterize factors affecting hunting behavior. The Theory of Planned Behavior provides our conceptual framework, and posits that behavioral intention is predicted by attitude, subjective

norms and perceived behavioral control. This is a powerful approach because analysis of the differential influences on behavior can help identify the most important barriers to change and targets for intervention. The protocol was developed and implemented in three areas of intense hunting in Sulawesi (Indonesia) and the Philippines. Here we report and compare our findings across hunting sites. Although all sites shared a positive attitude towards hunting (hunting is a "good thing" to do), they differed in the significance of social norms and perceived behavioral control as well as in specific behavioral, normative and control beliefs. We highlight how our findings are being used to guide pilot conservation programs to reduce hunting.

Bat Wing Skin pH

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Skin is a complex physical barrier and chemical landscape of distinct niches. Skin represents the primary interface between a host and its environment and is the body's first line of defense against pathogens. White-nose syndrome (WNS) is a cutaneous fungal infection of hibernating bats that damages wing membranes, causing physiological disruptions that can lead to death. Cutaneous pH varies with season, sex, age, and species, and may alter pathogen virulence or host susceptibility but has not previously been characterized in bats. To understand how skin pH varies between wing regions and species and how this might alter the "landscape" of the wing, we measured skin pH on the surface of bat wings of different species using non-invasive probes. Female bat skin was more acidic than male skin, and dorsal wing surfaces were more acidic than ventral surfaces. Acidity varied between species and locations. In Ontario, Canada, *Myotis leibii* were the most acidic (n = 10, mean = 6.03 ± 0.13), followed by *Eptesicus fuscus* (n = 67, mean = 6.04 ± 0.14) and *M. lucifugus* (n = 251, mean = 6.23 ± 0.12). Bats were more acidic in New Brunswick than in Ontario (*E. fuscus*, n = 27, mean = 5.73 ± 0.15; *M. lucifugus*, n = 34, mean = 5.80 ± 0.15), while *M. lucifugus* in Prince Edward Island were more alkaline (n = 35, mean = 6.38 ± 0.09). Variation in skin pH may impact the composition and diversity of skin microbiomes on bats and susceptibility to WNS.

A P53 Duplication Influences the Stress Response in the Long-lived Bat, *Myotis lucifugus*

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Cancer is a disease common to all complex life. Many life history traits, such as size and lifespan, are correlated with cancer risk between individuals of a species; however, this correlation does not hold when comparing between species. This phenomenon, known as Peto's Paradox, is resolved as species co-evolve cancer suppression mechanisms alongside increased sizes and lifespans. However, the exact mechanisms involved are largely unknown. Bats represent an ideal clade to study this paradox, as the combination of clade size, phylogenetic diversity, and recent divergence times preserves a detailed record of the genetic changes underlying their diversity in body size and lifespan. We show that the little brown bat, *Myotis lucifugus*, has two full copies of TP53, a central regulator of cellular stress responses; *M. lucifugus* is the only species to-date with such a full-locus duplication. To investigate how these two copies of TP53 influence the stress response of *M. lucifugus* relative to 4 other closely related bat species (*M. evotis*, *M. thysanodes*, *M. yumanensis*, and *Eptesicus fuscus*), we measured apoptosis, cytotoxicity, and viability in primary fibroblasts in response to chemically induced DNA-damage, unfolded protein response, and oxidative stress. We show that both loci are transcriptionally active in tissue RNA-seq and in primary fibroblasts via RT-qPCR, and that knocking down TP53 reduces apoptosis and necrosis in response to DNA damage. These results demonstrate a functional role for two copies of TP53 in mediating the stress response of the little brown bat, *Myotis lucifugus*, and resolving Peto's Paradox in this species.

***Gotta Catch'Em All! Using PNA-DNA Clamps to Increase Microbiome Read Numbers in a Diet Specialist**
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*** Luis Víquez-R.** received the **Luis F. Bacardi Bat Conservation Award.**

The popularization and further development of sequencing techniques has vastly increased the number of microbiome studies over the past 10 years. Although the actual objectives of these studies vary widely, they always rely on having high microbiome read numbers (MRN) for the bacterial taxa within a sample. We collected fecal samples from 550 lesser long-nosed bats (*Leptonycteris yerbabuenae*) from three different sites along the migratory route in Mexico. We extracted total DNA and sequenced the 16S V4 region from bacterial DNA. The first results showed a high level of "contamination" that was hijacking our reads and consequently greatly affected the MRN. Further exploration revealed that the V4 primer was highly effective in yielding chloroplast and mitochondria sequences. While this is normal in any microbiome study, the disturbing part was an extremely high percentage of the reads assigned to the genetic material of the cell organelles that in some cases reached 95% of all reads. After recognizing that the contamination came from a high percentage of pollen from the bat's temporary main diet—the cactus saguaro (*Carnegiea gigantea*) present in the fecal samples—we developed species specific PNA-DNA clamps for the cactus organelles. This way we were able to reduce the pollen-derived sequences in the microbiome from 95% to 20%, thus improving the MRN significantly. In the light of more studies exploring the microbiome of different bat species, the use of PNA-DNA clamps can be an excellent option when dealing with dietary specialists.

