

**99TH ANNUAL MEETING
& CENTENNIAL CELEBRATION
OF THE
AMERICAN SOCIETY OF MAMMALOGISTS
28 JUNE-2 JULY 2019
HYATT REGENCY WASHINGTON ON CAPITOL HILL
-WASHINGTON, DC-**



ABSTRACT BOOK

The 2019 American Society of Mammalogists Annual Meeting logo was designed by John Megahan. It features the African bush elephant (*Loxodonta africana*), which for decades has welcomed visitors to Smithsonian's National Museum of Natural History. The Smithsonian Institution Building (aka, The Castle) is featured in the background.

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AMERICAN SOCIETY OF MAMMALOGISTS (ASM)

The American Society of Mammalogists (ASM) was established in 1919 for the purpose of promoting interest in the study of mammals.

AN OVERVIEW

In addition to being among the most charismatic of animals, mammals are important in many disciplines from paleontology to ecology and evolution. We, of course, are mammals and thus are in the interesting position of studying ourselves in quest of a greater understanding of the role of mammals in the natural world.

The ASM is currently composed of thousands of members, many of whom are professional scientists. Members of the Society have always had a strong interest in the public good, and this is reflected in their involvement in providing information for public policy, resources management, conservation, and education.

The Society hosts annual meetings and maintains several publications. The flagship publication is the *Journal of Mammalogy*, a journal produced six times per year that accepts submissions on all aspects of mammalogy. The ASM also publishes *Mammalian Species* (accounts of individual species) and *Special Publications* (books that pertain to specific taxa or topics), and we maintain a mammal images library that contains many exceptional photographs of mammals.

We encourage you to peruse the ASM web site (www.mammalogy.org) for information about mammals and the American Society of Mammalogists. Check out our interesting history by clicking on the Our History tab on the Archives Committee page. We hope it will stimulate your interest in mammals and further your appreciation of their importance.

ASM LEADERSHIP

The ASM is led by a group of scientists who are elected by the membership.

ASM COMMITTEES

Much of the work that the ASM does is accomplished through a large number of volunteer committees. These committees work to further the aims of the Society and the science of mammalogy as a whole.

ASM ENDORSES HUMAN DIVERSITY

The ASM is dedicated to ensuring the opportunity for active, equal participation in all ASM functions by all members, regardless of gender, race, ethnic background, age, physical disabilities, or sexual orientation.

<http://www.mammalsociety.org/>

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WELCOME

Dear ASM Attendee,

Welcome to the 99th annual meeting of the American Society of Mammalogists (ASM), our Centennial Celebration! The ASM held its first (organization) meeting at the Smithsonian Institution in April 1919. The ensuing century has been good for the ASM, and the ASM has proven to be a leader in the promotion of mammalogy. Our Centennial Celebration is intended to highlight the current status of this engaging field.

This is our 10th meeting at the Smithsonian Institution; we last met here for our 75th annual meeting in 1994. We held our picnic at the National Zoo, and the rotunda of the National Museum of Natural History provided a fitting venue for our closing social. I look forward to a repeat of these memorable events this year. Given the tremendous diversity that comprises the Smithsonian, I hope you will have the opportunity to come early or stay late and see some of these remarkable museums.

This year's program reflects the diversity that we embrace in the ASM – diversity in our membership as well as our subject animals and thematic pursuits. The ASM has worked diligently to ensure that our annual meetings provide an intellectually exciting and engaging time for all, and that every member feels safe and comfortable at all times. The ASM has always been my “home society” and our meetings feel like an extended family reunion; I hope that you will share this sense of comfort and, indeed, of restoration.

In addition to a record-shattering number of submitted abstracts, we have eight workshops and five symposia scheduled this week. Workshops range from genome assembly and bat acoustics to telemetry, acoustics, scientific communication, student mentoring, and a hackathon for mammal diversity. We also are sponsoring an additional workshop on bias awareness in academia, which will have limited seating, so sign up early. Symposia will be equally dynamic and diverse, focusing on reconciling scientific collecting with conservation, the challenges (and rewards) of integrating museum specimens into global databases such as GenBank and Red Lists, the remarkable Ecuadorian mammal fauna, the hyperdiverse Murinae as a model of adaptive radiation, and the biology of urban mammals. Of course, we will have multiple poster and thematic sessions as well. #ASM100 will be a meeting to remember!

We all come to the annual meeting for a mixture of the scientific and the social but remember that the ASM is a member-run society. You decide our leadership, and you have a voice in how and where we speak up on issues. I encourage you to attend our two Member's Meetings, where your voice and your vote truly counts. You can also make your voice heard through participation in one of our committees. ASM committees are active throughout the year, and they address important matters; if any of these appear particularly interesting to you, I encourage you to introduce yourself to current committee members.

The meeting isn't all work, of course. I hope you brought your running shoes for the annual Run for Research, and that you will join us at the National Zoo for the picnic. We will have various social events for casual conversation as well. The auction and associated social is always a highlight. This year's Capstone will include three speakers, followed by a closing social where we will announce the recipients of our various awards.

Whether this is your first meeting or you're a long-time participant, ASM meetings should be both informational and enjoyable. We pride ourselves on our support of and for students. If you want to meet leaders of this society, please approach and introduce yourself. Nobody has ever caught rabies at an ASM meeting. Hopefully you will become as addicted as I did when I attended my first meeting (HSU – 1984).

Thank you for attending the meeting and making the ASM a priority in your lives. I especially thank our sponsors, exhibitors, and advertisers, whose support is critical to so many of our annual functions. Please take some time during the breaks and socials to visit their tables and displays and let them know how much you appreciate their participation and their support.

Enjoy the meetings, and enjoy the Smithsonian museums!



Douglas A. Kelt
President, American Society of Mammalogists

PROFESSIONAL CODE OF CONDUCT

STATEMENT OF INCLUSION

The American Society of Mammalogists (ASM) prohibits discrimination, harassment, and bullying against any member because of ancestry, color, national origin, marital status, veteran status, gender identity or expression, sexual orientation, race, ethnicity, religion, age, disability, political affiliation or any other characteristic protected by law. ASM expects its employees, volunteers, members and other constituents, whenever and wherever they are conducting Society business or participating in Society events or activities, to maintain an environment free of discrimination, harassment, bullying, or retaliation.

CODE OF CONDUCT

Ethical professional conduct is expected of all participants at ASM sponsored activities, including the annual meetings. Professional conduct applies to all professional, research, and learning environments. ASM is dedicated to ensuring the opportunity for active, equal participation in all ASM functions by all members, regardless of gender, race, national origin, ethnicity, age, physical appearance, disability, or sexual orientation. Discrimination and harassment are prohibited by the ASM; no individual should feel harassed, threatened, or unsafe at any ASM sponsored activity. All ASM members and participants in ASM sponsored activities are expected to follow the most recent version of ASM Professional Conduct policies (see QR Code and link below).

GENERAL GUIDELINES

1. ASM aims to operate in the best interest of the Society and its membership through policies and procedures, which are continually updated.
2. Unprofessional conduct by any ASM member or meeting attendee will not be tolerated and is subject to disciplinary action. Unacceptable behavior includes, but is not limited to, unwanted verbal attention, unwanted touching, intimidation, stalking, shaming or bullying in person or through social media outlets. If you experience such behavior, depending on the context and if you feel comfortable, you should let the offender know and tell him/her to stop and/or seek help from bystanders. Participants asked to stop any harassing behavior are expected to comply immediately. Concerns can also be presented to the Ombudspersons in person (contact information below) or reported anonymously online (see QR Code Below). Note that persistent offensive or unwelcome behavior may constitute harassment and that harassment presented in a joking manner is still harassment and both would be subject to disciplinary action.
3. Scientific presentations are expected to adhere to ASM standards of professional conduct and should not include inappropriate and/or graphic images or language that include (but are not limited to) pornography, demeaning or degrading images or language, or depictions of violence.
4. Established professionals and all ASM leaders should recognize that they hold positions of power, formal or informal, over students and aspiring professionals. These individuals are expected to lead by example regarding our high standards of professional and personal conduct.
5. All ASM members are potential bystanders to unprofessional or unwelcome behavior. Bystander intervention can prevent, divert, or mitigate harassment. Please do not look the other way.

REPORTING MISCONDUCT

Concerns or allegations of misconduct or harassment should be directed the Office of the Ombudsperson (John L. Koprowski [squirrel@ag.arizona.edu] and Jessica E. Light [jlight2@tamu.edu]) or reported anonymously online (see QR Code and link below).

ASM PROFESSIONAL CONDUCT POLICIES



<https://tinyurl.com/y4xbfm2j>

ASM ANONYMOUS ONLINE REPORTING



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ABSTRACTS

1^{HTA}: Forest structure and snow depth alter the movement and subsequent expenditures of a forest carnivore

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Achieving energetic balance is central to the survival, persistence, and ecology of free-ranging mammals. Approaches used to estimate expenditures in wild mammals are generally precise, but difficult to implement. The concurrent use of GPS-collars and accelerometers has emerged as an alternative for estimating expenditures, but has few validated applications in terrestrial mammals. To test the efficacy of movement characteristics in describing expenditures of a forest carnivore, the Pacific marten (*Martes caurina*), we concurrently implemented the doubly-labelled water technique to estimate field metabolic rate (FMR) and collected GPS-collar data (n=8). Then, we used a simple but explanatory linear model (FMR ~ movement velocity) to estimate expenditures of previously collared martens (n=32 individuals on 47 occasions). We also quantified the effects of influential landscape characteristics, such as forest openness and snow-depth, on expenditure. Average FMR (\pm SD) of female and male martens was 627 kJ (\pm 142 kJ) and 913 kJ (\pm 62 kJ), respectively. Movement velocity explained the majority of variation in FMR ($R^2=0.69$). Mass-specific FMR was positively related to both snow-depth (cm: $\beta=1.39 \pm 0.42$, $P<0.002$) and openness of used areas (%: $\beta=8.29 \pm 3.32$, $P=0.02$). Our work demonstrates that movement metrics can effectively explain variation in FMR and shows that landscape features influence the movement and consequent expenditures of martens. Our findings highlight the importance of energetics in forest carnivores, especially in rapidly changing landscapes. This research was not supported by an ASM grant, but culminated in the lead author receiving the Annie M. Alexander award in 2019.

2^{HTA}: An early burst of morphological diversification in a skeletal novelty in bats**

Kathryn Stanchak^{1,2}, Jessica Arbour¹, Sharlene Santana^{1,2}

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The role of novelty in evolution has long been debated among biologists. Neomorphic anatomical elements are scattered throughout the historical evolutionary record, but whether they impact the evolutionary trajectories of their respective clades is poorly understood. Here, we explore the anatomical diversification of the calcar—a neomorphic skeletal element found in the feet of bats (Chiroptera)—to clarify whether novel skeletal additions can become integrated into vertebrate body plans and subsequently evolve into a variety of forms. To reveal the macroevolutionary patterns that characterize calcar diversification, we examined variation in the length of the calcar across Chiroptera (1,392 specimens; 226 species; 21 families) and tested different models of calcar length evolution. We also investigated the anatomical diversity of the calcar with microCT scans (22 species; 16 families) and histological sectioning (18 species; 13 families). We found that calcar length diversified early in the evolutionary history of bats, mirroring patterns of species diversification documented in the fossil record. Our detailed anatomical studies revealed diversity in both structural and material parameters that might plausibly affect calcar function. This raises the possibility that the burst of morphological diversification in the calcar was adaptive, and that early in bat evolutionary history the calcar became an important part of the suite of adaptations that allowed bats to radiate. This research was supported by an ASM Grant-in-Aid of Research awarded to Kathryn Stanchak in 2017.

3^{E,HTA}: Dietary morphology of two island-endemic rodent clades is consistent with a persistent, incumbent-imposed biotic filter**

Dakota Rowsey¹, Lawrence Heaney², Sharon Jansa¹

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A lineage that colonizes a system in the absence of competitors may exhibit rapid diversification due to greater ecological opportunity to exploit underutilized resources. The resultant species diversity of this primary-colonizing (incumbent) clade may limit the ability of subsequent lineages to persist unless these

non-incumbent lineages are ecologically distinct. We compared the mandibular shape diversity of two sympatric clades of murine rodents endemic to Luzon Island, Philippines - incumbent Phloeomyini and secondary-colonizing Chrotomyini - to the Sahul “Old Endemic” (SOE) rodents, the sister clade of Chrotomyini and incumbent murine lineage on the Sahul supercontinent. This three-clade comparison allowed us to test the hypothesis that incumbent lineages force persistent ecological distinction of subsequent colonists both at the time of colonization and throughout the subsequent sympatry between the two clades. We recovered strong support for this hypothesis, finding both that Chrotomyini constitutes a biased subset of the total diversity of their clade plus the SOE to minimize overlap with Phloeomyini, as well as recovering this distinction has persisted through time from the stem ancestor of Chrotomyini and SOE. The patterns of dietary variation in these clades reveal that incumbency may have a prominent influence on the diversity of faunal assemblages at the island scale, and that lineages that pass this biotic filter may diversify freely provided they do so in ways that maintain distinction from incumbent species. This research was supported by an ASM Grant-in-Aid of Research and the A. Brazier Howell Award awarded to DMR in 2016 and 2019 respectively.

4^{HTA}: Loosening the Macroevolutionary Ratchet**

Brian Tanis¹, Larisa DeSantis², Rebecca Terry¹

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The macroevolutionary ratchet, exemplified in Canidae, is a pervasive pattern of clade replacement whereby increasingly specialized species are driven to extinction and replaced by younger, more generalized species. However, specialization and its link to extinction has traditionally been inferred from morphological traits rather than from direct dietary reconstructions. Dietary plasticity, which isn't captured by morphology, truly defines dietary specialization of species. We tested the association between specialization and extinction by quantifying the dietary niche of 9 extinct and 4 extant North American canids spanning 33.3 million years of evolution using Dental Microwear Texture Analysis (DMTA). DMTA quantifies microscopic wear patterns on tooth enamel to capture a comprehensive picture of dietary resource use. Species dietary specialization was calculated using multi-dimensional Bayesian ellipsoid volumes of DMTA parameter space and correlated with their duration as estimated using PyRate. We found dietary specialization as inferred from DMTA to be a better predictor of species duration than morphology. Counter to expectations, we observed a positive correlation between specialization and lineage duration, and that specialization was not correlated with traditionally-used dietary categories (i.e. hypo-, meso-, or hypercarnivory). Our results contradict the macroevolutionary ratchet hypothesis, suggesting that overspecialization in diet alone was not enough to drive iterative extinctions in canids. Instead, we suggest that dietary specialization offers selective advantages that facilitated the coexistence of a diverse canid community through time. This research was supported by a Grant-In-Aid of Research awarded to Brian Tanis in 2015.

5: Ecology and conservation of African lions exposed to poaching and pastoralism**

Kristoffer Everatt

Nelson Mandela University, Port Elizabeth, EC, South Africa. Panthera, New York, NY, USA

Apex predators are crucial for maintaining ecological patterns and processes, yet humans hinder their ability to fulfill this role by displacing them from the landscape. Many apex predator species such as African lions (*Panthera leo*) are experiencing catastrophic declines as a result of competition with growing human populations. We investigated the relative and cumulative influences of anthropogenic pressures on lion occurrence across a 73 000 km² multi-use landscape in southern Africa using occupancy models from replicated detection/non-detection spoor surveys. We hypothesized that lions were most limited by 1) interference competition, or 2) exploitive competition with humans. Interference competition with pastoralism was the biggest driver limiting lion occupancy, with a clear disturbance threshold for lions resulting in the near complete loss of lions from the landscape where cattle surpass 20% occupancy. This study emphasizes the top-down impacts of the human ‘super-predator’ on apex carnivores. Using abundance and mortality data collected from 2011-2018 and found that the sub-populations of lions which are exposed to poaching and pastoralism have declined by up to 68%. The targeted poaching of lions for body parts was the greatest single cause of death, with associations between lion-livestock conflict and a

trade in lion body parts. To counter this immediate threat to the viability of this lion population, we have initiated a dedicated lion protection anti-poaching project.