Movements and In-roost Behavior of the Wooly False Vampire Bat, *Chrotopterus auritus*
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Carnivorous bats represent an ultimate extreme in specialization of bats in the New World. The woolly false-vampire bat, *Chrotopterus auritus*, is the second largest bat in the Americas but little is known about its ecology. We tracked the movements of 10 individuals from 2 colonies on 32 occasions for a total of 72 foraging nights, the largest sample size for any study on *Chrotopterus*. One roost was surrounded completely by undisturbed forest whereas the other was surrounded by deforested habitats used for agriculture and cattle pasture. Using miniature GPS tags, we documented an average home range of 108 ha, a core foraging area of 3.78 ha, and average maximum flight distances of 2.06 km. The bats ranged farther and flew significantly longer distances in from the roost in a relatively more disturbed landscape than on the undisturbed landscape. Males flew longer and more variable distances. Bats used the well-preserved semi-deciduous forest more often than secondary forest and agricultural fields for traveling and foraging, but the bats occasionally moved and foraged along the borders of secondary forest and agricultural fields adjacent to semi-deciduous conserved forest areas. Although this carnivorous bat might cope with some fragmentation, large well-preserved forested areas are highly important for its conservation. We also present the first evidence showing food supplementation in a variety of combinations. Genetic studies are under way to understand the identity of the bat involved.

Impacts of Habitat Conversion by Hyperabundant Moose on Summer Bat Activity in Newfoundland, Canada
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Large herbivores can drastically alter local vegetation structure, subsequently affecting biotic communities. In Gros Morne National Park, Newfoundland, hyperabundant moose populations have exacerbated the conversion of mature forest stands into open meadows: "moose meadows" (MM). This shift in vegetation structure has affected habitat use by other fauna (e.g., songbirds). We hypothesized that bats and insects would use MM differently than they would regenerating or mature forests. We predicted that reduced vegetation in MM habitat would result in lower insect biomass and consequently, lower bat activity. We acoustically monitored bats and collected nocturnal insects during summer 2017 and 2018 from four habitat types ranging from MM to mature forests. Insect activity differed among habitat types ($F_{df=3} = 5.555$, $p < 0.01$), with the lowest mean biomass in MM, but contrary to the prediction,

bat activity did not ($F_{df=3}$ = 0.306, $p > 0.05$). To further explore drivers of bat activity, generalized linear mixed models were used. Three model sets were generated, each incorporating a different category of explanatory variables——vegetation, environmental, and insect—and compared using second-order Akaike information criterion (AICc). The vegetation model had the best fit (AICc = 1130.6) and suggested that average snag abundance, percent deciduous dominance, bat species interactions with vegetation height classes, and sampling year were the most influential predictors of bat activity. While pre-established habitat designations did not predict variation in bat activity, vegetation structure was important and may still indicate a potential effect of forest conversion by moose on summertime bat activity.

Variation in Bat Use of an Ephemeral Wetland in Western Tennessee

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During the summer months, most species of bats in Tennessee use the forested landscape to both raise their offspring and to forage. We examined the variation in bat use of an ephemeral wetland located in the Beech Ridge Unit of the Obion River Wildlife Management Area June–October 2018 using both mist net and acoustic surveys. We hypothesized that there would be variation in species richness from summer through early fall, and that both the mist net and acoustic surveys would reflect those differences. We netted bats, identified them to species, and collected morphometric data every 3 weeks beginning mid-June. Simultaneously, we used a bat detector near the net survey site to record bat activity and species richness for at least two weeks after almost all net nights. After files were scrubbed for non-bat noise, species were identified, when possible, and bat activity was examined with SonoBat v. 4.2.2. The bat passes identified to species by SonoBat were then manually vetted. During the study, species richness varied by net night and month, and similar variation was reflected in both the net and the acoustic surveys. Eight species were captured either by mist net, by acoustic survey, or by both. All of the species captured via mist net were also captured acoustically, but one species was captured via acoustic survey but not mist net. The variation in bat species assemblages within this seasonal examination of the bat community at this site may have implications for future habitat management strategies.

BatAMP's New Visualization Tool Provides Novel Insights into the Seasonal Ecology of Bats

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Knowing the distributional range of a species is fundamental to understanding its ecology and providing for its conservation and management. Generally, the first level of understanding is based upon static species range maps, which include many historic locational records. However, as species ranges shift due to environmental change, it is increasingly important to base conservation decisions on current areas of occupancy. In addition, many species of bats shift their distribution and activity areas seasonally; something not reflected in conventional range maps. Fortunately, across the United States and Canada, acoustic monitoring efforts for bats are generating multitudes of new species occurrence records each year. Increasingly, results from these local research and monitoring efforts are shared to the Bat Acoustic Monitoring Portal (BatAMP) for use in understanding regional- and continental-scale seasonal occurrences of bats. As of July 2019, over 6 million detections of 34 species from 35 states and provinces have been compiled in BatAMP during the years 2006–2018. The recently launched data visualizer (https://visualize.batamp.databasin.org/) provides users interactive filtering capabilities to focus on particular species, geographic extent, and time periods of interest. I demonstrate the use of this tool as it relates to documenting survey effort, exposing potential range extensions, and generating hypotheses about the seasonal occurrences of bats at large spatial scales.

Intra-annual Isotope Sampling of Red Bats in Nebraska Raises Questions

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Wind turbines are estimated to kill hundreds of thousands of bats in North America every year. Reported mortality indicates that long-distant migrant species are the most impacted, with red bats (*Lasiurus borealis*), hoary bats (*L. cinereus*), and silver-haired bats (*Lasionycteris noctivagans*) comprising approximately 80% of mortality. Because most mortality occurs during the fall migratory period, effective conservation actions rely on information about these movements. Stable isotope analysis is increasingly used to infer migratory movements of bats. We used the method in a novel way, focusing on changes in isotope values at one place over time. We captured red bats during the summer and fall of 2016 at one location in east-central Nebraska. We compared the mean and distribution of stable hydrogen isotopes in summer and fall to infer possible migratory timing. For comparison to other studies, we also calculated catchment area of bats using previously published models. No difference in hydrogen isotope values of red bat fur was observed between seasons. Consequentially, mapping catchment areas showed high probability that both summer and fall bats originated locally. Potential catchment areas for red bats encompassed most of the species range, leading to questions about the usefulness of such mapping activities. Additionally, the lack of change in isotope values raises questions about the generally accepted theories about migratory behavior of red bats. Our study emphasizes that caution should be used when interpreting isotope analysis. Fundamental research to understand isotope patterns in bats has not been done as it has with insects and birds.

Insights from Monthly Species Distribution Models for Three Migratory Bat Species Impacted by Wind Energy

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Understanding seasonal variation in the distribution and movement patterns of migratory species is essential to their monitoring and conservation. Bats are a group of species that are migratory, yet, when compared to birds, we know much less about their seasonal distributions or migratory movements. This is significant because of the impact wind energy has on migratory bat populations through increased fatalities. Here we describe more accurate seasonally resolved distributions for the three species (*Lasiurus borealis* [Eastern Red Bat], *L. cinereus* [Hoary Bat], and *Lasionycteris noctivagans* [Silver-haired Bat]) most impacted by wind farms that can be used to make inferences about migratory paths and behavior. To accomplish this, we used 2880 occurrence points collected from the Global Biodiversity Information Facility over five decades in North America. We used five approaches to infer species-specific distribution patterns: regression (GLM), maximum entropy (MaxENT), BIOCLIM algorithm SDM, random forest, and an ensemble. Our results suggest that all three species exhibit variation in distributions from north to south depending on season, with each species showing potential migratory pathways during the fall migration. Additionally, we observe the largest potential for interactions between wind turbines and species distributions during summer months for both Hoary and Eastern Red Bats, while Silver-haired Bats show more potential interactions during winter months. Overall, this study generated inferences of the migratory behavior for three impacted bat species that can be used to minimize the impact of future wind farm locations and for improving the accuracy of biomarker-based assignment studies by providing spatially-based priors.

An Ounce of Prevention: Using Infra-red Technology to Proactively Manage a Bat Roost

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Advances in technology allow improved management of species that historically have been challenging to study and may allow researchers and managers more insight into behavior. We installed an infra-red beam-break system on a Mexican free-tailed bat seasonal roost in central Nevada to monitor roost activity. The system runs continuously and passively and provides data on a daily basis to managers via cellular connection, thus requiring minimal field maintenance. While this beam-break system and the data it provides are instrumental to a nearby commercial wind

production facility, the use of this technology has broader implications. Relying on six years of data, we'll provide insight into changes in activity patterns across different scales. Variables, such as weather, which can affect activity patterns, may also be investigated.

Historical Reconstruction of Bat Diets using Stable Isotope Analyses

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Agricultural intensification has been linked with population declines and reduced diversity among arthropods and their predators. In recent history, the Midwestern region of North America rapidly transitioned from a complex, dynamic system to the largely agricultural landscape seen today. To assess whether and to what extent bats may have shifted their diets in response to human-mediated landscape changes, we compared carbon and nitrogen isotopic ratios from little brown and big brown bat tissues collected in Wisconsin and Illinois. Using hair from museum specimens, we measured bulk $\delta^{13}C$ and $\delta^{15}N$ to reconstruct historical bat diets. Additional hair and bone samples from contemporary bats were also measured to calculate seasonal and long-term dietary niche widths. Preliminary results show that for both bat species, historical samples were significantly more enriched in $\delta^{13}C$ than contemporary samples. For big brown bats, historical samples were also significantly more enriched in $\delta^{15}N$. These results demonstrate that bats have shifted their dietary niches over time and suggest that agriculturally-dominated landscapes do not support the main prey base of these bat species.

Nuclear Phylogeography and Distribution Modeling of the Widespread Species Big Brown Bat

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The big brown bat (*Eptesicus fuscus*) is a common hibernating bat distributed across most of North America, several Caribbean Islands, and northern South America. A previous range-wide study of big brown bat populations identified mitochondrial phylogeographic patterns that roughly corresponded to the morphological subspecies and indicated clear geographic divergence. However, the previously generated nuclear structure showed a lack of differentiation, reflecting either sex-biased gene flow or insufficient power of the markers used. Further clarification of nuclear divergence using more powerful markers is thus important for the understanding of population structure and patterns of gene flow. Here we hypothesize that mitochondrial and nuclear genomes have similar population structures shaped by both unbiased contemporary gene flow and historical vicariance among glacial refugia. We used the more powerful SNP data generated by bestRAD sequencing, and we did species distribution modeling (SDM) in MaxEnt to identify historical refugia using Bioclimatic variables on WorldClim and occurrence records on the Global Biodiversity Information Facility. Preliminary results from 96 samples confirmed nuclear divergence among populations in the western and eastern United States and the Caribbean Islands, similar to the patterns of mitochondrial phylogeography. The SDM reconstruction showed that Central America was the main glacial refugia but is faced with a loss of suitable habitats under future climate change scenarios. Our data supported the geographic nuclear divergence and particularly suggested genetic diversity and distinction of populations on the Caribbean Islands, which are proposed to be evolutionarily significant units (ESUs) and a focus of conservation under impacts of climate change.