6^{E}: Episodic gene flow repeatedly impacts the evolution of high-latitude mesocarnivores**

Jocelyn Colella

University of New Mexico, Albuquerque, NM, USA. Museum of Southwestern Biology, Albuquerque, NM, USA. University of New Hampshire, Durham, NH, USA

How does hybridization and the transfer of genetic material between species (i.e., introgression) influence mammalian evolution? The consequences of hybridization are relatively well studied in plants, with outcomes ranging from hybrid vigor and occasionally speciation to the complete fusion of previously distinct lineages. Once thought to play a relatively minor role in mammalian evolution, genomic investigations have recently highlighted the ubiquity of hybridization, suggesting that identifying instances of introgression (e.g., humans and Neanderthals) may be critical for understanding evolution and processes of diversification. Here, I investigate introgression dynamics in multiple meso-carnivores, ermine (*Mustela erminea*) and marten (*Martes americana* and *M. caurina*). Four ermine lineages and two marten species diverged during refugial isolation in the Late Pleistocene, and both clades subsequently formed insular and mainland hybrid zones in North America. We use whole-genome sequences and geometric morphometrics to contrast introgression dynamics between these clades to understand the role of periodic gene flow in high-latitude evolution. We identify evidence of repeated introgression with varying evolutionary consequences, ranging from hybrid speciation to apparent genetic swamping. These refined historical perspectives provide a foundation for future research and management of these species, given recent actions that may impact these species (e.g., widespread translocations, habitat modification, potential pathogen introductions). This research was supported by the Shadle Fellowship awarded to Jocelyn P Colella in 2018.

7^{E}: Interactions between invasive *Opuntia stricta* and native mammals in Central Kenya**

Anne-Marie Hodge

University of Wyoming, Laramie, WY, USA

Introduced plants often interact with native pollinators and seed dispersers, facilitating further establishment and spread. Prickly pear cactus (*Opuntia stricta*) was introduced to Kenya in the 1940s. We assessed how dispersal by olive baboons (*Papio anubis*) affected the dominant mode of reproduction in *O. stricta*, which reproduces both sexually and asexually. *Opuntia stricta* density and relative abundance of seed-derived individuals (from sexual reproduction) were significantly higher at baboon roosts than control sites, suggesting that baboons disperse *O. stricta* seeds and facilitate sexual reproduction. Recent biocontrol efforts target mature plants, and by identifying factors that influence relative abundance of seed-derived individuals, future control efforts can target areas with substantial deposits of seeds that could regenerate the population in the future. We also investigated how a biocontrol campaign using the hemipteran *Dactylopius opuntiae* affected *O. stricta* density and fruit availability, as well as mammal visitation to infested areas. *Opuntia stricta* declined significantly after the initiation of biocontrol. We found a negative functional response in visitation associated with *O. stricta* declines. Baboons consumed *O. stricta* out of proportion to its availability, and post-biocontrol scats contained seeds of native fruits that were absent from all pre-biocontrol samples, suggesting that baboons compensate for lower *O. stricta* availability by increasing consumption of native species. These findings highlight the reach of both biological invasions and subsequent biocontrol efforts on mammal activities throughout an ecosystem. The research was supported by Grants-in-Aid awarded to Anne-Marie Hodge in 2013 and 2015, and an ASM Fellowship awarded to Anne-Marie Hodge in 2017.

8^{}: Mammals on mountainsides revisited: functional diversity gradients and change in Great Basin small mammal communities**

Brooks Kohli

University of New Hampshire, Durham, NH, USA

Understanding how biodiversity is distributed, maintained, and altered is a fundamental goal of ecology that is especially important during the current period of rapid environmental change. Traditionally, diversity has been described in taxonomic terms using the number and abundance of species (e.g., species richness).

However, biodiversity is multi-faceted and includes functional (ecological traits) and phylogenetic (evolutionary relationships) dimensions that emphasize the similarities and differences among species. Functional diversity is particularly appealing because it quantifies the range and prevalence of traits in an assemblage and helps link patterns of diversity to the ecological processes that generate them. I leveraged a multi-dimensional diversity approach to investigate elevation-diversity patterns, community assembly processes, and change in small mammal communities over the last century in three mountain ranges in the Great Basin of western North America. In contrast to the well-established mid-elevation peak in species richness, functional and phylogenetic diversity generally increased with elevation. This suggests that the various dimensions of diversity are regulated by different processes. The functional structure of these assemblages was most strongly influenced by environmental factors, but competition also played a role. Over time, climate and habitat change led to decreases in small mammal functional diversity despite stability of species richness. Functional restructuring of communities likely represents an early warning of more dramatic diversity declines and helps to identify specific mechanisms of change. This research was supported by an ASM Fellowship awarded to Brooks Kohli in 2018.

9: Advantages of 3D microCT imaging for studying prenatal development in bats

James Ryan

Hobart & William Smith Colleges, Geneva, New York, USA

The nearly 6,400 species of mammals exhibit tremendous morphological diversity. Despite the important role of early embryonic development in shaping adult diversity, embryonic development has been studied in only a few mammalian species. Bat development, in particular, remains poorly known. Traditional staging charts based on external morphology have been produced for a number of bat species including *Carollia perspicillata*. While these staging systems provide useful guides for embryological studies, they lack the internal anatomical details provided by three-dimensional microCT imaging. Here, a series of *Myotis lucifugus* embryos is used to demonstrate the advantages of using microCT imaging for studying mammalian prenatal development. MicroCT imaging is a non-invasive technique that does not require difficult and lengthy dissection yet affords accurate and detailed three-dimensional views of the smallest mammalian embryos. MicroCT can resolve details with resolutions up to 1.5 $\mu\text{m}/\text{voxel}$. In addition, internal organs can be segmented to yield accurate volumes for each organ. Furthermore, microCT volumes provide information on the timing of development of internal structures such as aortic arches, sensory structures (e.g. cochlea), and brain regions. Finally, because the technique is non-destructive, it does not compromise valuable museum specimens.

10^E: Reassessing the taxonomy of Caucasian tur by means of cranial morphometry

Kai Caspar^{1,2}, Eva Bärmann¹

¹Section of Theriology, Zoological Research Museum Alexander Koenig, Bonn, North Rhine-Westphalia, Germany. ²Department of General Zoology, University of Duisburg-Essen, Essen, North Rhine-Westphalia, Germany

Caucasian tur are wild goats occurring in the Greater Caucasus mountains. Traditionally, these animals are grouped as two parapatric species, *Capra caucasica* and *Capra cylindricornis*, which are assumed to hybridize at the shared border of their ranges East to the Elbrus massive. While remarkably similar in general morphology and ecology, these two groups differ profoundly in the males' horn shape. However, tur taxonomy is not consolidated and it remains unclear if the mentioned groups represent distinct species or result from clinal variation of just one. Here we show that *C. caucasica* and *C. cylindricornis* are distinct taxonomic entities by applying morphometric methods to the largest sample of crania of these wild goats yet studied, encompassing 107 skulls. A notable overlap in character variance is observable, which likely reflects a very recent split of Eastern and Western tur populations. Nevertheless, both sexes in the two species can clearly be separated in a discriminant function analysis and display several diagnostic traits which distinguish them from each other. Skull morphology does not vary in the same fashion as horn shape, which follows a latitudinal cline. Instead, individuals originating from identical localities can vary greatly in their craniomorphometric traits. Upcoming sequencing of the studied tur material from diverse localities will complement the morphometric dataset, aiming to create a comprehensive picture of the phylogeography of these enigmatic mountain ungulates.

11: Whale watching tours, conservation attitudes, and cetacean behavior in Kenai Fjords Alaska

Lauren McCaslin, Bruce Schulte

Western Kentucky University, Bowling Green, KY, USA

Marine mammals are in a precarious conservation position because of historic and current anthropogenic activities. Conservation legislation has helped protect species, but the greatest public ground swelling may be evident through the advent of the commercial whale watching industry. The summer feeding grounds around Seward Alaska have made this area a prime tourism location. These protected waters have a confluence of marine mammal species, including the appealing and abundant humpback whale (*Megaptera novaeangliae*) that may associate with three ecotypes of killer whales (*Orcinus orca*). These species may travel together to feed or be adversaries in a predator-prey relationship. Using whale watching as a platform, this study evaluated the effects of the presence of these two species separately and together, and of the type of interaction between them, on human perception. Data were collected via opportunistic observations and a pre- and post-survey instrument. Both species were often observed travelling and tourists reported enhanced conservation attitudes after whale watching tours. These tours provide an opportunity for collecting meaningful scientific data and providing more in-depth education such as enhancing the appreciation for ecosystem services provided by marine mammals.

12: The mammal collections at Instituto Politécnico Nacional, México

Celia Lopez-Gonzalez¹, Cynthia Elizalde-Arellano², Miguel Briones-Salas³, Juan Lopez-Vidal²

¹CIIDIR Unidad Durango, Instituto Politécnico Nacional,, Durango, Durango, Mexico. ²Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, Mexico City, Mexico City, Mexico. ³CIIDIR Unidad Oaxaca, Instituto Politécnico Nacional,, Oaxaca, Oaxaca, Mexico

We summarize the scientific achievements of the mammal collections at Instituto Politécnico Nacional. The oldest, at Escuela Nacional de Ciencias Biológicas (ENCB), was founded in 1955. CIIDIR Durango (CRD) followed in 1984, and CIIDIR Oaxaca (OAXMA) in 1985. In 2018, they held 61,267 catalogued specimens (43,985, 12,160, and 5,122 respectively). Together they are the largest mammalian repository in Mexico. Individually, ENCB is the second largest in the country. All Mexican terrestrial orders are represented, as well as 145 genera (84%) and 343 species (69.1%), 108 of which are endemic (62%). All Mexican states are represented; CRD covers mostly the north, ENCB mostly central and southeastern Mexico, and OAXMA the southeast. Their personnel have conducted 89 research projects, and mentored 95 thesis and dissertations; 30 more, from other institutions, used specimens under our care. At least 285 peer-reviewed publications have used specimens deposited in our collections. OAXMA and CRD have tissue collections with over 9,000 samples. All three meet most curatorial standards, but lack some basic ones, which threatens their long-term existence. Our results are the basis to establish a sound institutional policy to ensure that these and other institutional collections are prepared to face the challenges of the XXI century.

13^F: Species accumulation analysis for endoparasites of North American pocket gophers (Rodentia: Geomyidae)

Altangereh Dursahinhan, Sebastian Botero-Canola, Scott Gardner

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Species of the family Geomyidae, known collectively as “pocket gophers,” are a monophyletic group of subterranean/fossorial rodents that inhabit a wide geographic range, extending from a northernmost limit in southwest and south-central Canada through United States, throughout the west, south through Mexico and Central America into Panama and northern Colombia. The family includes six genera and about 45 species. Relative to the importance of these rodents through the Nearctic and northern Neotropical ecological landscapes, the study of endoparasite diversity of pocket gophers is incomplete. A species accumulation curve was produced incorporating more than 47 species of endoparasites collected from the literature representing good data on 14 species of pocket gophers from a wide range of habitats distributed throughout the Nearctic and northern Neotropics. Our analysis of data from a literature search shows that the expected species accumulation curve for parasites of these mammals has not yet reached an asymptote, indicating the recorded diversity will likely increase as more gophers are collected and necropsied. We also summarize the network analysis of the host-parasite ecological interactions that we

observed from the connectivity patterns among species of Geomyidae. The results show that both *Thomomys talpoides* and *Geomys bursarius* have larger networks of parasite-ecological connections than other species of gophers. This may be due to actual biology, or the fact that sampling of endoparasites has not been comprehensive.

14: Melanocortin-1-receptor (MC1R) gene sequence variation in native and introduced populations of *Sciurus carolinensis*

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The eastern gray squirrel (*Sciurus carolinensis*) is native to North America. This species was introduced to multiple locations in Britain during the 1800s, and it has since spread throughout most of the island. As part of a larger study, we sequenced the melanocortin-1-receptor (MC1R) gene in populations of *S. carolinensis* from the United States and Britain. MC1R encodes a key regulatory protein involved in fur color; a 24-basepair deletion in this gene is associated with melanism in *S. carolinensis*. We extracted DNA, amplified the MC1R gene by polymerase chain reaction, and sequenced MC1R alleles from 118 animals: 37 from 7 states in the U.S. and 81 from 4 counties in Britain. We identified 11 alleles in the U.S. populations; only 5 of these alleles were present in the British populations. We detected 12 variable sites, 11 of which were single nucleotide polymorphisms; the other 1 was the 24-basepair deletion. Only 2 polymorphisms were non-synonymous. As expected, variation in native populations was higher than in introduced populations. Evenso, we documented a surprisingly high number of MC1R alleles in Britain, given the small numbers of animals in the founding populations. The high level of synonymous substitutions suggests that this gene is under purifying selection. Furthermore, all melanic animals were associated with the 24- basepair deletion, suggesting that this deletion is a relatively recent mutation.

15^E: Range dynamics of a high-elevation rodent (*Neotoma mexicana*) in the American Southwest

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The geographic distribution of species is dependent on numerous biotic and abiotic factors that comprise a species' fundamental niche. Elevation can dictate where species live and move, as it is associated with hypoxia and temperature differentials. The negative relationship between temperature and elevation creates ecological separation along elevational gradients. Under projected climate warming scenarios, North American species are hypothesized to potentially expand their ranges northward and/or contract their southern ranges to higher elevation areas. The American Southwest is a region with tremendous topographical relief, resulting in the convergence of biomes (e.g. deserts, mixed conifer and alpine forests). The Mexican woodrat (*Neotoma mexicana*) is found in the coniferous forests of the Southwest at higher elevations relative to the distantly related, but largely parapatric white-throated woodrat (*N. albigula*). Their area of sympatry is narrow, suggesting these species maintain distinct elevational zonation. In this study we compare the evolutionary histories of two *Neotoma* species to determine the direction and extent of post-glacial population expansion in the Southwest. We examine the occurrence of these two species in the mountains and surrounding lowlands of New Mexico. Using museum specimens, we confirm morphological identification of species with mitochondrial DNA sequences and then test whether these species conform to post-glacial expansion expectations with regard to elevation. Our results contribute to the understanding of species range limits in an ecologically diverse region.

16^E: Fecal microbial communities differ by intrinsic and extrinsic variables in *Urocyon littoralis*

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This project investigates the scat microbiome of *Urocyon littoralis* (island fox) to find correlations with extrinsic (island environment, captivity, collection time) and intrinsic variables (sex, age, weight). Paired samples of *U. littoralis* blood and scat were collected from the Channel Islands, along with scat samples of captive *U. littoralis* specimens in zoos and mainland *Urocyon cinereoargenteus*. The fox exome was sequenced from blood samples using commercial *Canis familiaris* baits, while bacterial 16S rRNA v4

amplicons were sequenced from scat samples. Both the *U. littoralis* scat microbiome and exome significantly differed by geographical origin, and genetic distance of the exome correlated with Euclidean distance of the 16S community across all islands. Significant differential bacterial abundance was also found between males and females on Santa Catalina, fall and winter samples on Santa Rosa, and low and medium weight samples on San Clemente. Captivity and species were not found to be significant correlates.

17: Evolutionary analyses unveil the molecular mechanism of fast inactivation in calcium-permeable TRP channels

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Fundamental for calcium homeostasis in vertebrates, TRPV5 and TRPV6 are calcium-selective ion channels belonging to the Transient Receptor Potential (TRP) gene family. Detailed phylogenetic analysis suggests that duplications from which TRPV5 and TRPV6 originated occurred independently in the ancestors of mammals, sauropsids, amphibians, and chondrichthyans. Coincident with the conquest of land and the physiological changes needed to maintain calcium homeostasis, our expression analyses suggest a change in the expression pattern from gills to kidney. Within amniotes, we identified a traceable sequence signature of three amino acids at the amino-terminal intracellular region that correlates well with both of the duplication events and the phenotype of fast inactivation observed in TRPV6 channels. Electrophysiological recordings and mutagenesis suggest that calcium-induced fast inactivation is an evolutionary innovation that emerged independently from each duplication event. Molecular dynamics simulations suggest that calcium-induced channel rearrangements are important modulatory regions of TRP channels.