Genomic, Morphological, and Developmental Basis of Olfactory Evolution in Phyllostomids

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Neotropical leaf-nosed bats (Phyllostomidae) are well known for their dietary radiation and accompanying morphological adaptations for the consumption of new food resources. The evolution of frugivory, nectarivory, and sanguivory from an insectivorous ancestor suggests novel mechanisms of food detection must have also evolved, and behavioral evidence shows phyllostomids strongly rely on olfaction while echolocation is supplemental. When the profound morphological or genetic changes necessary for dietary diversification emerged is unknown, but enable

new diets, these changes must precede dietary diversification. We compared the olfactory turbinate morphology (nasal cavity structures in which chemosensory epithelial tissue is distributed), olfactory receptors sequenced from olfactory epithelium transcriptomes, and ontogenetic sequences of turbinate development in phyllostomids with differing diets to test if adaptive selection or novel morphologies occurred in the olfactory system prior to dietary divergence. We discovered: 1) metrics of olfactory turbinate complexity suggest turbinate shapes are highly variable, but have strong phylogenetic signal; 2) gene duplication within particular olfactory receptor subfamilies, but more recent than the evolution of plant-visiting in bats; and 3) ontogenetic development of turbinates remains relatively simple earlier in development and the complexity of the structures occurs at very late stages. This is the first study to integrate a synergistic view of the olfactory system in bats, considering the morphological, genetic, and developmental basis of chemosensory diversity.

Land Use Predicts Occupancy of Bats in an Agricultural Landscape

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Bats provide crucial pest control services in heavily agricultural landscapes. However, their populations are vulnerable to dramatic declines due to wind turbines, habitat fragmentation, disease, and climate change. Habitat preferences of vulnerable species must be identified in order to develop appropriate management strategies. To determine habitat preferences, we acoustically recorded bats at 22 sites throughout Dubuque County, Iowa, for 4 nights per site during summer 2018. Calls were identified to species in Kaleidoscope. We gathered site-level data on landscape condition from ArcGIS and weather covariates of detection from regional weather stations. To investigate how weather and landscape variables impact bat detection and occupancy, respectively, we ran single-season occupancy models in Program Presence. We identified 18,399 bat calls, representing all 9 species previously documented. We implemented occupancy models for 4 species (*Eptesicus fuscus*, *Lasiurus borealis*, *Myotis lucifugus*, *Perimyotis subflavus*); the other 5 species were detected too infrequently for reliable modelling. Detection probability of 2 species, *L. borealis* and *P. subflavus*, was impacted by moon illumination and minimum temperature, respectively. Occupancy of all 4 modeled species was influenced by landscape variables. Larger bat species preferred agricultural areas while *M. lucifugus* preferred forested areas, possibly due to prey availability. Only *P. subflavus* avoided urban areas. The larger species and *P. subflavus* avoided areas near rivers or wetlands, which may be explained by correlated geographic characteristics of the sampling sites. Additionally, multiple detections of *M. septentrionalis* and *M. sodalis*, both federally-listed species under ESA, indicate the need to proactively protect bats in Dubuque County.

RECENT LITERATURE

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ANATOMY/HISTOLOGY

Curtis, A. A., T. D. Smith, K. P. Bhatnagar, A. M. Smith, and N. B. Simmons. 2018. Maxilloturbinal aids in nasophonation in Horseshoe Bats (Chiroptera: Rhinolophidae). The Anatomical Record, https://doi.org/10.1002/ar.23999 [kpbhat01@louisville.edu]

Gaudioso, P. J. 2019. Morfologia y morfometria del esqueleto postcraneal de murcielagos (Mammalia: Chiroptera) de Argentina. Publicaciones Especiales N° 2, PIDBA (Programa de Investigaciones de Biodiversidad Argentina), 302 pp. [ISBN 978-987-86-1760-2]

Jubilato, F. C., M. T. Comelis, L. M. Bueno, S. R. Taboga, R. M. Góes, and E. Morielle-Versute. 2019**.** Histomorphology of the glans penis in Vespertilionidae and Phyllostomidae species (Chiroptera, Mammalia). Journal of Morphology, https://doi.org/10.1002/jmor.21062 [eliana.morielle-versute@unesp.br]

Wirawati, V., N. D. A. Widiati, G. Gunawan, G. R. Saragih, P. Hening, and H. Wihadmadyatami. 2019. The distribution of serotonergic nerve on the hippocampus of the fruit bats (*Rousettus amplexicaudatus*). Veterinary World, 12(9): 1460–1466. [heviwihadmadyatami@ugm.ac.id]

BAT POOP BACTERIOLOGY

Dhivahar, J., A. Khusro, P. Agastian, and S. S. Isaac. 2019. Isolation and characterization of hyper-xylanase producing *Bacillus* spp. from faeces of the Indian flying fox (*Pteropus giganteus*). Acta Chiropterologica, 21(1): 229–236. [isaacsuthakar@gmail.com]

Modesto, M., M. Satti, K. Watanabe, E. Puglisi, L. Morelli, C.-S. Huang, J.-S. Liou, M. Miyashita, T. Tamura, S. Saito, K. Mori, L. Huang, P. Sciavilla, C. Sandri, C. Spiezio, F. Vitali, D. Cavalieri, G. Perpetuini, R. Tofalo, A. Bonetti, M. Arita, and P. Mattarelli. 2019. Characterization of *Bifidobacterium* species in feaces [*stet*] of the Egyptian fruit bat: Description of *B. vespertilionis* sp. nov. and *B. rousetti* sp. nov. Systematic and Applied Microbiology, 42: 126017. [paola.mattarelli@unibo.it]