18: Caching and building behaviors of woodrats in captivity during longer term studies

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The woodrat (genus *Neotoma*), is known for its prolific caching and building behaviors. While these behaviors have been studied in both natural and lab settings, the majority of studies lasted only a few days. We therefore completed longer term (2 week) caching and building trials utilizing large double-decker cages. Woodrats were provided with a mixture of essential items (cotton and sticks for nest building) and non-essential items (jingle bells) over two trials. We compared speed of caching between animal groups (*N. albigula* and two populations of *N. lepida*), caching items, and experimental trials. We also categorized level of organization and nest building at the end of each trial. We found that all woodrats demonstrated significant and observable caching and building behavior during the trials. As expected, essential items were cached more quickly than non-essential items. During the second trial, both species cached the non-essential items more quickly than during the first trial, showing that experience mattered. Based on field observations, we expected *N. lepida* to display more organized caching and building behavior than *N. albigula*. However, we found that during the first trial, *N. albigula* was more likely to make large, well-built nests than *N. lepida*. Overall, the large double-decker cages serve as ideal home cages for woodrats by allowing them to express innate caching and building behaviors.

19^E: Genetic diversity of blue wildebeest (*Connochaetes taurinus*) in the Liuwa Plains of Zambia

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The blue wildebeest (*Connochaetes taurinus*) acts as a keystone species in the savannahs of southern Africa, where it maintains shortgrass plains by grazing and serves as the primary prey source for the region's carnivores. Though the second largest wildebeest migration occurs in the Liuwa Plains of western Zambia, this population remained largely unstudied until recently. Monitoring efforts in the field have increased understanding of survival, movement, and resource dependence, but the level of genetic diversity and patterns of gene flow in this population remain unknown. Few genetic studies have been conducted on wildebeest elsewhere in their range, particularly for a large, migratory population such as this. We used

restriction-site associated DNA sequencing (RAD-seq) to assess genetic diversity, population structure, and demographic history of blue wildebeest in Zambia. Next generation sequencing of DNA from 85 wildebeest generated a dataset of 220 million sequence reads, from which we identified 1,980 high-quality polymorphic RAD loci. We analyzed 3,351 single nucleotide polymorphisms (SNPs) within these loci to quantify genetic variation in Liuwa Plains wildebeest, calculate effective population size, test for historical demographic change, and assess population structure. This genetic information could supplement data collected in the field to assist in developing effective conservation plans for wildebeest as they face threats of habitat destruction and overhunting.

20^E: Estimating white-tailed deer population sizes using unmanned aerial vehicles (UAVs)

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Estimating population sizes, recruitment, and sex ratios is essential for managing wildlife populations. Helicopters are commonly used to conduct surveys of white-tailed deer; however, they are expensive, risky, and not always practical. Camera surveys and spotlight counts are also used but are labor intensive. Unmanned aerial vehicles (UAVs) are an emerging technology that has yet to be fully evaluated for wildlife surveys in Tamaulipan thornscrub. We conducted UAV surveys on 5 ranches with known numbers of deer. Surveys were conducted in November and February to assess count variation with changes in canopy coverage. Further, daytime and nighttime surveys were conducted on each ranch to evaluate variation under different conditions. The UAV was equipped with a dual thermal and optical video camera. Heat signatures were detected on the thermal imagery, then identification was confirmed, when possible, via optical imagery. Our UAV counts were compared to raw counts from September helicopter surveys. Preliminary data shows 10.5% difference in daytime vs nighttime counts on the first ranch analyzed. During the daytime survey, 51.9% of thermal heat signatures were identified in optical footage giving us a 6.2% difference between confirmed ID detections and the raw helicopter counts. Daytime and nighttime thermal-only detections were 57.8% and 48.0% higher than the raw helicopter counts, respectively. Further analysis is in progress and additional results will be discussed.

21: Adaptive management to promote an imperiled native cottontail over a non-native competitor

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The New England cottontail (*Sylvilagus transitionalis*) is a shrubland obligate species that has experienced drastic population declines in the last century notably due to forest maturation and anthropogenic development. The species also faces widespread invasion of their historic range by eastern cottontails (*Sylvilagus floridanus*), an introduced species occupying similar habitat. Recent research in New York strongly suggested that as a result of competitive interactions with eastern cottontails, the niche of the New England cottontail has shifted from open, low-canopy closure early successional shrublands to older, high-canopy closure shrublands. Management strategies retaining a higher degree of residual canopy closure may lessen competitive interactions, as eastern cottontails avoid such shrublands; however, these areas may not provide high quality forage and cover resources for New England cottontails. We evaluate the effectiveness of forest management strategies prescribed to promote New England cottontails over eastern cottontails. Both species were trapped and outfitted with radio-collars within designated management and control areas. Resting and active locations were obtained each week for individuals, and vegetation surveys were conducted to assess used and available resources. By comparing cottontail resource selection among plots with varying types of management and population sizes of eastern cottontails, we will inform land managers and owners of the effectiveness of current management practices for New England cottontails, and provide guidance for improving cover and food resources to promote populations.

22^{E,HTA}: Genetic data reveal paraphyletic taxa and cryptic species diversity in the greater galagos (*Otolemur garnettii*)

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Primates are one of the most diverse mammalian radiations, yet our understanding of phylogenetic relationships within several primate clades remains unclear. Galagids are small nocturnal primates from sub-Saharan Africa characterized by high levels of cryptic species diversity. This is the case of the neglected *Otolemur* clade (greater galagos), where deficient geographic sampling and taxonomic assessments based on conserved morphological attributes obscure true species diversity. We present the first comprehensive genetic sampling ($n = 64$) of *Otolemur garnettii* across continental and insular Kenya and Tanzania to elucidate evolutionary relationships among three subspecies traditionally delimited based on distributions and morphology (*O. g. panganiensis*, *O. g. garnettii*, *O. g. lasiotis*). We sequenced ~2.5kbp of the mitochondrial genome (encompassing cytochrome b gene and the d-loop hyper-variable region I) to infer phylogenetic relationships under a Bayesian framework. Preliminary results suggest that specimens from Kenya (corresponding to *O. g. lasiotis*) form a clade. However, samples from mainland Tanzania (*O. g. panganiensis*) form two paraphyletic clades, one of which is sister to all other samples. Furthermore, samples from Zanzibar (*O. g. garnettii*) were recovered nested within mainland Tanzania samples (*O. g. panganiensis*). Our findings indicate paraphyletic taxa in *Otolemur* and suggest that geographically delimited subspecies do not correspond to natural groups. This investigation supports that the incorporation of genetic data will further our understanding of Galagidae systematics, evolutionary history, and biogeography.

23: Mammals behind bars: teaching marine mammalogy in a super-maximum security prison

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Many studies report that prison education significantly reduces recidivism and lowers violence amongst incarcerated individuals within a prison environment. Prison education in the science disciplines presents challenges in that hands-on, active learning opportunities are rare because of the inherent security risks that laboratory-based courses present (i.e., use of museum specimens, laboratory equipment, chemicals, etc.). Many of the students in this program have limited formal schooling and none have completed a college-level biology course. Here I present information on the implementation, obstacles encountered, and successes of teaching a college-level, non-majors course in marine mammalogy at Pelican Bay State Prison, the only supermax prison in California. This course offers incarcerated students the opportunity to practice science literacy and critical thinking skills in an environment that fosters scholarship, collegiality, and personal growth. Although this course does not have a laboratory component, integration of museum specimens (e.g., bones, teeth, baleen) into the curriculum allows students to get hands-on experience with identification skills and offers insight into the biology of marine mammals. This course has been taught three times without incident and fulfills the non-majors science requirement for students interested in earning an associate's degree.

24^E: Temporal prevalence of ecto-parasites considering mammal community turnover and woody encroachment within the Great Plains

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Human practices (development, agriculture, cessation of burning) have fragmented Native Prairie habitats through the Great Plains. Consequences include woody encroachment, mosaic communities of grassland and woodland mammals, and increase in zoonotic pathogens. We present a first diagnosis of ectoparasite prevalence across a prairie-woodland experimental landscape to investigate the influence of climate, mammal host, and habitat on parasite distributions. We test hypotheses: H_0 : Distribution of ectoparasites will be uniform across habitats (suggesting host generalists across mammals); H_1 : Ectoparasites will have a greater density in woody habitats (reflecting the observation that both woody encroachment and vector-borne disease are increasing); H_2 : Ectoparasite distributions will be variable across groups (e.g., fleas vs. ticks), habitats, and years. Small mammals were sampled for two years across three prescribed fire treatments including annual, 4-year, and 20-year burns on Konza Prairie LTER. All fleas, ticks, lice, and mites were collected from small mammals, separated by group and quantified by both presence/absence, and general densities (low, medium, high). We analyzed differences among years, fire treatments, and small mammal species, using pairwise and multi-variate statistics. Preliminary results indicate that in years with low rainfall and mammal density, ectoparasites persist primarily in woody habitats. In productive years

with high mammal densities, ectoparasites are more widespread across habitats but exhibit group-specific trends. Woody encroachment appears to increase source habitats for maintaining prevalence of parasites through time.

25^F: What are the evolutionary origins of Kansas mammals? Community assembly dynamics through the Great Plains

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The Great Plains, ranging through the center of North America, support both grassland and woodland mammal species that often have broad distributions, and high intra-specific diversity with multiple geographic lineages. Purely endemic communities should be more stable and exhibit shared evolutionary histories. Mixed communities with species having distant origins may reflect community turnover, and higher potential for new interactions, including transfer of parasites across the continent. We test the competing hypotheses: H0: Lineages within small mammal species in northeast Kansas all share the same origins; H1: Lineages have varying evolutionary histories, stemming from different geographic origins through North America. Small mammals from eight species were sampled from a mosaic of multiple habitat types (grassland, shrubland, woodland) across the Konza LTER site. We extracted DNA from five individuals of each species, and sequenced the Cytochrome-b gene, a common barcode locus for mammals. For each species, we downloaded existing range-wide sequence data from GenBank, and estimated phylogenetic trees using Bayesian methods, to assess lineage placement of Kansas specimens. Preliminary results indicate multiple geographic and evolutionary origins among current prairie mammals, indicating community mixing through time. Increasingly heterogeneous habitats through the Great Plains due to human land practices will promote continued mixing of mammals with distant origins across North America, increasing new host-parasite associations, and risk of emerging disease.

26^F: Analyzing the cortisol profile in wild vs. captive North American porcupines

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Cortisol, its production and its effects are being discussed more frequently as studies share new findings about stress. Wildlife, like the North American porcupine (*Erethizon dorsatum*) experience harsh conditions throughout the cold winters in northern New York, likely leading to higher cortisol levels than their captive counterparts. To test this potential difference, I collected fecal samples from wild and captive porcupines from October 2018 to March, 2019. I quantified cortisol using an ELISA test. Preliminary results support the finding that captive porcupines experience less stress in winter than their wild counterparts. Understanding the stress profiles of wild animals may be extremely helpful in the effort to conserve species and their habitats. If we can discover which environmental and anthropological factors cause stress and thus influence cortisol profiles, conservationists can work more efficiently to preserve and protect species globally.

27: oVert: a collaborative effort to produce 3D data for all vertebrate genera

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The oVert (openVertebrate) Thematic Collection Network (TCN) is a collaboration among 18 natural history museums in the U.S. whose goal is the production of high-resolution digital 3D data for internal anatomy across the vertebrate tree of life. At a network of digitization centers, we are CT-scanning ~20,000 fluid-

preserved specimens representing ~80% of the living genera of vertebrates, focusing primarily on data-rich specimens of type species. We also are generating contrast-enhanced scans to reveal soft tissues and organs for a majority of the living vertebrate families. This collection of digital imagery and 3D volumes is being shared outwardly on the MorphoSource 3D data repository for open exploration, download, and use. Our network of leading U.S. collections will develop best practices and guidelines for high-throughput CT-scanning, including efficient workflows, preferred resolutions, and archival formats that optimize the variety of downstream applications. We also will upgrade the interface and functionality of MorphoSource, improving its capacity to explore media, capture standardized metadata, ingest legacy data from previous and existing projects, supply media information to data aggregators, and engage educators and students. To date, we have CT scanned more than 7,100 fluid-preserved specimens, representing approximately 2,900 vertebrate genera and nearly 50% of all vertebrate families. In total, 297 representatives of known mammalian genera have been scanned. An additional 586 specimens have been identified for scanning.

28: Forestry and prescribed burns attract wildlife but may limit species diversity

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Prescribed burns and forestry cuts are land management tools used to increase wildlife populations by promoting habitat diversity. We were interested in what vegetative and landscape features attract wildlife as a result of these management techniques, and how wildlife presence and diversity differed across forest stands with varying tree density. We established 15 camera trap stations at Fort A.P. Hill in Bowling Green, VA across forest stands with low, medium, and high basal area. We deployed camera traps for a total of 532 trap nights (TN) of effort. At each site, we measured the distance to trafficable roadways and water sources, vegetation composition, and the percent groundcover, canopy cover, and understory. We used an information theoretic approach and linear regression to test and rank several possible models to explain trap success. The cameras captured 9 different species and a total of 398 trap events. The most predictive model included basal area and displayed an inverse relationship between basal area and trap success. Although cameras in low basal areas had the highest trap success, they had lower species diversity compared to those in high basal areas. Our results suggest that reduced tree density attracts large numbers of early successional specialists but doesn't promote species diversity as well as a forest with high tree density.

29: Microhabitat use by the Texas kangaroo rat along roadsides dominated by cropland

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The Texas Kangaroo Rat (*Dipodomys elator*) is endemic to north-central Texas and currently known from only 5 counties. Knowing its microhabitat use is crucial to make management decisions given the restricted range and scarcity of this species. Previous surveys have revealed individuals existing in landscapes dominated by cropland where the only natural cover is a thin strip of vegetation along roadsides. This is the first study to use tracking techniques to quantify nightly foraging movements of this species. We used radio-telemetry to ascertain nightly movement, general activity, and burrow usage at 3 roadside locations. We followed 16 individuals for an average of 5 - 6 nights and obtained a total of 480 fixes. Over several days, individuals used from 2 to 6 burrows with inter-burrow distance up to 400 m, although most movements were restricted around burrows while foraging (mean distance from fix to nearest burrow ranged from 2 to 21.9 m). A relatively high number of fixes (30 to 100%) represented individuals inside burrows, indicating that kangaroo rats spend a lot of time in their burrows each night. Foraging individuals tended to remain within 10 m of the roadside habitat strip with minimal incursions into cropland and no use of rangeland. Our findings indicate the potential relevance of thin roadside vegetation strips as habitat for this species and perhaps as corridors to connect populations.

30: Snowshoe hares alter behavior in response to coyote and moose cues at diverse vegetation densities

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Prey avoid chemical cues from predators at feeding sites because the risk of death outweighs the benefit of food. However, we lack information regarding avoidance of chemical cues from competitors as well as how foraging behavior changes alongside vegetative cover. To test if chemical cues and vegetative cover alter prey vigilance, number of visits, and time spent at feeding sites, I observed snowshoe hares (*Lepus americanus*) in plots containing coyote (*Canis latrans*; predator) and moose (*Alces alces*; competitor) urine across a spectrum of vegetation densities. Snowshoe hares significantly reduced the number of visits to feeding plots when coyote or moose urine was administered. In plots containing coyote urine, number of visits decreased significantly as plots became more densely vegetated. Neither chemical cues nor vegetation density had a large effect on snowshoe hare vigilance or time spent in plots. These results suggest that competition between snowshoe hares and moose has selected for an avoidance response. This study also reinforces the idea that an increase in vegetation density could prove disadvantageous to prey, perhaps because sit-and-wait predators use dense vegetation to stalk and ambush while on the hunt.

31: Populations of small mammals, tallgrass prairie, and prescribed fire: a fire-reversal experiment

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Prairie fires are a natural feature of native grasslands in the Flint Hills of Kansas. Small mammals respond indirectly to fire via vegetation changes that result following fire and also to fire suppression. Previously, we have shown that most species respond either positively or negatively to burning of native tallgrass prairie. Herein, we investigate how small mammals respond to the reversal of a fire regime (i.e., a change from an annual burn to a long-term unburn and vice versa). We sampled small mammals in two contiguous ungrazed treatments in native tallgrass prairie for 2 years before the reversal occurred and then for 10 years after the fire reversal. One experimental treatment was burned in spring for >20 years and then switched to an unburned regime after the spring fire in 2000, whereas the other was left unburned for over 5 years and then switched to an annual burn regime beginning with the prescribed fire in spring 2001. Overall, we recorded 11 species of rodents and 2 of shrews and a total of 2,444 individuals. *Peromyscus leucopus* was the most abundant species followed by *Sigmodon hispidus* and *P. maniculatus*. Six of seven common species were strongly associated with one of the treatments. Several species showed positive associations with some part of the landscape and with time after the fire reversal within each treatment.

32: Communities of small mammals, tallgrass prairie, and prescribed fire: a fire-reversal experiment

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Fire, grazing, and weather and associated changes in vegetation and environmental conditions affect small mammals in native tallgrass prairie in the Flint Hills of Kansas. In ungrazed sites, presence or absence of recurring fires influences plant production as well as structure of live and standing dead vegetation and density of plant litter. Based on studies on the Konza Prairie, most small mammals (rodents and shrews) respond either positively or negatively to fire-induced changes, which should change community structure and composition. Herein, we examine community characteristics (community abundance; species diversity, richness, and evenness; community composition; and inter-site similarity of communities) in annually burned and unburned sites (2-year period) and then changes that occur when the fire regimes are reversed (subsequent 10-year period). Community abundance varied widely among years in both reversal sites, but showed no directional temporal change. Species diversity and evenness, however, increased significantly from before to after fire reversals in both sites. The original unburned site included encroached woody vegetation so *Peromyscus leucopus* dominated this site before the fire reversal and then declined through time as expected. In contrast, but as expected, *P. maniculatus* dominated the annually burned site and then declined through time. Overall, communities of small mammals in the two experimental sites were highly dissimilar before fire reversals, but after the reversals, community similarity increased through our study period.

33^{E,HTA}: Reciprocity in restoration ecology: when might large carnivore reintroduction restore ecosystems?**

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Carnivore reintroduction is often expected to revert community and ecosystem properties to their natural states via risk effects and the direct killing of prey. Because large carnivore extirpation and reintroduction are usually believed to have symmetric and offsetting effects, fulfilling this “assumption of reciprocity” is crucial to realizing the restorative potential of large carnivores for community structure and ecosystem function. Because we were able to find few studies of this phenomenon centered on large carnivore reintroductions, we used studies that included but were not limited to large carnivores involving (1) the reintroduction of a native apex predator or (2) the removal of an introduced apex predator to examine the assumption of reciprocity. Reintroduction of native apex predators did not affect any of four trophic groups (mesopredator, omnivore, herbivore, primary producer) in a positive or negative way, but removal of introduced apex predators consistently increased the abundance and biomass of mesopredators. Further, outcomes of apex predator reintroduction and removal were variable across study systems, regardless of system complexity. The assumption of reciprocity, in which predator extirpation and reintroduction are believed to have consistent, counterbalancing effects is largely unsupported by current evidence. Rigorous experimental studies of large carnivore reintroductions are needed to more thoroughly assess this widely accepted idea. This research was supported by a Grant-in-Aid awarded to Jesse Alston in 2018, and by a Shadle Fellowship awarded to Brett Jesmer in 2017.

34^E: Ocelot (*Leopardus pardalis*), bobcat (*Lynx rufus*), and coyote (*Canis latrans*) coexistence patterns in South Texas

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Interspecific competition among carnivores has been linked to differences in behavior, morphology and resource use. Insights into these interactions facilitate a stronger understanding of the local processes, which can have impacts on the recovery of endangered species, such as the ocelot (*Leopardus pardalis*). Ocelots, bobcats (*Lynx rufus*), and coyotes (*Canis latrans*) share a small geographic range overlap from southern Texas to south-central Mexico, but relationships between the three are poorly understood. From 2011 to 2018, we conducted a camera trap study to examine co-occurrence patterns between ocelots, bobcats, and coyotes on the East Foundation’s El Sauz Ranch in South Texas. We used a novel multi-season extension to multi-species occupancy models with two or more interacting species to identify the mechanisms of interspecific interactions and examine potential resource partitioning within this carnivore guild. Ocelots, bobcats, and coyotes mutually coexisted, and species-specific detectability varied seasonally on El Sauz. Seasonal co-occurrence patterns were best explained by increasing distance to a high-speed roadway. These results revealed a unique dynamic between ocelots, bobcats, and coyotes across a heterogeneous landscape in South Texas. We were unable to find clear evidence of resource partitioning, which may indicate the niches of our focal species may be too discrete for interspecific competition among species. However, our results have important implications for road mitigation for carnivores on ranchlands adjacent to rapidly developing areas.

35: Preliminary investigation of resident and transient margays at Wildsumaco Wildlife Sanctuary, Ecuador

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Margays (*Leopardus wiedii*) are small, elusive cats found in the Neotropics. Like many wild felids, margays are on the decline and listed as a Near Threatened species by the International Union for Conservation of Nature (IUCN). We began a camera trap study in 2008 at Wildsumaco Wildlife Sanctuary (WWS) in the eastern Andean foothills of Ecuador. The margay was one of our most frequent captures and has become a flagship species for the Sanctuary and Wildsumaco Biological Station. Our data indicate that WWS may have one of the highest densities of margays in the Neotropics. The population of margays at WWS consists of resident and non-resident individuals. Some individuals, such as Female 2 and Male 3, have been captured throughout the study during every month, whereas other individuals are only captured a few times over several months. The high abundance of margays at WWS may indicate that margays are using the Sanctuary as a corridor to move from areas around WWS to the nearby Sumaco National Park, and/or buffer zones within the UNESCO Sumaco Biosphere Reserve. Many of the non-resident individuals at WWS may be dispersing juveniles or mating season transients. We examined images from camera traps to investigate the spatial and temporal relationship between resident and transient individuals for this presentation.

36: Tunnel diameter as an alternative method to determine pocket gopher (*Thomomys*) occupancy

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Due to their subterranean lifestyle and aversion to live traps, members of the Family Geomyidae are challenging to study in the field. The Wyoming pocket gopher (*Thomomys clusius*) is one of the least-studied mammals in North America, primarily because of its rarity within a restricted geographic range. A scarcity of information regarding its ecology has impeded formal listing decisions and further conservation action. We evaluated an alternative method to live-capturing to assist agencies with monitoring *T. clusius*. We show that tunnel diameter can distinguish between occupancy by *T. clusius* and a co-occurring, more widespread congener (*T. talpoides*). These measurements could reduce reliance on invasive methods, such as live-trapping, to identify species of co-occurring pocket gophers, and potentially could be extended to other species of fossorial mammal.

37^E: The future of museum mammalogy collections

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Museum mammalogy collections have served as a resource to demonstrate changes in biodiversity over time. However, with a growing focus on genetics and more federal restrictions in place that limit the collection of certain specimens, mammalogy collections have had to adapt. Surveys of museum collections suggest that tissue samples are becoming more important than other types of specimens because of the increasing demand for genetic samples. In order to better understand the ways that mammalogy collections are changing and the challenges those changes cause, we focused on two questions. Are collections changing to adapt to new research needs? What methods can mammalogy collections use to grow in the future? We conducted a survey of collections in museums to determine what types of collection specimens (tissue, fluid, skin, or skeletal) have increased the most in recent years and the results will be discussed. In addition, we conducted a literature review to determine what types of methods could be used to expand collections. Some methods include establishing partnerships with wildlife organizations to collect specimens that have died naturally, collecting skin puncture samples and blood in the field instead of whole specimen collection, and increasing the number of specimens digitized so that they are accessible to more people. Understanding how mammalogy collections are currently changing can help focus specimen preservation and collecting efforts in the future.

38: Predicting new records for an endangered shrew in a poorly explored mountain range in Mexico

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Finding and monitoring new populations of endangered species is critical for establishing priorities for conservation actions. The Nelson's small-eared shrew (*Cryptotis nelsoni*) is a poorly known and critically

endangered species, which is only found in small patches of cloud forests in Los Tuxtlas, an isolated mountain range in eastern Mexico. It is likely that the scarcity of records of *C. nelsoni* is a consequence of incomplete surveys in Los Tuxtlas. Here we (1) identified climatically suitable and stable areas through the last cycle the last glacial-interglacial cycle, (2) investigated the sampling bias to identify poorly sampled areas, and (3) conduct fieldwork in three poorly sampled localities predicted as suitable habitat for this species in Los Tuxtlas. We identified new suitable areas for *C. nelsoni* in the highest and most inaccessible parts of Los Tuxtlas, which have been climatically stable over time. These remote areas also lack small mammal records probably due to insufficient or non-existent sampling effort. Our fieldwork resulted in 15 new specimens from an area relatively close to the type locality. However, we did not find new records in two other sampled localities. We highlight the importance of continuing long-term surveys in poorly sampled and climatically suitable areas to accurately characterize the geographic distribution and evaluate the current conservation status of this shrew.

39^{E,HTA}: Pika glucocorticoid metabolites within latrines

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Noninvasive measurements of stress (glucocorticoid metabolites/GCM) from scat are becoming a popular method for assessing population health in wildlife. Pikas are small mammals (order: Lagomorpha) that do not hibernate and are relatively active throughout the year. Evidence suggests that climate change may be causing declines in pika populations, leading to widespread use of noninvasive methods to assess population health within pika ranges. We sought to understand how GCM varied during a summer season within a territory. We collected scat in 2018 from 6 different latrine sites on the Grand Mesa from June through early November. We extracted GCM from the scat and performed an ELISA to measure GCM concentration. We observed a decrease in stress in August, but the exact timing of this decrease was variable between individuals. These results were consistent with a similar study conducted at Niwot Ridge Ecological Station, where lower stress levels were also observed in August. Variability in our results may be due to territory intrusion, which could result in scat being collected from multiple individuals. Understanding seasonal patterns of stress in this species is important for conservation and management, as well as assessing population health and viability.

40^E: Exploratory behavior and response to novelty in two montane chipmunks of the Sierra Nevada

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Phenotypic plasticity – particularly of behavioral traits – provides an immediate mechanism through which animals can respond to rapidly changing environmental conditions. Little empirical work, however, has been done to relate individual-level behavioral plasticity to population- or species-level responses to environmental change. Individual variation in exploratory behavior is one common metric of behavioral flexibility that likely has implications for a population's resilience to environmental change. In the Sierra Nevada Mountains of California, the alpine chipmunk (*Tamias alpinus*) has undergone a significant upward contraction in elevational range over the past century; while the lodgepole chipmunk (*Tamias speciosus*) has experienced no significant change in elevational distribution over this period. These differences in range response are associated with marked interspecific stress physiology, and habitat specialization, both of which suggest that *T. alpinus* should be less exploratory than *T. speciosus*. As a result, these species provide a compelling system in which to study the adaptive importance of individual-level behavioral plasticity in response to climate change. To assess interspecific differences in exploratory behavior in *T. alpinus* and *T. speciosus*, we subjected free-living members of each species to an open-arena hole-board trial (a standard test of exploratory behavior). Preliminary results indicate significant individual variation in exploratory behavior within each species. Future experiments will extend these trials to determine the repeatability of individual differences in behavior and to assess behavioral differences between species.

41: Methods to manage woodchucks

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Woodchucks (*Marmota monax*) damage residential properties by eating vegetation and burrowing, which may cause people to translocate them. However, translocation is not always humane. Thus, our objective was to gather information about alternatives to translocation. We used an online survey to compile examples of successful and unsuccessful methods that people use to manage woodchucks and to understand human attitudes toward those methods. We examined methods used in rural, urban, and suburban areas and compared attitudes toward control methods in those areas. Of 475 respondents, 72% lived in a rural area. Throughout all areas, blocking holes was the least successful method (21%). However, in urban areas, blocking holes was the most successful method (20%). In rural areas, shooting and reliance on predators accounted for 39% of successful methods. Comparing across locations, shooting was overrepresented in rural areas. The most cited reasons for not using particular methods were personal beliefs (21%) and negative effects on other animals (19%). Reasons did not differ depending on location. Ironically, the same control method may work for some people but not for other people. Other factors may play a role, such as how those methods are deployed. Despite differences in methods, people showed similar concerns when making decisions about types of control they opt to use. This information could be used to create educational material related to human-woodchuck conflicts.

42^E: Using camera traps to assess winter mammal diversity and porcupine occupancy in New York State

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Camera trapping is a useful and non-invasive way to determine species diversity and measure habitat use. This study had two aims: 1) Comparative analysis of the general winter species diversity in deciduous versus pine forests and 2) Occupancy modeling for the North American Porcupine in St. Lawrence County, New York. We selected 6 state forests in St. Lawrence County, 3 deciduous and 3 replanted pine. We placed cameras out in 2 phases, with 24 camera deployments during each phase. We deployed the cameras at 4 randomly generated sites per forest. In the second phase, we relocated each camera to a new random site within the same forest. Photos were uploaded to Zooniverse, a citizen-science platform that enables the public to assist with species identification. We measured mammal species richness in each forest and across forest types and modelled occupancy using R. Preliminary results suggest that there is a higher mammal species richness in deciduous forests than in managed pine forests during the winter. We will also report on porcupine occupancy. Understanding how many different species are present in an ecosystem, and understanding how different habitats support species within an ecosystem, is critical when planning conservation strategies.

43^{E,HTA}: Modeling thermal properties of fisher reproductive dens: implications for artificial den boxes

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Female fishers (*Pekania pennanti*) use cavities in large-diameter trees for parturition and to raise kits. Large cavity trees are relatively rare on managed landscapes, causing researchers and managers to test if artificial den boxes would enhance fisher habitat. Thermal properties of natural and artificial cavities could influence their relative value to fishers, but information on thermal properties of natural or artificial cavities is limited. Our objectives were to model heat transfer processes in tree dens used by female fishers and in artificial den boxes to describe thermal properties during the denning season, measure potential energy conservation in female fishers based on thermal properties of cavities, and use results to improve design of artificial den boxes that mimic the microenvironment of natural cavities. We modeled heat transfer and internal temperature of cavities based on ambient temperatures during the denning season and thermal conductivity values for natural cavities, artificial den boxes, and fishers. We considered artificial den box designs with and without polystyrene insulation. Overall, natural cavities maintained a high thermal gradient between the internal and external temperatures early in the denning season, while the thermal gradient decreased over time as ambient temperatures warmed. Artificial den boxes made with polystyrene

insulation maintained similar thermal gradients to natural cavities. Insulated den boxes will reduce heat loss of female fishers and kits consistent with thermal properties of natural cavities.

44^{E,HTA}: Role of nasal cavity morphology with diet and olfactory activity in bats

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New World leaf-nosed bats (Phyllostomidae) are one of the most ecologically diverse mammal families, feeding on a wide variety of food groups. However, it is not fully understood how phyllostomid bats locate food and how their olfactory function relates to structure. Their nasal cavity consists of two chemosensory morphologies related to smell: vomeronasal organ (VNO), which primarily detects pheromones, and main olfactory turbinals, which primarily detects odorants. In this study, we compare sizes and shapes of VNO and turbinal sets of different species to see how nasal cavity morphology correlates to diet and olfactory activity. We hypothesize that plant-visiting phyllostomid bats will have greater olfactory surface area because of fruit and flower odor compounds, while carnivorous bats will have greater VNO surface area because of the prevalence of animal pheromones. Phyllostomid bat heads stained with iodine- based contrast agents underwent contrast-enhanced CT (diceCT) scans. This is the largest 3D soft tissue data set of bat nasal cavity to exist. We reconstruct VNO and turbinals using diceCT scans and VGSTUDIO, software that allows for 3D visualization of data. Quantitative measurements are made including surface area, volume, and length to identify patterns with nasal cavity morphology and known feeding patterns. Preliminary results suggest that differences in VNO and turbinal morphology correspond to diet variation, which is expected as olfaction plays a crucial role in animal feeding behavior.