BEHAVIOR

Haarsma, A.-J., P. H. C. Lina, A. M. Voûte, and H. Siepel. 2019. Male long-distance migrant turned sedentary; The West European pond bat (*Myotis dasycneme*) alters their migration and hibernation behaviour. PLoS ONE 14(10): e0217810. [ahaarsma@dds.nl]

Ramanantsalama, R. V., O. S. Noroalintseheno Lalarivoniaina, A. P. Raselimanana, and S. M. Goodman. 2019. Seasonal variation in diurnal cave-roosting behavior of a Malagasy fruit bat (*Rousettus madagascariensis*, Chiroptera: Pteropodidae). Acta Chiropterologica, 21(1): 115–127. [rianaval@yahoo.fr]

CONSERVATION

Kwon, Y., A. C. Doty, M. L. Huffman, V. Rolland, D. R. Istvanko, and T. S, Risch. 2019. Implications of forest management practices for sex-specific habitat use by *Nycticeius humeralis*. Journal of Mammalogy, 100(4): 1263–1273. [annacdoty@gmal.com]

Martino, A. M. G., D. Borges, and J. M. Nassar. 2019. Activity records of the endangered Paraguaná moustached bat, *Pteronotus paraguanensis*, in the main vegetation types of the Paraguaná Peninsula, Venezuela. Acta Chiropterologica, 21(1): 165–174. [jafet.nassar@gmail.com]

McHugh, N. M., B. L. Bown, J. A. Hemsley, and J. M. Holland. 2019. Relationships between agri-environment scheme habitat characteristics and insectivorous bats on arable farmland. Basic and Applied Ecology, 40: 55–66. [nmchugh@gwct.org.uk]

Straka, T. M., S. Greif, S. Schultz, H. R. Goerlitz, and C. C. Voigt. 2020. The effect of cave illumination on bats. Global Ecology and Conservation, 21: e00808. [tana.straka@tu-berlin.de]

DEVELOPMENT/ONTOGENY

Chi, T., M. Liu, X. Tan, Y. Li, K. Sun, L. Jin, and J. Feng. 2019. Vocal development of Horsfield's leaf-nosed bat pups (*Hipposideros larvatus*). Acta Chiropterologica, 21(1): 193–204. [jinlr915@nenu.edu.cn]

DISEASE

Bowen, L. E. 2019. Chapter 27. Natural History and Medical Management of Chiroptera. Pp. 353-362 *in* S. M. Hernandez, H. W. Barron, E. A. Miller, R. F. Aguilar, and M. J. Yabsley, Eds.. Medical Management of Wildlife Species: A Guide for Practitioners. Wiley and Sons, Inc., 482 pp. [ISBN: 9781119036586]

Hranac, C. R., J. C. Marshall, A. Monadjem, and D. T. S. Hayman. 2019. Predicting Ebola virus disease risk and the role of African bat birthing. Epidemics, 29: 100366. [c.r.hranac@massey.ac.nz]

Rocha, F., and R. A. Dias. 2020. The common vampire bat *Desmodus rotundus* (Chiroptera: Phyllostomidae) and the transmission of the rabies virus to livestock: A contact network

approach and recommendations for surveillance and control. Preventative Veterinary Medicine, 174: 104809. [ricardodias@usp.br]

Selvin, J., S. Lanong, D. Syiem, S. d. Mandal, H. Kayang, N. S. Kumar, and G. S. Kiran. 2019. Culture-dependent and metagenomic analysis of lesser horseshoe bats' gut microbiome revealing unique bacterial diversity and signatures of potential human pathogens. Microbial Pathogenesis, 137: 103675. [josephselvinss@gmail.com]

Warrell, D. A. 2020. Bats. Pp. 1021–1029 *in* E. T. Ryan, D. R. Hill, T. Solomon, N. E. Aronson, and T. P. Endy, Eds. Hunter's Tropical Medicine and Emerging Infectious Diseases (Tenth Edition). Elsevier. [ISBN 9780323555128]

DISTRIBUTION/FAUNAL STUDIES

Tanshi, I., A. E. Ogbeibu, and P. J. J. Bates. 2019. Complementary bat (Mammalia: Chiroptera) survey techniques uncover two new country records for Nigeria. Journal of Threatened Taxa, 11(14): 14788–14801. [iroro.tanshi@uniben.edu]

Weber, M. M., R. L. M. Novaes, M. Delgado-Jaramillo, E. Barbier, V. C. Cláudio, E. Bernard, and R. Moratelli. 2019. Is *Myotis lavali* (Chiroptera, Vespertilionidae) endemic to the South American dry diagonal? Journal of Mammalogy, 100(6): 1879–1888. [mweber.marcelo@gmail.com]

ECOLOGY

Appel, G., A. López-Baucells, W. E. Magnusson, and P. E. D. Bobrowiec. 2019. Temperature, rainfall, and moonlight intensity effects on activity of tropical insectivorous bats. Journal of Mammalogy, 100(6): 1889–1900. [giu.appel@gmail.com]