45^{HTA}: Genomic footprints of postglacial colonization in the Patagonian olive mouse (*Abrothrix olivacea*)

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During glacial phases, the andean slopes of southern South America were covered by ice sheets, forcing distributional changes in many species. Restriction to glacial refugia, including possibly one in what currently is the valdivian forest, have been proposed for many taxa. Rodent species in the region show phylogeographic units arranged latitudinally, rather than separating andean forests from open steppes and grasslands. The Patagonian olive mouse *Abrothrix olivacea*, however, showed a distinct mtDNA clade in Tierra del fuego, suggesting an additional, southern refugium. To establish the sources and direction of colonization events and test the proposed refugium in Tierra del fuego, we genotyped 172 *A. olivacea* and 6 specimens from 2 other species of *Abrothrix* with an exon-capture protocol. The final dataset consisted of 7900 loci, encompassing a total of 8 million base pairs and including thousands single nucleotide polymorphisms. Values of heterozygosity, Tajima's D and the directionality index support a single source in northwestern forests, in line with a valdivian forest refugium and ruling out a separate southern refugium in Tierra del fuego. In contrast to earlier, mtDNA studies, we found a longitudinal break, separating populations in the andean forests from those from open Patagonia. Furthermore, whereas continental forests show a marked geographical subdivision, the eastern populations present limited geographical structure compatible with a stepwise pattern of rapid southward expansion.

46: Is the distribution of *Peromyscus leucopus* (and Lyme disease) shifting northward: a preliminary analysis?

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The deer mouse, *Peromyscus maniculatus*, and the white-footed mouse, *P. leucopus*, are two of the most common species of small mammals in New Hampshire, and are notoriously difficult to identify based on field characteristics alone. Both species have a widespread but overlapping distribution in New Hampshire (Choate, 1973). The objective of this study was to document the distribution of these two species in New Hampshire and determine if their distributions have shifted in the last 45 years. In addition, the white-footed mouse, but not the deer mouse, has been implicated as the major reservoir for *Borrelia burgdorferi*, the bacteria that causes Lyme disease (Mather, 1989). We trapped mice throughout the state and collected

tissue samples. We used a microsatellite technique (Tessier, et. al., 2004) to determine species identity and tested the same samples for the presence of *B. burgdorferi* DNA (Aliota, 2014). We tested 48 samples from 8 locations. All captured mice were identified as *P. leucopus*. No *P. maniculatus* were trapped, even in locations where they were previously documented by Choate (1973). 69% of the samples were positive for *B. burgdorferi*. These results are consistent with the suggestion by Roy-Dufresne (2013) that *P. leucopus* is expanding its range northward due to climate change. This may, in turn, influence the potential spread of Lyme disease in New Hampshire.

47^{E,HTA}: The role of fire succession in dietary competition among small mammal species

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Fires have increased in season length and area burned in the United States over the last 3 decades, potentially altering their impact on biological communities. Thus, understanding what drives ecological responses to fire may help us predict how changes in fire regimes will affect ecosystem functions. In western North America, fire succession in mammal communities is marked by a transition between a few dominant species: southern red-backed voles (*Myodes gapperi*) dominate old-growth forests but are largely replaced by North American deermice (*Peromyscus maniculatus*) immediately after a fire. These abundance shifts have been observed in multiple studies, but the processes that mediate these shifts are debated. One possibility is a competitive exclusion-release model, which suggests coexisting species occupy different dietary niches due to competition and exclusion in resource-limited habitats. We tested whether the observed post-fire increase in deermice might be explained by competitive release from voles, which often fare poorly in post-fire environments. Here, we examine dietary shifts between deermice and voles before and after a fire using stable isotope analyses. Furthermore, we evaluate the degree to which deermice and voles fit a competitive exclusion-release framework. Our results indicate that deermice transitioned to a more varied diet, enriched in ¹³C (i.e., more C4 plants) after the fire. This research provides important insights into how small mammals are impacted by fire succession and competition for similar foods.

48: Diet switching in mammalian herbivores: dietary specialization and toxin tolerance in two woodrat species

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Herbivores face many dietary challenges including those presented by the toxins that are produced as defense mechanisms by many plants. To understand the evolution of toxin tolerance in dietary specialists, we are investigating two species of woodrats, *Neotoma lepida* and *Neotoma bryanti*, and their hybrids. Both species experienced a shift in their diet about 18,000 years ago, as creosote bush (*Larrea tridentata*) expanded its geographic range and replaced the ancestral diet of juniper (*Juniperus spp.*). Creosote bush contains numerous toxic compounds that differ from the compounds found in juniper and require different detoxification mechanisms. We conducted feeding trials with woodrats from 2 species and their hybrids from 13 geographic locations to determine the maximum tolerable dose (MTD) of creosote resin. Some populations are creosote feeders, whereas others feed on the ancestral diet of cactus and juniper. We found that MTDs vary between species, where the MTD of *N. lepida* is approximately 1.5 times higher than that of *N. bryanti*. Hybrids showed intermediate tolerances. This pattern was reflected across all the populations, including sites where both species and their hybrids are found. We found that the presence of creosote explains some of the variation in MTD. Furthermore, MTD is negatively correlated with distance from the origin of creosote invasion suggesting that evolutionary history (duration of exposure) with creosote has allowed for greater adaptation to this diet.

49^E: The effect of winter severity on reproductive timing in two species of congeneric mice

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Climate change can affect how species interact when individuals of one species migrate into the range of another. If these species are closely related, they may compete for resources, including territories. For seasonal breeders, milder winters and warmer springs due to climate change may allow one species to begin reproduction earlier, giving it a possible advantage in securing quality territories over a competing species that reproduces later. Two species of field mice in the genus *Peromyscus* have shifted their ranges in the past 30 years as temperatures warm in the Great Lakes region. *P. leucopus* has expanded its range to overlap with *P. maniculatus* in the Upper Peninsula, while *P. maniculatus* has been lost throughout the Lower Peninsula. Mice were captured on both peninsulas over the course of three summers to assess how winter severity affects reproductive timing and community composition. Winter was the least severe in 2016 and most severe in 2018. Where the two species co-exist, *P. leucopus* had higher overwinter survival compared to *P. maniculatus* when winters were less severe, but not when winters were more severe. *P. leucopus* began reproduction earlier in 2016, following the least severe winter, while *P. maniculatus* reproductive timing did not vary with winter severity. However, more *P. maniculatus* juveniles were caught throughout 2017 and 2018 following more severe winters, when *P. leucopus* had a lower reproductive output.

50^E: The proof is in the poop: estimating population density of recovering Ohio bobcat (*Lynx rufus*)

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Wildlife populations are dynamic and continually fluctuating in response to anthropogenic change. Understanding and documenting these changes is important for sustainable management and conservation of wildlife. Bobcats (*Lynx rufus*) are currently recovering in Ohio from local extinction due to habitat loss and overharvesting. Evidence of bobcats recolonizing the state have sparked debate about opening a fur trapping season for bobcats, yet there is no baseline population estimate for bobcats in Ohio. The aim of this study is to determine the density of bobcats in two subpopulations using genetics-based spatial capture-recapture (SCR) methodology. Between July 2018 and March 2019 we surveyed the two core areas three times. Covering 270.3 km of transects in each survey, we collected 560 scats total. I extracted DNA from scats using Qiagen mini stool kits and ran quantitative polymerase chain reaction (qPCR) to amplify segments of DNA. My PCR product was sent to Ohio State genomics lab where 7 microsatellite loci were used to identify species, individuals, determine sexes, and analyze population structure. Density will be determined using SCR. The results from my analyses will provide important data on population density and structure for a recovering carnivore, and contribute to our overall understanding of carnivore recolonization in disturbed landscapes. Additionally, these data will be used to conduct a population viability analysis of bobcats in Ohio, to inform management and conservation strategies.

51^{E,HTA}: Urban coyotes differ genetically from coyotes in natural habitats

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The Los Angeles metropolitan area consists of highly urban, suburban, rural, and undeveloped mountainous habitats. Coyotes (*Canis latrans*) are found in each of these very different habitat types, making them an exemplary model organism to investigate the effects of urbanization on animals in this fragmented landscape. The purpose of this study was to investigate whether urban coyotes differ genetically from coyotes in less developed habitats. We hypothesized that due to natal habitat biased dispersal, coyotes living in natural habitats will be more genetically related to other coyotes in similar natural habitats and less related to coyotes living in more urban habitats, despite geographic distance. We analyzed 10 microsatellite genetic markers from 126 individual coyotes and combined the genetic data with detailed land cover data. Our results reveal that coyotes in the Los Angeles metropolitan area cluster into four significantly different genetic populations. Three populations are associated with primarily urbanized habitats in Los Angeles and Orange Counties. In contrast, the remaining population is associated with more naturally vegetated land near the Santa Monica Mountains, Santa Susana Mountains, Santa Ana Mountains, and Simi Hills. Coyotes living in natural areas are genetically similar despite long geographic

distances separating them. In a very short amount of time, urbanization has already affected the microevolution of coyotes, a species typically thought to be relatively insensitive to human disturbance.

52^E: Investigating the range of *Peromyscus maniculatus* in south Texas

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The geographic range of *Peromyscus leucopus* and *P. maniculatus* overlaps throughout much of Texas, with the former known from almost every county. Although *P. maniculatus* is believed to occur across the entire state, records of *P. maniculatus* from the southern parts of Texas are patchy and supported by few specimens in collections. To investigate the southern range of *P. maniculatus* in Texas, we used museum specimens and 2D geometric morphometric analyses to distinguish between *P. leucopus* and *P. maniculatus*. Specimens were examined from across the southernmost distribution of *P. maniculatus* in Texas. Morphometric data were gathered from landmarks placed on images of skulls, using control specimens that were assessed genetically to determine species identification. Our morphometric analyses revealed distinct morphological differences between *P. leucopus* and *P. maniculatus*. These results suggest that many of the previously identified *P. maniculatus* specimens fall into *P. leucopus* morphospace, which may imply that these specimens were misidentified and that the currently accepted range of *P. maniculatus* extends too far south.

53^E: Maternal effects on birthweight, growth, and survival of mule deer fawns

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Maternal effects are the influence of maternal phenotype and the maternally provided environment on the phenotype of her offspring. Frequently, maternal effects are manifest both pre- and post-parturition. Pre-parturition effects are primarily direct allocation of energy to the offspring that is in utero. However, there are both direct and indirect maternal effects during post-parturition. While both direct and indirect effects are often discussed, there is a paucity of information on the relative importance of each type due to the difficulty in monitoring mothers prior to parturition and mother-offspring relationships after parturition in free-ranging animals. We use mule deer (*Odocoileus hemionus*) to study these direct and indirect effects because they are iteroparous and long-lived. Our objective is to determine the relative importance of direct and indirect maternal effects on birth mass, growth rates, and survival of mule deer fawns through the first twelve months of life. Preliminary findings suggest that maternal condition is directly translated to offspring in utero, dams in better condition produce offspring with greater birth mass. However, climatic variables may diminish the direct effect of maternal condition on growth and survival. Understanding the interaction of direct and indirect maternal effects on mule deer offspring will provide valuable insight into fawn recruitment and population dynamics.

54^E: GIS analysis of the range shift in *Cynomys* from the Quaternary to the present

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Using ArcGIS, fossil records from the FAUNMAP database were compared to current distributions of *Cynomys* across North America in order to determine two important geographic questions. First, has the extant range of certain species of mammals been used to refine identifications of fossils to the species-level? Second, absent bias in the identification, how have the geographic ranges changed from the Pleistocene to the present? Within the genus, we focused on four species: *gunnisoni*, *leucurus*, *ludovicianus*, and *parvidens*. These species were selected based on the availability of fossil record data, and each had broad extant ranges. Once separated by species, the fossil record data was further divided by the North American land mammal ages (NALMA), focusing on the Irvingtonian and Rancholabrean, as well as the Holocene. Using ArcGIS Pro v.2, we calculated a directional distribution ellipse that corresponds to where one standard deviation of the fossil localities were found. These directional distributions were determined for each species by age in order to easily compare the fossil distributions with the current

mammal ranges. Our analysis revealed both evidence of dispersal due to environmental change, and that there is the possibility that the identification of the fossils was biased by the modern ranges.

55: Modeling the behavior of escape, should a heard school or swarm?

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Aggregation behaviors such as heading or schooling are thought to be adaptive, in part, as predator avoidance mechanisms. These behaviors have been studied extensively through mathematical modeling. There are generally two categories of aggregation behavior models: (1) “schooling” models, in which group members match each other’s movement, and (2) “swarming” (aka. “selfish herd”) models, in which individuals swarm to the group center, without matching movement. Because both behaviors may be important for escape, animals might use either strategy to avoid predators. Most models only employ one strategy. To understand which strategy acts as a better defense, we created an object oriented program in which we encoded four classic models of both types. In each model, “prey” used their type’s movement rule. We asked whether there is a “safer” movement strategy (school/swarm) in the presence of a nearest target predator. Because swarms exhibit less directional movement, we predicted higher capture rates in swarming models than schooling models. To test this prediction, we simulated a single predator attacking from a random location. We did not allow prey to detect the predator before or during the attack. Preliminary data suggest that swarming models may result in higher capture rates, but further analysis is required. We will present these initial results and future directions with the model system. This research was funded by NSF grant IOS-1149302.

56^{E,HTA}: Movement and microhabitat selection in southern flying squirrels (*Glaucomys volans*)

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Flying squirrels (genus *Glaucomys*) have a direct link to forest trees for food, shelter, and travel, making them a good model to understand the effects of fragmentation on forest mammals. This study examined the southern flying squirrel (*Glaucomys volans*) in urban and rural fragments in southwestern Illinois. Squirrels were collared and tracked using radio-telemetry. Nighttime tracking established home range sizes. Daytime tracking determined nesting tree preferences. Hypotheses tested included: (1) squirrel sex affects home range size, (2) tree mast type affects nesting tree selection, (3) tree size affects nesting tree selection. 95% minimum convex polygon (MCP) and 95% kernel density estimator (KDE) determined home range sizes. No significant difference between sexes in home range size was found. MCP and KDE in this study are among the lowest observed. Squirrels selected soft mast trees for nesting significantly more than expected. Tree size preferences were significant, with medium and large trees (>40 cm diameter) being preferred over small trees (<40 cm diameter). The finding of larger tree usage was consistent with most other studies. During the course of tracking, one male squirrel was observed crossing a road, indicating gap crossing potential for flying squirrels in urban environments. Understanding the spatial behavior and habitat characteristics provides crucial insight to better understand the effect of fragmented landscapes on small mammal communities.

57^{E,HTA}: Shifting small mammal community diversity due to wildfire succession in the Greater Yellowstone area

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Given the increase in wildfire frequency and severity throughout the intermountain west, it is increasingly important to understand the effect fires have on ecological communities. Understanding the effects of fire succession on community structure allows us to better predict the influence future fires will have on species occurrence, interactions, and persistence. In this study we use 4 grids, established after the 1988 Yellowstone fires, to examine the effects of subsequent fires on small mammal diversity. We contrasted species richness and abundance two years before and after the 1988 and 2016 fires. Prior to the 2016 fire, communities were dominated by red-backed voles (*Myodes gapperi*; >50% of captures) and shrews (*Sorex*

spp.; ~25% of captures), with a mixture of other small mammal species. After the 2016 fire, species richness remained relatively constant but abundance fluctuated, with deermice (*Peromyscus maniculatus*) comprising 75% of captures and dominating all four trapping grids. In contrast, red-backed voles and shrews dropped to 6-7% and 3-4%, respectively. We hypothesize the reason this shift may be in part due to dietary generalism in deermice. Results suggest that fire regime (timing and intensity) may be key to understanding post-fire community assemblages. Long-term studies, such as this, are critical for predicting the impacts of wildfires on ecological habitats and their communities. This research was supported by a Undergraduate Honoraria awarded to Robert Beers in 2019

58^E: Establishing a historical baseline for the presence of white-nose fungus in *Perimyotis subflavus* in Oklahoma

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More than five million North American bats have died since 2007 due to infection by *Pseudogymnoascus destructans* (Pd), also known as white-nose fungus (WNF). Transmitted through skin-to-skin contact and contact with contaminated surfaces, Pd is most dangerous to bats in winter, due to their reduced immune system response during hibernation. Biogeographic studies suggest that the fungus has most likely been contracted from Europe and has been swiftly moving across the US, detected for the first time in Oklahoma in 2014. For this project, we investigated the historical presence of Pd in Oklahoma bats by swabbing museum specimens of *Perimyotis subflavus* collected in Oklahoma, using collections dating back to 1925. *Perimyotis subflavus* is a species of special concern to the state; it also has been confirmed in the state with diagnostic symptoms of WNF. This investigation was intended to evaluate the possibility of the historical presence of the fungus in the state and provide a baseline from which to test future bats captures. For this study, each bat specimen was swabbed along the wing and rostrum; DNA extraction and qPCR were used to detect the fungus and quantify the concentration, if present. Other than our positive control samples none of the bats swabbed tested positive for the fungus, suggesting low-to-no prevalence of Pd in all historical and recently collected museum specimens of Oklahoma *Perimyotis subflavus*.

59^E: Differences in reproductive bet-hedging within a family of long-lived mammals

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For interparous species, there is a trade-off between one's current reproductive value (CRV) and residual reproductive value (RRV). When resources are limiting, an individual must make an evolutionary choice between a current reproductive opportunity that decreases likelihood of survival and foregoing a current reproductive opportunity to increase the likelihood of future reproduction. This choice is called "bet-hedging". Our objective was to determine if bet-hedging can be used to differentiate reproductive strategies within a single family of mammals, Cervidae. We tested the hypothesis that elk would be more likely than mule deer to bet-hedge based on female condition (i.e., fat storage) because of their longer lifespan and relatively high annual survival. We captured female elk (*Cervus canadensis*) and mule deer (*Odocoileus hemionus*) across the state of Utah during February and March from 2015-2019 to test for pregnancy and obtain physiological data. We used mixed-effects generalized linear regression models to examine factors influencing the likelihood of pregnancy. We found that the likelihood of pregnancy was generally high and stable for mule deer and was influenced most strongly by body weight of yearling individuals, but not fat reserves. In contrast, likelihood of pregnancy of elk was lower and more variable, and was influenced strongly by variation in fat reserves among individuals. Consistent with our hypothesis, elk were more likely to use a bet-hedging strategy than mule deer.

60: Seasonal changes in mass of three species of bats suggest differential energy allocation strategies

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In temperate-zone mammals, decisions about energy allocation are often governed by seasonal changes in weather and food availability. In addition, energy allocation strategies usually differ between males and females. The study of energy allocation is challenging for bats, especially those that do not roost in areas known or accessible to humans. We evaluated year-round changes in body mass for 3 species of bats in northern California: silver-haired bats (*Lasiorycteris noctivagans*), California myotis (*Myotis californicus*), and Yuma myotis (*Myotis yumanensis*). The two species of myotis are considered resident species that do not migrate. Silver-haired bats are considered migratory species with females likely migrating further than males. Body mass of all species peaked in late-autumn and was at a minimum during spring. There were significant differences in body mass between sexes and among seasons in all 3 species. We used sex- and season-specific multiple linear regression models of change in body mass to quantify these changes. Interspecific comparisons provided valuable insights into the energy allocation and overwintering strategies of these species and are an important first step toward understanding their ecology over the full annual cycle.

61: Functional skeletal morphology of pencil-tailed tree mice (Rodentia: Muridae: *Chiropodomys*)

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Pencil-tailed tree mice (Muridae: *Chiropodomys*) are small arboreal mammals endemic to the rainforests of Southeast Asia. They are capable of manual and pedal grasping and have nails rather than claws on their pollex and hallux, but their limb morphology has never been analyzed from a functional perspective. Here we compare two species of *Chiropodomys* to the similarly sized but terrestrial *Mus musculus* using quantitative morphometric osteological data recorded from six limb bones. Principal components analysis (PCA) and discriminant function analysis (DFA) clearly separate *Chiropodomys* from *Mus*. Both PCA and univariate analyses reveal several features linked to arboreality in *Chiropodomys* and characteristics associated with terrestriality in *Mus*. PCA and DFA also distinguish mainland *C. gliroides* from island *C. calamianensis* of the Palawan Faunal Region, with the latter exhibiting larger body size as predicted by the island rule. Finally, PCA and DFA clearly separate northeastern *C. gliroides* specimens collected east of the Mekong River from southwestern specimens collected on the Malay Peninsula south of the Isthmus of Kra; these preliminary results may indicate that there are two taxonomically distinct populations in this sample, but this must be tested further with more specimens and craniodental data. Overall, our study of *Chiropodomys* postcranial morphology revealed functional differences related to substrate preference, larger body size in an island endemic species, and possible evidence for a previously unrecognized mainland taxon.

62^E: Testing range limits of two cryptic species of *Neotoma*: Is the Rio Grande a barrier?

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Neotoma leucodon, previously considered a subspecies, was elevated to species status in 2001 by Edwards and Bradley when paraphyly was detected in the *Neotoma albigula* species complex. The geographic ranges of the two species were hypothesized to be separated by the Rio Grande, with *N. albigula* occurring only west and *N. leucodon* occurring only east of the Rio Grande. Recently, however, specimens identified as *N. albigula* were found east of the river in New Mexico. We aim to delineate the range limits of *N. leucodon* and *N. albigula* in New Mexico through intensive sampling of woodrats in multiple transects across the Rio Grande. Given the intermittent flow of the Rio Grande in southern New Mexico, we hypothesize that this border will be more permeable in southern than central New Mexico. We sequence cytochrome b to test our identifications of specimens of these two species. Further, we apply demographic expansion statistics to gain insight into their historical demographic expansion and contraction dynamics. As episodes of drought become longer and more severe in the Southwest, understanding how rivers influence species' geographic boundaries and interspecific dynamics at contact zones could be crucial for guiding conservation efforts.

63^{E,HTA}: Upward to heaven? Climate change risks and the future for collared pikas

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A primary objective of conservation is understanding the effects of climate change on the habitat suitability of naturally fragmented populations. High latitude montane regions have experienced increased levels of warming throughout the last 50 years. Consequences of climate change within these regions give probable cause for a shift in the range of iconic alpine flora and fauna. We use species distribution models (SDMs) to predict changes in distribution of an alpine mammal, the collared pika (*Ochotona collaris*), under future climatic conditions. We modelled the pika's current climatic niche and geographical distribution using museum records spanning a 113-year period and projected the niche onto climate models for 2055 and 2085 under a variety of plausible greenhouse scenarios. Collared pikas follow a metapopulation model, which indicates a naturally fragmented distribution that has the potential to be augmented due to climate-driven fragmentation. Preliminary findings suggest that temperature variability is the limiting factor for range shifts. The pika's acute sensitivity to heat and cold stress has led them to be considered a sentinel species for monitoring climate change in the subarctic. SDMs facilitate the identification of dispersal corridors and species' preferred habitat suitability, which can be directly implemented into conservation management schemes. Thus, understanding the impacts of climate change on habitat suitability and species distribution may help provide a framework for future pika conservation efforts.

64: Systematic characterization of the species of the genus *Ctenomys* (Rodentia: Ctenomyidae) of northern Argentina

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The genus *Ctenomys* comprises 69 nominal species of subterranean South American rodents known as tuco-tucos, which diversified in the last 3.5 million years into an explosive cladogenesis, possibly mediated by chromosomal changes. It has been proposed as an exceptional model in several fields of evolutionary biology. However, the main difficulty for such studies and to resolve its systematics is the lack of available information of the recognized species. In northern Argentina, there are 28 out of 45 species described for the country, and 18 were described by Oldfield Thomas about a century ago. Descriptions are limited to few lines of qualitative information, restricted to few external and cranial morphological measurements of specimens from type localities and near surroundings, and holotypes are deposited in British Museum, not available for local studies. We planned to visit all the type localities of northern Argentina, and to collect, prepare skin and skeleton, take tissue samples and deposited vouchers in public Argentinean museum, and at the end do morphological and molecular comparisons with species previously characterized. Now, we were able to extend the description of *C. bergi*, *C. coludo*, *C. famosus*, *C. fochi*, *C. johannis*, *C. juris* and *C. tulduco* and to phylogenetically position them within the known phylogeny of the genus. New information available will allow us to propose a complex phylogeographic scenario in the evolution of the genus.

65^{E}: Metabarcoding illuminates dietary diversity in a neotropical bat community**

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Classical conceptions of trophic guilds are useful for organizing mammals based on their dietary ecologies, but species often fail to fit nicely into a single dietary guild. Neotropical bats are especially prone to issues with defining guild membership because their feeding habits are often poorly known or inferred indirectly

from morphology and echolocation call characteristics. To better understand the fit of neotropical bats diets to their traditional guilds, we used fecal metabarcoding to examine the arthropod, plant, and vertebrate components of the diets of 28 bat species from Belize ($n = 80$). Our dataset included all classic terrestrial feeding guilds (insectivory, frugivory, nectarivory, piscivory, omnivory, and carnivory) with the exception of sanguivory. Preliminary results suggest that bats previously defined as strictly frugivorous engage in facultative insectivory, and that bats commonly classified as carnivorous, such as *Chrotopterus auritus* and *Trachops cirrhosus*, routinely supplement their diet with insects. Further, our data more precisely document the taxonomic identity of arthropods, plants, and vertebrates these mammals are eating at this site in Belize. Future application of metabarcoding methods has the potential to contextualize differences in diet both within and among widely distributed bat species, offering new insights into bat dietary diversity and flexibility. This research was supported by an ASM Grant-in-Aid of Research awarded to Melissa Ingala in 2018.

66: Highly disparate life history patterns among rodents of Luzon Island, Philippines; implications for conservation

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The island of Luzon supports a diverse rodent fauna that includes both highly specialized species (e.g., arboreal “cloud rats” and earthworm predators) along with species that are ecological generalists. Additionally, there are widespread non-native species introduced through human agency. We use information from museum specimens obtained during surveys across elevational and habitat disturbance gradients throughout Luzon to assess life history patterns among these different groups. In forested habitats, species-rich local assemblages are dominated by members of two clades endemic to the Philippines (Chrotomyini and Phloeomyini) derived from separate ancient colonization events. These species have small litters of 1 or 2 young once annually. Native species derived from more recent colonization events have slightly larger litters. Among native species, there are differences in seasonality of reproduction as assessed through frequency of pregnancies, male testicular cycles, and population age structure. In many, reproductive maturity is delayed, and adults may live several years. In sharp contrast, non-native species (*Rattus* spp.) grow rapidly, are sexually mature when less than full grown, have multiple, large litters, and appear to reproduce year-round. Although life history traits of non-natives facilitate invasion of severely disturbed areas, they confer no competitive advantage over native species in forested habitat.

67^E: Linking the gut microbiome and inflammatory bowel disease in captive adult red wolves (*Canis rufus*)

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Captive management of many wildlife species has proven to be challenging. Individuals often suffer from suboptimal health and display disease syndromes that are not generally described in the wild population. Inflammatory bowel disease (IBD) is a debilitating gastrointestinal (GI) disorder that severely impacts the sustainability of the critically endangered North American red wolf (*Canis rufus*). Retrospective studies have identified that GI diseases are the second leading cause of captive adult red wolf mortality. Recent molecular studies show that imbalanced gut microbial composition is tightly linked to IBD in the domestic dog. We investigated two questions: (1) what is the relationship between the gut microbiota and GI health and (2) how does the relative abundance of gut microbiota differ between wolves in poor GI health versus wolves in good GI health? Fresh fecal samples were collected from 55 individuals from eight facilities and scored based on a fecal consistency index, a proxy for GI health. We characterized gut microbiome composition from the samples using 16S rRNA metabarcoding. Preliminary results showed that bacterial taxa differed in relative abundance between healthy GI and unhealthy GI individuals. We are currently delineating the relationship(s) among diet, gut microbiota, and health of individuals. The findings obtained from our study will increase our understanding of the interplay between various captive environmental factors and IBD, which can inform captive red wolf management.

68: Examining shifts in mammal diversity in a semi-natural ecosystem during the rise of suburbia

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Mammals provide far-reaching ecological functions and ecosystem services, including top-down ecosystem regulation, seed dispersal, and insect control. Furthermore, the presence of mammals can reflect the levels of human impact and climate change on natural systems, and mammal diversity serves as a proxy for ecosystem health. Despite its importance, a thorough assessment of mammal diversity is lacking in the Crum Woods ecosystem (CW), a semi-natural temperate forest that includes the Crum Creek and is part of the Delaware River watershed. The CW features a mosaic of management activity and presents a natural experiment for the examination of diversity across a human-use gradient as it encompasses unmanaged forest to restored habitat to manicured arboretum. In the scientific literature, the most recent systematic mammal survey in Delaware County occurred in 1952. Though the 1952 survey did not include the CW directly, it can provide a baseline for historical levels of species diversity in the area. Using live traps, trail cameras, and passive ultrasonic acoustic recording devices, we documented the current mammal assemblage in the CW and contrasted today's diversity with the 1952 Delaware County survey in order to examine changes over the past 67 years. Preliminary results provide insight into the response of this mammal assemblage to suburban spread and yield useful information for the responsible management of this managed and semi-natural setting.

69^E: Systematics and ecology of the brush-tailed mice, *Calomyscus*, based on *Cytb* and *Rbp3*

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Family Calomyscidae is a group of muroid rodents consisting of the single genus *Calomyscus*. They are small pale colored mice with large ears and tufted tails. *Calomyscus* prefer dry rocky mountainsides with sparse vegetation and are found in South Central Asia. Populations tend to be isolated due to uneven habitat. Currently only eight species are recognized based on morphological characteristics and phylogenetic analyses. *Calomyscus* can be informally separated into three species groups; this project focuses on one of these, the *C. bailwardi* species group. This group contains three of the eight recognized species, *C. baluchi*, *C. hotsoni*, and *C. bailwardi*, which are distributed in Iran, Afghanistan, and Pakistan. We analyzed how species present in this group are related and investigated potential species suggested by other datasets. Cytochrome b (*Cytb*) sequences were obtained from 229 individuals and a phylogenetic tree was constructed to test relationships among species. Interphotoreceptor retinoid-binding protein (*Rbp3*) sequences were obtained from 30 individuals and a maximum parsimony network was constructed. The *Cytb* tree suggests up to six species, more than the recognized three. Specifically, both *C. baluchi* and *C. bailwardi* appear to be comprised of more than one species. The *Rbp3* network supports these distinctions, but less robustly. Ecological niche modeling indicates habitat requirements for the suggested species are different.