Azofeifa, Y., S. Estrada-Villegas, J. Mavárez, and J. M. Nassar. 2019. Activity of aerial insectivorous bats in two rice fields in the northwestern Llanos of Venezuela. Acta Chiropterologica, 21(1): 149–163. [jafet.nassar@gmail.com]

Barti, L., Á. Péter, I. Csősz, and A. D. Sándor. 2019. Snake predation on bats in Europe: new cases and a regional assessment. Mammalia, 83(6): 581–585. [bartilev@yahoo.com]

Chávez-Estrada, A., A. Salinas-Melgoza, and Y. Herrerías-Diego. 2019. Do activity patterns and the degree of foraging specialization enable niche partitioning in nectarivorous bats? Acta Chiropterologica, 21(1): 139–148. [cuixmaloso@gmail.com]

Duque-Márquez, A., D. Ruiz-Ramoni, P. Ramoni-Perazzi, and M. Muñoz-Romo. 2019. Bat folivory in numbers: how many, how much, and how long? Acta Chiropterologica, 21(1): 183–191. [munozml@si.edu]

Goerlitz, H. R., H. M. ter Hofstede, and M. W. Holderied. 2020. Neural representation of bat predation risk and evasive flight in moths: A modelling approach. Journal of Theoretical Biology, 486: 110082. [hgoerlitz@orn.mpg.de]

Linton, D. M., and D. W. Macdonald. 2019. Roost composition and sexual segregation in a lowland population of Daubenton's bats (*Myotis daubentonii*). Acta Chiropterologica, 21(1): 129–137. [daniellemlinton@gmail.com]

Pérez-Cárdenas, N., K. Porras-Brenes, L. V. Auccacusi-Choque, J. J. Suárez-Torres, R. M. Brooks, and G. Chaverri. 2019. Microclimate of developing tubular leaves used as roost sites by bats. Acta Chiropterologica, 21(1): 175–181. [gloriana.chaverri@ucr.ac.cr]

EVOLUTION

Reyes-Amaya, N., and D. Flores. 2019. Hypophysis size evolution in Chiroptera. Acta Chiropterologica, 21(1): 65–74. [nrreyesa@unal.edu.co]

FLIGHT

Cichocki, J., M. Warchałowski, A. Ważna, I. Gottfried, A. Bator–Kocoł, T. Gottfried, A. Koscielska, J. Bojarski, M. Pietraszko-Warchałowski, and G. Gabrys. 2019. Frequent or scarce? Damage to flight–enabling body parts in bats (Chiroptera). PLoS ONE 14(7): e0219783. https://doi.org/10.1371/journal.pone.0219783 [j.cichocki@wnb.uz.zgora.pl]

GENETICS

Endo, K., K. Iida, M. Nunome, Y.-K. Kim, S.-H. Han, J.-H. Sohn, Y. Ohmori, H.-S. Oh, J. Kimura, and E. Hondo. 2019. Phylogeography of *Miniopterus fuliginosus* (Chiroptera) with special reference to Jeju Island, South Korea. Mammalia, 83(6): 610–614. [ehondo@agr.nagoya-u.ac.jp]

Gürün, K., A. Furman, J. Juste, M. J. R. Pereira, J. M. Palmeirim, S. J. Puechmaille, P. Hulva, P. Presetnik, D. Hamidovic, C. Ibáñez, A. Karatas, B. Allegrini, P. Georgiakakis, D. Scaravelli, M. Uhrin, H. Nicolaou, M. R. Abi-Said, Z. L. Nagy, S. Gazaryan, and R. Bilgin. 2019. Phylogeography of the bent-wing bat, *Miniopterus schreibersii* (Mammalia: Chiroptera), using new microsatellite data. Journal of Mammalogy, 100(6): 1865–1878. [kanat.gurun@boun.edu.tr]

Najafi, N., M. Sharifi, and V. Akmali. 2019. First insights into the population genetic structure and the phylogeographic status of the Mehely's horseshoe bat *Rhinolophus mehelyi* (Chiroptera: Rhinolophidae) in Iran inferred from mitochondrial genes. Mammalian Biology, 99: 97–108. [v_akmali@razi.ac.ir]

Torres-Morales, L., A. Guillén, and E. Ruiz-Sanchez. 2019. Distinct patterns of genetic connectivity found for two frugivorous bat species in Mesoamerica. Acta Chiropterologica, 21(1): 35–49. [arualtm@hotmail.com]

HIBERNATION

Meierhofer, M. B., S. J. Leivers, R. R. Fern, L. K. Wolf, J. H. Young, Jr., B. L. Pierce, J. W. Evans, and M. L. Morrison. 2019. Structural and environmental predictors of presence and

abundance of tri-colored bats in Texas culverts. Journal of Mammalogy, 100(4): 1274–1281. [melissa.meierhofer@ag.tamu.edu]

MIGRATION AND HOMING

Avila-Flores, R., A. L. Bolaina-Badal, A. Gallegos-Ruiz, and W. S. Sánchez-Gómez. 2019. Use of linear features by the common vampire bat (*Desmodus rotundus*) in a tropical cattle-ranching landscape. Therya, 10(3): 229–234. [rafaelavilaf@yahoo.com.mx]

Roby, P. L., M. W. Gumbert, and M. J. Lacki. 2019. Nine years of Indiana bat (*Myotis sodalis*) spring migration behavior. Journal of Mammalogy, 100(5): 1501–1511. [plroby@copperheadconsulting.com]

NATURAL HISTORY

Flores-Quispe, M., G. Calizaya-Mamani, G. Portugal-Zegarra, G. A. Alvarado, J. Pacheco-Castillo, and E. M. Rengifo. 2019. Contributions to the natural history of *Mormopterus kalinowskii* (Chiroptera: Molossidae) in the southwest of Peru. Therya, 10(3): 343–352. [fq.marisel@gmail.com]

PALEONTOLOGY

Galán, J., C. Núñez-Lahuerta, R. Moya-Costa, J. M. López-García, and G. Cuenca-Bescós. 2019. Fossil bat assemblages as palaeoenvironmental and palaeoclimatic indicators: A case study in the Lower to Middle Pleistocene Gran Dolina sequence of Sierra de Atapuerca, Northern Spain. Palaeogeography, Palaeoclimatology, Palaeoecology, 535: 109365. [galanj@unizar.es]

Rossi, V., M. E. McNamara, S. M. Webb, S. Ito, and K. Wakamatsu. 2019. Tissue-specific geometry and chemistry of modern and fossilized melanosomes reveal internal anatomy of extinct vertebrates. Proceedings of the National Academy of Sciences, 116(36): 17880–17889. [valentina.rossi@ucc.ie]

PARASITOLOGY

Cai, Y., X. Wang, N. Zhang, J. Li, P. Gong, B. He, and Z. Zhang. 2019. First report of the prevalence and genotype of *Trypanosoma* spp. in bats in Yunnan Province, Southwestern China. Acta Tropica, 198: 105105. [xczhang@jlu.edu.cn]

Clément, L., M. Dietrich, W. Markotter, N. J. Fasel, A. Monadjem, A. López-Baucells, D. Scaravelli, P. Théou, R. Pigeault, M. Ruedi, and P. Christe. 2019. Out of Africa: the origins of the protozoan blood parasites of the *Trypanosoma cruzi* clade found in bats from Africa. Molecular Phylogenetics and Evolution, doi: https://doi.org/10.1016/j.ympev.2019.106705 [laura.clement@unil.ch]

Lopez-Berrizbeitia, M. F., and M. M. Diaz. 2019. Siphonaptera associated with small mammals (Didelphimorphia, Chiroptera, and Rodentia) from northwestern Argentina. Therya, 10(3): 279–308. [mflopezberri@hotmail.com]

Michalik, J., B. Wodecka, J. Liberska, M. Dabert, T. Postawa, K. Piksa, and J. Stańczak. 2020. Diversity of *Borrelia burgdorferi* sensu lato species in Ixodes ticks (Acari: Ixodidae) associated with cave-dwelling bats from Poland and Romania. Tick and Tick-borne Diseases, 11: 101300. [michalik@amu.edu.pl]

PHYSIOLOGY

Miguel, P. H., P. Kerches-Rogeri, B. B. Niebuhr, R. A. S. Cruz, M. C. Ribeiro, and A. P. d. C. Neto. 2019. Habitat amount partially affects physiological condition and stress level in Neotropical fruit-eating bats. Comparative Biochemistry and Physiology, A, 237:110537. [pedrohmiguel2@gmail.com]

POPULATION BIOLOGY

Noroalintseheno Lalarivoniaina, O. S., F. I. Rajemison, R. V. Ramanantsalama, A. Andrianarimisa, and S. M. Goodman. 2019. Population size and survival of the Malagasy fruit bat *Rousettus madagascariensis* (Pteropodidae) in Ankarana, northern Madagascar. Acta Chiropterologica, 21(1): 103–113. [olivasantarni@gmail.com]

REPRODUCTION

Arandas, M. J. G., Á. A. C. Teixeira, V. W. Texeira, F. R. Silva, K. S. N. Marinho, N. B. Lima Junior, F. C. A. A. Júnior, and K. R. P. Santos. 2019. Seasonal influence on testicular morphophysiological parameters of bat *Carollia perspicillata* in fragments of the Atlantic Forest, northeastern Brazil. Pesquisa Veterinária Brasileira, 39(6): 429–433. [julianaarandas@hotmail.com]

Silva, S. F. M. d., M. E. d. L. Vieira, M. B. Freitas, S. L. P. d. Matta, and D. B. Motais. 2020. Duration of the seminiferous epithelium cycle in the frugivorous bat *Artibeus lituratus*. Theriogenology, 142: 363–367. [daniellebmorais@gmail.com]

TAXONOMY/SYSTEMATICS/PHYLOGENETICS

Demos, T. C., P. W. Webala, J. C. K. Peterhans, M. Bartonjo, and B. D. Patterson. 2019. Molecular phylogenetics of slit-faced bats (Chiroptera: Nycteridae) reveal deeply divergent African lineages. Journal of Zoological Systematics and Evolutionary Research, https://doi.org/10.1111/jzs.12313 [tdemos@fieldmuseum.org]

Hutterer, R., J. Decher, A. Monadjem, and J. Astrin. 2019. A new genus and species of vesper bat from West Africa, with notes on *Hypsugo*, *Neoromicia*, and *Pipistrellus* (Chiroptera: Vespertilionidae). Acta Chiropterologica, 21(1): 1–22. [r.hutterer@leibniz-zfmk.de]

Loureiro, L. O., M. Engstrom, B. Lim, C. L. González, and J. Juste. 2019. Not all *Molossus* are created equal: genetic variation in the mastiff bat reveals diversity masked by conservative morphology. Acta Chiropterologica, 21(1): 51–64. [livia.loureiro@mail.utoronto.ca]