70: Improving species range estimates for an arboreal species group with a parapatric distribution

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Three-toed sloths (genus *Bradypus*) include three species distributed parapatrically across mainland Central and South America: *B. variegatus*, *B. tridactylus*, and *B. torquatus*. The distributions of these arboreal species are constrained by forest cover, as well as by the presence of their parapatric congeners. Traditional species distribution modeling (SDM) techniques typically rely on abiotic variables without accounting for the effects of competition on range boundaries. We sought to improve range predictions for *Bradypus* by using the ranges of the parapatric congeners to mask abiotic SDM range predictions. To account for the presence of parapatric species, we used support vector machines (SVMs) to delineate borders between ranges using occurrence data and predicted SDM habitat suitabilities for each species. We found that the SVM range estimates were more closely aligned with ecological expectations than those

generated from unmodified species distribution model predictions. The SVM estimates were also less likely to include occurrences of parapatric species in the predicted range and better accounted for known contact zones between species. Finally, we masked the range estimates with a forest cover threshold calculated by temporally matching occurrence points with remotely sensed forest cover data. This mask quantified the differential effects of deforestation and habitat fragmentation across the three species' ranges.

71: Across time and space: social structure of the highland tuco-tuco in multiple ecological contexts

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Social relationships are key determinants of individual fitness. As such, identifying the social structure of a population is a critical component to understanding finer scale biological processes of individuals. In free-living species, conspecifics often socialize in multiple ecological contexts, including those that are constrained (e.g. dens, nests) and those that are unconstrained (e.g. open spaces). Despite this, little is known about how social organization varies between ecological contexts. These contexts may prove especially important when considering species who split their time above- and belowground where selective pressures such as predation and foraging ecology likely differ. We used paired radiotracking and visual scan sampling techniques to examine the social organization of live-trapped individuals within a population of highland tuco-tucos (*Ctenomys opimus*) from northwestern Argentina. We tracked individuals above- and belowground as well as during daytime (active period) and nighttime (resting period) to investigate 2 critical questions regarding the social structure of this species. Is the highland tuco-tuco social? Does social organization vary across time or ecological contexts? Our findings suggest that the highland tuco-tuco is facultatively social, with some individuals living alone while others live in groups of varying size and composition. Social groups were stable across ecological contexts but varied between daytime and nighttime. Understanding how social organization varies across ecological contexts may provide critical insight about the function of sociality in a given population.

72^F: Ecogeographic patterns of craniodental morphology within *Zapus luteus*: primary productivity vs climate

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Within mammals, body size often varies across space and time, but requires the integration of ecology and evolution (eco-evolutionary) to advance our understanding of the processes that shape and maintain biodiversity. Here, we unite geometric morphometrics with environmental informatics to evaluate how alternative eco-evolutionary hypotheses including heat dissipation, environmental seasonality, and resource availability best explain observed physical features of an endangered rodent. More specifically, we examine skull centroid size (a proxy for body size, $N = 319$) across ~40 populations of *Zapus luteus* that occupy the southern reaches of the Rocky Mountains (*Z. l. luteus*) and the southern Great Plains (*Z. l. pallidus*). With disjunct distributions across different physiographic regions and habitats (montane vs grasslands), hibernation, and recent evolutionary history, this system offers a rare opportunity to assess how eco-evolutionary processes shape ecogeographic variation within a species. Results indicate that subspecies significantly differ for both size and shape suggesting that montane versus grassland associated populations have responded to a complex interaction of climate and net primary productivity. These preliminary data and analyses yield support for re-evaluating taxonomy, but also, for implementing novel conservation measures for federally listed populations that improve protections for adaptive variation.

73: Reproductively viable population of American Black Bears (*Ursus americanus*) in desert lowlands of Trans-Pecos Texas

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During a three-year camera-trap study in Big Bend Ranch State Park, situated in the Trans-Pecos region of West Texas, we documented a persistent breeding population of American Black Bears (*Ursus*

americanus) in The Solitario region of the park. The habitat in The Solitario, which is an isolated eroded remnant of volcanic activity, is typical low elevation Chihuahuan Desert scrub, but includes significant localized rocky relief. From July 2016 to May 2018 a total of 219 images of American Black Bears was captured. Based on size, color, body markings, facial patterns, presence of cubs, and dates of images, we determined these images to be of a minimum of 11 individuals. Large adults and smaller subadults were identified during each year, and at least two different females with small cubs were documented during two consecutive years. Based on these data, we consider The Solitario bears the northernmost reproductively viable population of American Black Bears in Trans-Pecos Texas. Available plant resources in the area are compared with the documented diets of American Black Bears from other Chihuahuan Desert localities in Texas and northern Mexico. This American Black Bear population is in an area spatially separated from other black bear populations in the region, and its relevance to the mainland-island metapopulation recolonization concept previously proposed for the species in northern Mexico and Trans-Pecos Texas is discussed.

74: Cave-exiting behavior of hibernating bats in 12 Idaho caves

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Cave-exiting behavior of bats during winter in western North America is poorly understood, especially at multiple, adjacent caves. Quantifying this behavior of hibernating bats in this area is important for understanding the behavioral ecology of these mammals, especially before white-nose syndrome arrives in Idaho. We set acoustical monitors at 12 caves that are biologically important hibernacula (up to 1,740 hibernating bats) in southeastern Idaho, USA, during winter (November to March) from 2011 to 2018. We will investigate if nightly activity of western small-footed myotis (*Myotis ciliolabrum*) and Townsend's big-eared bats (*Corynorhinus townsendii*) fluctuates by cave characteristics, number of hibernating bats, bat species, moon phase, and weather variables. Preliminary results indicate that bat activity occurred during all months; however, 70% of bat passes (≥ 2 bat call pulses) occurred in November and March, and 30% of activity occurred from December to February. Western small-footed myotis were detected 4.5 times more than Townsend's big-eared bats. Our study documents cave-exit behavior during winter outside of 12 caves for 2 bat species of conservation concern in an area that is crucial for both species in western North America. Our results provide a unique insight into the behavioral ecology of these species in this area. Additionally, our data will provide baseline levels of bat activity in winter prior to the arrival white-nose syndrome in Idaho.

75: Hand it to the red panda

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In organisms with bilateral symmetry, lateralization has occurred across various lineages. Most likely ecological pressures shape lateralization in limb use (=handedness) and brain asymmetry (=laterality). Unsurprisingly, the majority of studies on the former have focused on humans and other primates, with a small number in marsupials, parrots, and domestic mammals; leaving many opportunities for additional research. Given that lifestyle and ecological pressures exerted on an animal are strongly correlated with the occurrence/non-occurrence of handedness, the red panda (*Ailurus fulgens*) is an excellent candidate for study due to the presence of a highly modified radial sesamoid (=“false thumb”), which allows increased manipulation of objects. However, because of the elusive nature of red pandas, field studies have proven remarkably difficult, even in determining population densities accurately, making zoos a viable alternative. Collaborative observations with zoo keepers and random sampling has allowed us to evaluate handedness in *A. fulgens* and shows favor for the right hand among unrelated individuals when feeding or manipulating objects. Such observations can be coupled with fossils from the extinct *Pristinailurus bristoli*, which shows evidence of left-handedness; suggesting that handedness has existed for at least the past 5 million years in the lineage (Ailuridae). Moreover, recently recovered cranial material will be CT scanned to generate endocasts to assess brain asymmetry.

76^E: Habitat associations of key deer fawns: pairing spots as unique identifiers with N-mixture models

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Key deer (*Odocoileus virginianus clavium*) are an endangered subspecies of white-tailed deer endemic to the lower Florida Keys. Habitat loss, hunting, and expanding urbanization were historically associated with population decline prior to their protection. A variety of techniques have been used to estimate their population size, but none have focused on estimating fawn abundance or fawning habitat associations. We validated and applied a new technique to estimate fawn abundance using camera traps deployed at 56 sites throughout the National Key Deer Refuge on Big Pine Key, Florida, to capture photos of spot patterns as unique identifiers for individual fawns. We used the photos of fawn flanks in the WildID program to compute and distinguish individuals within and across sites and examined landscape associations of the female deer with their fawns. Our results suggest a stronger relationship between increasing elevation and decreased fawn abundance, which can have impacts on the conservation of the Key deer, particularly in the face of climate change and rising sea-levels. Fawn counts were also negatively associated with human trails. Finally, distance from development had a positive, but weak, relationship with fawn site abundance. This study showcased that temporary spot patterns can be used to identify individual fawns while their spots are present, which corresponds with the closure assumptions of capture-recapture and N-mixture models.

77^{HTA}: Skeletal variation among island populations of large treeshrews (Scandentia, Tupaiidae)

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The large treeshrew (Scandentia: Tupaiidae: *Tupaia tana*) is a small terrestrial mammal endemic to the tropical rainforests of Southeast Asia. *Tupaia tana* has a complicated taxonomic history; currently, 15 subspecies are recognized from Borneo, Sumatra, and smaller islands, which were connected to one another as recently as the Last Glacial Maximum. Many of the subspecies were originally differentiated based on pelage and small sample sizes. Here we explore patterns of intraspecific variation using quantitative morphometric osteological data obtained from the hands of museum specimens. Principal components analyses reveal extensive overlap among these populations in morphospace, suggesting that several currently recognized subspecies are not morphometrically distinct. However, we do find some variation between Bornean and Sumatran populations of *T. t. tana*, the only subspecies shared between these islands; discriminant function analysis of these two populations correctly classifies 81% of the specimens. Additional data and analyses are required to determine whether this variation should be recognized taxonomically. Comparisons of Bornean specimens to subspecies on small, offshore islands reveal an island effect, with island populations averaging smaller body size. This result is inconsistent with Foster's island rule, which predicts that island populations of small mammals average larger body size relative to mainland forms. A similar lack of support for ecogeographical rules has been noted in *T. glis*, suggesting that these "rules" do not apply universally across small mammals.

78: Activity patterns of American pikas (*Ochotona princeps*) on camera traps in low-elevation lava flows

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The American pika (*Ochotona princeps*) is a small lagomorph that typically resides in high-elevation alpine boulder fields and relies on cool climates. However, at Craters of the Moon National Monument, these animals thrive in low-elevation lava fields that have consistent daytime temperatures of over 32°C in the summer. We placed camera traps at Craters of the Moon (1,800 meters) and on Grays Peak in the Pioneer mountain range (3,200 meters) to observe pika behavior in each habitat. Motion-activated cameras were placed near active haypiles from May to October 2017. We captured over 20,000 videos and images, 1,133 of which were of pikas. Pikas at Craters tended to be active early in the morning before 9:00 and again after 20:00. In contrast, pikas at Grays Peak were most active between the morning hours of 6:00 and 10:00 and

were not as active in the evenings. These data will advance our understanding of how pikas at Craters use behavior modifications to inhabit an atypical habitat compared to alpine habitats. Since pikas are known to be affected by climate change, these data will also serve as a baseline to which we can compare activity patterns of these animals in the future and to inform conservation assessments and management plans for this unique population.

79:** Molecular identification of nonvolant mammals along an elevation gradient in the Western Andes of Colombia

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Colombian biota has a unique ecology and geological history, something to attribute to its location in northwestern South America and its greatest variation in bio-geographical terms. Colombia has two of the most critical biodiversity hotspots of the world: the Andes and Choco. Both hotspots account for 50% of 1700 species of neotropical mammals. Based on recent fieldwork, we documented the small terrestrial mammals along an elevation gradient (10 to 3610 meters) in the Humid Rainforest of the Choco and the Andean forests in the Western Cordillera of Colombia. To further corroborate our morphological identification of all collected species we sequenced part of the mitochondrial marker Cytochrome-b (CYTB), insomuch as it has an abundant representation and denser taxon sampling in GenBank. CYTB also provides a detailed framework for mammal species identification. To avoid misidentifications, due to the use of traditional molecular identification analyses like “distance-based,” we performed a Maximum likelihood (ML) phylogenetic analysis, and for each species registered we included all the available CYTB sequences from GenBank. Herein, we present the results of the five different systematic surveys; a total of 581 specimens representing 30 species were collected, and 130 sequences were obtained for all species. So far, this has been the most extensive trapping effort for Colombia. This research was supported by a Latin American Student Field Research Award awarded to Juan M. Martínez-Cerón in 2018.

80: Effects of transfer on fecal glucocorticoid metabolites in red pandas (*Ailurus fulgens*)

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The endangered red panda (*Ailurus fulgens*) is a favorite of zoo visitors because of its charismatic personality and behavioral antics. In spite of their popularity, red pandas have a reputation of being sensitive to environmental stressors. Like many *ex-situ* species, red pandas are frequently transferred between institutions due to breeding recommendations; however, their adrenal stress response to relocations has not been previously researched. This study focused on animals transferred between four zoological facilities in the US. Fecal samples were collected 3-7 days per week from each individual (n = 5), with collections occurring for up to three months before and after relocation. Samples were dried and fecal glucocorticoid metabolites (fGM) extracted using 80% methanol and a modified shaking technique. Concentrations of fGM were then quantified using a corticosterone assay (CJM006). Red pandas demonstrated a physiological response to relocation. Both individual variation in baseline fGM concentrations and response to transfers occurred in study individuals. Preliminary results show a variety of responses in fGM, including increases or decreases in fGM the day after transfer. These analyses indicate an acute adrenal response to translocation, but long-lasting changes were not observed. Understanding how red pandas react to stressors, such as relocation, is important for guiding and improving transfer methods to support the long-term health of each animal.

81: Understanding dietary diversity takes a diversity of approaches and individuals

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At every meal, mammalian herbivores face the possibility of being poisoned by their food. Plants typically produce a complex battery of secondary compounds to deter consumption by herbivores. For the past three

decades, my research has focused on understanding the physiological, behavioral and microbial mechanisms employed by herbivores in dealing with the myriad plant toxins in their diets. I have been privileged to work with a variety of inspirational mentors and collaborators who have helped to hone my scientific acumen and to shape my mentoring capabilities. My research group has consisted of dozens of talented trainees (postdocs, graduate, undergraduate and high school students) from diverse backgrounds, and together we have worked on a miscellany of herbivore systems, predominantly mammalian ones, to uncover mechanisms that enable the ingestion of toxic diets. I have also been fortunate to teach Mammalogy and to work with several of my trainees on moving this course from a lecture-based format to a more interactive one. In this presentation, I will highlight some of our past scientific discoveries and introduce some of our newest projects. I will also present some of the active-learning components that my trainees have added to our Mammalogy course.

82: Mammal research and conservation on Madagascar: A review of the past 30 years

Steven Goodman

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The past decades have seen a remarkable augmentation in information on the native land mammals of Madagascar, which includes four endemic groups -- tenrecs (Tenrecidae), rodents (Nesomyinae), carnivorans (Eupleridae), and lemurs (Lemuroidea) -- as well as nine bat families, one of which is endemic to the island (Myzopodidae). On the basis of fieldwork and laboratory analyses, particularly molecular genetics, something on the order of 130 species of land mammals new to science have been described, many of which are endemics with limited distributions. In parallel to these advances, the protected area system has been greatly expanded, covering more than 12% of the island, including different ecosystems and the ranges of many micro-endemics. Further, the distributions of many of these mammals and aspects of their natural history are now better known. Largely based on different social-economic problems and human population growth, levels of deforestation on the island, within and outside of the protected area system, remain high, and other forms of natural resource exploitation have increased. These different aspects are reviewed, highlighting important advances, including several generations of national field and conservation biologists, as well as other positive aspects and remaining problems with the island's reserve system.

83: A brief history of change in the mammals at Kluane Lake, Yukon

Stan Boutin*

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Resource pulses, population cycles, and changing climate present opportunities for researchers to study how and why individuals and populations change over short and long time frames. I have been fortunate to be part of two long-term projects that study hares, lynx, and red squirrels in the boreal forests of Canada. I cut my "research teeth" on the longstanding riddle of why snowshoe hares and Canada lynx show 10-year cycles but, as for many mammalian population ecologists, was frustrated by the challenge of tracking individuals during their critical juvenile stage. North America red squirrels, however, have characteristics that allow us to track individuals from birth to death with ease, and we have done so for over 15,000 individuals spanning 10 generations. Red squirrels are part of a resource pulse system that has revealed a remarkable and unexpected repertoire of phenotypic and evolutionary changes as the system flips from boom to bust food availability. In recent years students in my lab have taken me back to my roots using new technology to revisit some unresolved questions about the snowshoe hare-lynx cycle. Finally, given we now have 40 years of data, I will touch on how these systems are being altered as a result of climate change.