Patterson, B. D., P. W. Webala, J. C. K. Peterhans, S. M. Goodman, M. Bartonjo, and T. C. Demos. 2019. Genetic variation and relationships among Afrotropical species of *Myotis*

(Chiroptera: Vespertilionidae). Journal of Mammalogy, 100(4): 1130–1143. [bpatterson@fieldmuseum.org]

Uvizl, M., J. Šmíd, T. Aghová, Z. K. Varadínová, and P. Benda. 2019. Molecular phylogeny and systematics of the sheath-tailed bats from the Middle East (Emballonuridae: *Taphozous* and *Coleura*). Acta Chiropterologica, 21(1): 23–34. [marek.uvizl@gmail.com]

TECHNIQUES FOR STUDYING BATS

Banner, K. M., K. M. Irvine, T. J. Rodhouse, D. Donner, and A. R. Litt. 2019. Statistical power of dynamic occupancy models to identify temporal change: Informing the North American Bat Monitoring Program. Biological Indicators, 105: 166–176. [katharine.banner@montana.edu]

Bartonička, T., N. Miketová, and P. Hulva. 2019. High throughput bioacoustic monitoring and phenology of the greater noctule bat (*Nyctalus lasiopterus*) compared to other migratory species. Acta Chiropterologica, 21(1): 75–85. [hulva@natur.cuni.cz]

Faure-LaCroix, J., A. Desrochers, L. Imbeau, and A. Simard. 2019. Going beyond a leap of faith when choosing between active and passive bat monitoring methods. Acta Chiropterologica, 21(1): 215–228. [julie.faure-lacroix.1@ulaval.ca]

Harrington, A. P., D. B. O'Meara, T. Aughney, K. McAney, H. Schofield, A. Collins, H. Deenen, and C. O'Reilly. 2019. Novel real-time PCR species identification assays for British and Irish bats and their application to a non-invasive survey of bat roosts in Ireland. Mammalian Biology, 99: 109–118. [andrewpharrington16@gmail.com]

Locatelli, A. G., S. Ciuti, P. Presetnik, R. Toffoli, and E. Teeling. 2019. Long-term monitoring of the effects of weather and marking techniques on body condition in the Kuhl's pipistrelle bat, *Pipistrellus kuhlii*. Acta Chiropterologica, 21(1): 87–102. [emma.teeling@ucd.ie]

Schlottau, K., E. Eggerbauer, C. M. Freuling, M. Beer, T. Muller, and B. Hoffman. 2020. Rapid molecular species identification of indigenous bats from Germany for surveillance purposes. Infection, Genetics and Evolution, 78: 104140. [kore.schlottau@fli.de]

Teets, K. D., S. C. Loeb, and D. S. Jachowski. 2019. Detection probability of bats using active versus passive monitoring. Acta Chiropterologica, 21(1): 205–213. [djachow@clemson.edu]

Tuneu-Corral, C., X. Puig-Montserrat, C. Flaquer, M. Mas, I. Budinski, and A. López-Baucells. 2020. Ecological indices in long-term acoustic bat surveys for assessing and monitoring bats' responses to climatic and land-cover changes. Ecological Indicators, 110: 105849. [carme_ctc@hotmail.com]

York, H. A., B. Rodríguez-Herrera, R. K. Laval, R. M. Timm, and K. E. Lindsay. 2019. Field key to the bats of Costa Rica and Nicaragua. Journal of Mammalogy, 100(6): 1726–1749. [heather.a.york@gmail.com]

ANNOUNCEMENTS

Reminder—Renewal Time!

Just a reminder that this is the last issue of the 2019 series of *Bat Research News*. That means many of you will be receiving renewal information in your e-mail inbox fairly soon. We hope you will continue to support *BRN* for the 2020 volume-year. All of us at *Bat Research News* wish you a safe and happy 2020!

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Original research/speculative review articles, short to moderate length, on a bat-related topic would be most welcomed. Please submit manuscripts as .rtf documents to Allen Kurta, Editor for Feature Articles (akurta@emich.edu). Also please consider submitting short articles, notes, or letters on a bat-related topic. If you have questions, please contact Al. Thank you for considering *BRN*.

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Please consider submitting news from your lab group, your field work, or any bat-related news. Thank you in advance for considering us as a place for bat, bat worker, and bat lab news items.

Back Issues

Are you missing any back issues of the print edition of *Bat Research News*? If you would like to replace them, please contact Margaret Griffiths (margaret.griffiths01@gmail.com). Most are available from Volume 45, 2004 through Volume 60, 2019. Depending on what you need, we may ask you to cover postage. We are reducing the inventory of back issues, beginning with the oldest (i.e., Vol. 45, 2004).

FUTURE MEETINGS and EVENTS

2020

The 15th European Bat Research Symposium will be held 3–7 August 2020, in Turku, Finland. Please visit https://www.ebrs2020.fi/ for updates and information.

The **NASBR** will celebrate their **50th anniversary** where it all began, in Arizona. The annual meeting will be held 28–31 October 2020, in Tempe, Arizona, at the Tempe Mission Palms. The NASBR also plans to publish an edited volume that highlights bat biology research to coincide with their 50th annual meeting. Check the NASBR website for more information and updates — https://www.nasbr.org/annual-meetings.

2021

The 51st Annual NASBR will be held in Winnipeg, Manitoba, Canada, dates to be determined. Check the NASBR website for updates — https://www.nasbr.org/annual-meetings.