84: Potential for citizen photography to help evaluate molt phenology in a high-elevation, high-latitude mammal

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Mountain goats (*Oreamnos americanus*) molt their double-layer winter coats yearly. To evaluate their molt patterns and phenology, we combined data extracted from crowd-sourced, spatially explicit photographs of mountain goats from across their range with data from 2018 fieldwork at their northern range extent. We hypothesized that earlier onset of warmer temperatures associated with climate change will be associated with earlier molt dates for mountain goats. We evaluated effects of intrinsic (sex and presence of offspring) and environmental (latitude and elevation) factors using linear mixed-effects models. Effects of sex and offspring on molting were consistent between our 2018 data from the Yukon on wild and captive animals (presumed to have superior nutrition). These patterns also held with crowd-sourced data. Males molted first followed by females without offspring and lastly females with new kids. Molt onset occurred earlier at higher latitudes and later at higher elevations. Acknowledging limitations inherent in our dataset compiled thus far (N=500 images, mainly from 2000 to present), we did not find evidence that molt has shifted to earlier in the year. Our findings possibly lend support to existing evidence that molt plasticity is limited and molt is primarily photoperiod-driven. While participatory approaches like citizen photography engage the public and hold promise in helping scientists address questions, our study will require additional effort to source historical photographs to adequately evaluate potential phenological shifts.

85^{HTA}: Engaging citizen scientists in post-fire monitoring of Columbia River Gorge pikas

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Wildfires have increased in both frequency and severity; however, little evidence exists regarding the potential influence of altered fire regimes on at-risk species, particularly small mammals with limited dispersal ability. An ideal mammal for studying these interactions is the American pika (*Ochotona princeps*), a small lagomorph that typically inhabits high-elevation rockslides but that also occurs at low elevations in the Columbia River Gorge. In 2017, the Eagle Creek Fire burned nearly the entire low-elevation distribution of pikas on the Oregon side of the Gorge, destroying the moss cover and dense forest canopy at many sites. In this study, we engaged local volunteers to document pika recolonization dynamics in this nationally unique, refugial habitat. In summer 2018, we trained 60 citizen scientists to collect pika-abundance and fire-severity data at 36 sites. Although the population as a whole survived, pika occupancy was sharply reduced post-fire (44%) compared to pre-fire surveys (84%). Resurveys of 12 sites by experienced observers also revealed that volunteers were more likely to detect pikas when they surveyed for at least 50 minutes, underscoring the importance of clear, standardized protocols and assessing the reliability of team leaders. This fire represents a unique opportunity to use a 'natural experiment' to study post-fire changes in the distribution and abundance of pikas and, more broadly, apply citizen science in resource management and conservation.

86^E: A black-tailed prairie dog translocation in the Trans-Pecos ecoregion of Texas

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Prairie dog (*Cynomys spp.*) populations throughout North America have declined because of sylvatic plague (*Yersinia pestis*), shooting, poisoning, and habitat conversion. To aid this keystone species, wildlife managers have used translocation to restore prairie dogs to areas of extirpation. In this study, we translocated black-tailed prairie dogs (*C. ludovicianus*) to a site 60 km from Alpine, TX. We prepared the translocation site to prevent the immediate dispersal of the prairie dogs. The prairie dogs were captured from Marathon, TX (n = 156) and from Lubbock, TX (n = 59); all 215 prairie dogs were translocated to the same site. The prairie dog population at the translocation site was regularly monitored post-translocation

and predators were removed from the site. Vegetation was measured pre-translocation and will be measured at the same time of the year post-translocation to assess the ecological impacts of prairie dog reintroduction. Fecal samples (n = 39) from prairie dogs were taken to measure glucocorticoid levels during the capture of 153 prairie dogs from Marathon, TX and at various time periods post-translocation at the translocation site. We analyzed the effects of translocation on the stress level of the prairie dogs over time. This study will help wildlife managers with future translocations of prairie dogs and will aid in the restoration of black-tailed prairie dogs to their extirpated habitat in the Trans-Pecos ecoregion of Texas.

87: Mammals, lyssaviruses and the rabies paradigm revisited

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A majority of newly recognized and re-emerging diseases are zoonotic in nature, and not surprisingly, many involve wildlife. Rabies, with the highest case fatality of any infectious disease, is an acute progressive encephalitis, caused by a lyssavirus. Lyssaviruses are bullet-shaped, single-stranded, negative-sense RNA viruses (Family Rhabdoviridae), adapted for replication within the central nervous system as a fundamental niche. Although appreciated as one of the oldest recorded diseases, when, where and how rabies originated is poorly described. A century ago, rabies was believed to be caused by only one type of lyssavirus and the domestic dog was considered as the primary mammalian maintenance host. Today, throughout Africa, the Americas, Australia and Eurasia, more than 16 distinct lyssaviruses have been characterized. All mammals are believed susceptible and potential vectors, but reservoirs responsible for viral perpetuation appear limited to specific taxa among carnivores, bats, and perhaps non-human primates. Major carnivores include representative canids, herpestids, mephitids, mustelids and procyonids, yet most lyssaviruses are represented in bats. Intriguingly, within the New World, rabies virus is the only lyssavirus species documented in the Chiroptera. During 2015, FAO, OIE and WHO announced a plan for elimination of human rabies mediated via dogs by 2030. To promote success, given their unique knowledge, skill set and diverse abilities, mammalogists have a key role to play in this global program, particularly from a trans-disciplinary context.

88: Integrating residents' perceptions and ecoepidemiological measures of zoonotic disease risk: *Leptospirosis* in Argentina

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Leptospirosis is a zoonotic disease of global distribution caused by bacteria of the genus *Leptospira*, acquired by direct or indirect contact with urine of infected mammalian hosts. We used a One Health approach to investigate leptospirosis in two marginal neighborhoods of the city of Santa Fe by considering aspects of animal, human and environmental health. Our goal was to achieve a more comprehensive understanding of overall leptospirosis risk and ways to reduce it by involving multiple sectors and disciplines in a participatory action research program with two complementary approaches. The eco-epidemiological approach involved the analysis of biological samples, surveys and observations made in the field. The anthropological-cultural approach involved ethnographic methods, including interviews, workshops, and collective mappings to inquire about public risk perception. The articulation of the two approaches enabled obtaining results from samples collected from sites relevant for the community, integrating popular knowledge on the biology of the synanthropic mammals with those obtained from traditional methods, and to consider common human-wildlife interactions when evaluating potential transmission risk. Here, we present some of the insights gained on the multiple dimensions of this zoonotic disease and discuss some of the challenges faced when working collectively with citizens in promoting actions to reduced risk.

89: State-wide citizen science mammal survey as science, conservation, and engagement: North Carolina's Candid Critters

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Citizen science can engage the public with nature while also accelerating the rate of data collection, which is critical to track the rapid pace of modern environmental change. Camera traps are ideal tools for citizen science because their photographs can be verified by experts, and the unique animal pictures provide an enjoyable experience for volunteers. Although not a replacement for traditional museum collections, these archives of photo-vouchers can be accumulated faster, over larger areas, and are noninvasive. Through the North Carolina Candid Critters project, we have developed field protocols, training modules, education materials, and the cyberinfrastructure to enable large citizen science camera trapping programs. We have worked with >1300 volunteers across the state to monitor over >3200 sites on public and private land, recording ~1 million animal detections in ~185 camera-years of monitoring effort. We use the eMammal system to manage data, checking the identification of all pictures and making all data available through online databases and visualizations. We are using these data to documenting the distribution and relative abundance of wildlife across the state and to create statistical models evaluating the impacts of human and natural factors on animal populations. Furthermore, the act of running camera traps and examining the photos is very engaging for our citizen scientists, who become stronger advocates for mammals after participating.

90: Extreme drought and adaptive resource selection by a desert ungulate

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Studies of wildlife-habitat relationships that focus on the influence of resources, but ignore constraints on resource use frequently fail to identify underlying mechanisms. We investigated resource selection in desert bighorn sheep (*Ovis canadensis mexicana*) across periods of highly variable climatic conditions and at multiple scales. Sheep altered use of escape terrain in response to drought, decreasing their use of ridgelines, using areas with lower ruggedness and slope, and increasing use of valleys. Forage biomass and quality were frequently not associated with resource selection, likely due to water and nitrogen content of forage being more limiting for desert ungulates than digestible energy. At the population scale, sheep exhibited strong selection for areas near perennial water, and their proximity to water decreased with declining precipitation. However at the home range scale, sheep used areas further from water in autumn and winter, and distance to water was generally uninformative in summer models. Sheep selected more northerly aspects and locations with lower solar radiation during summer days. In early summer, sheep use of cooler locations coincided with periods when forage covariates and several topographic features were less important for habitat selection. Previous studies of habitat selection in desert bighorn sheep have primarily focused on components of the landscape and vegetation associations; however, abiotic factors in a desert climate likely exert a significant influence on selection of these features.

91^E: Into the light: atypical diurnal foraging of Blyth's horseshoe bat on Tioman Island, Malaysia

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Diurnal flight and foraging activity in insectivorous bats are atypical behaviours which have been recorded from islands with few avian predators, and from locations with extended daylight hours. We present the first known observations of diurnal activity of *Rhinolophus lepidus* in forest on Tioman Island, Malaysia recorded using visual surveys and acoustic monitoring. The bats were first observed flying during the day in 2014.

Targeted fieldwork conducted in July and September 2017 confirmed their diurnal and nocturnal activity, and feeding buzzes detected using bat detectors suggest that they were actively foraging during the day. Based on 29 sightings, some of up to three individuals, the diurnal flight and foraging behaviour of the bats appear to be a regular phenomenon on Tioman Island. The absence of resident diurnal avian predators that hunt below the forest canopy may account for the diurnal activity of *R. lepidus* in forests there.

92: A walk in the woods: Mammalian responses to trails in urbanized forest fragments

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Many natural areas retained in the urbanized landscape are divided by recreational trails which have both physical footprints and increase human presence. We investigated how three different trails affect movement of mice and other, larger, mammalian wildlife in small forest fragments in upstate New York: a wide gravel path with low foot traffic, a medium dirt path with moderate traffic, and a narrower woodchip path with heavy traffic. At each site, we set Sherman traps in three aligned grids, with the trail running in one of the gaps between grids. We marked and recaptured mice to count movements among the grids. Logistic regression showed that all intervening paths reduced movement by close to 50%. We also looked for larger wildlife presence on and off the trails with paired camera traps. Coyotes, red fox, and gray fox were all found more often on trail, while raccoons showed no preference. Deer showed slight avoidance, which was more pronounced on the higher-traffic trails, suggesting deer may be reacting to human presence. It is unlikely that diurnal human presence is responsible for nocturnal mouse path avoidance, but the physical gap and potential predator use of the paths may increase their perceived risk. Nature preserve designers should be aware of the alterations in animal activity brought by trails and the associated human presence.

93: Foraging decisions: patterns of interspecific and sexual variation in three frugivorous neotropical phyllostomid bats

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Decision-making processes involve multiple levels of complexity and result from selective pressures that ultimately impact individual fitness. I present a comparison of the strong interspecific differences among three species of neotropical leaf-tent-making bats (*Ectophylla alba* (1), *Uroderma convexum* (2), and *Artibeus phaeotis* (3)) that engage in decision making regarding several key resources that influence fitness—food, roosts, and mates. (1) With a highly specialized diet based mostly on fruits of a single fig species, *E. alba* makes foraging decisions based on distance and quality of food resources, and female and male foraging strategies do not differ significantly. (2) As a feeding generalist, *U. convexum* shows highly marked differences in foraging pattern between males and females, with males restricting their foraging movements close to their roosts while females forage further abroad. (3) Another dietary generalist, *A. phaeotis*, builds roosts in a highly aggregated tree species, and males and females both forage at a considerable distance from their roosts when food resources are not available nearby. This foraging pattern of *A. phaeotis* results in spatio-temporal fluctuations of the seed rain in relation to roost proximity, influencing distance-dependent effects of the dispersed seeds. Explaining the similarities and differences in foraging decisions among species and between sexes is strengthened by comparing details of the natural history, behavior, and morphology of each species.

94: Reliance on visual, olfactory, and acoustic cues in flower choice by nectar bats (*Lonchophylla robusta*)

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Nectar-feeding bats in the Family Phyllostomidae serve as important pollinators of wild and agricultural plants in the Neotropics, yet the way these bats use their sensory systems in flower choice is not well understood. We experimentally examined the use of vision, olfaction, and echolocation in flower choice in 34 wild-caught individuals of the species *Lonchophylla robusta* at the Wildsumaco Biological Station in Ecuador. To assess the role of visual cues, individual bats were acclimated to a flight tent and presented

with a 3x2 array of artificial flowers of three colors (white, light green and pink), and two size classes, large (petals 35 mm in length) and small (petals 20 mm in length). We also conducted experiments on the use of olfactory and acoustic cues to test bat preferences for three experimental concentrations (0%, 20%, and 40%) of honey-water solutions under conditions of minimal light while using an ultrasonic bat detector to monitor echolocation activity. In our tests of visual cues, we found that these bats exhibited a significant preference for large and white flowers, while our olfactory/ acoustic cue tests suggest that *L. robusta* primarily uses echolocation to locate a food source, but then switches to using olfaction when choosing on which flower to feed.

95^{E}: On using a non-hibernating squirrel (*Ammospermophilus harrisi*) to inform models of communication complexity**

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Ground squirrels exhibit a common alarm communication system that varies in complexity across species, such that comparative analyses provide insight into which ecological characteristics select for greater complexity. Conspecifics in many species respond to alarm calls and studies find sociality to be a strong selective force favoring more informative alarm calls. However, whether calls function primarily as a predator deterrent or warning to conspecifics is unresolved. If predators are the intended receiver of alarm calls, there may be selected variation in alarm systems not accounted for by sociality. We conducted a two-year study to determine the potential function of alarm calls in a solitary, non-hibernating squirrel, *Ammospermophilus harrisi*. We hypothesized that if calls function as a predator-deterrent, callers should be of equal sex ratio and vocalize year round. If calls function primarily as a warning to offspring, callers should be predominantly female and vocalize only when juveniles are above ground. We found that callers were predominantly female but vocalized throughout the year. We also found that call bouts varied considerably in duration, amplitude, rate, and call type, which could hold additional layers of information. Our results suggest that although alarm calls may function as a predator deterrent, calling behavior is still shaped by kin selection even in solitary species. This talk will discuss these findings and their implications for current models of communication complexity. This research was supported by an ASM Grant In Aid of Research awarded to Alexandra Burnett in 2017.

96^{E,HTA}: Arctic fox winter diet revealed by next-generation sequencing of fecal DNA**

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Climate-caused changes in prey abundance may alter predator-prey dynamics in the simple Arctic food web. Lemmings (*Dicrostonyx spp.*) are important prey for Arctic foxes (*Vulpes lagopus*) and their annual population fluctuations drive Arctic fox reproduction, creating strongly linked predator-prey population cycles. Winter diet directly impacts Arctic fox reproduction, but few prey species persist on the tundra during winter. Strategies to accommodate for decreased lemming availability, such as foraging in marine habitat, have allowed Arctic foxes to reproduce during years with low lemming abundance, but warming winters have decreased snowpack quality, preventing lemmings from reaching their previous high densities. We reconstructed Arctic fox winter diet at the southern edge of the Arctic, to investigate alternative prey consumption over years of varying lemming abundance. Next-generation sequencing of fecal DNA, from samples collected annually from 2011-2018, provided high taxonomic precision and identified prey previously undetected with traditional methods. Arctic foxes consumed a range of prey items from both terrestrial and marine environments. Lemmings and voles were the most important prey in most years, but alternative prey (seals and shrews) were consumed more when rodent densities were low. Climate change may be reducing historic prey abundances but also creating new foraging opportunities. Identifying species interactions provides information about how climate caused disturbances may be altering predator-prey dynamics. This research was supported by a Grant-In-Aid of Research awarded to Megan Dudenhoeffer in 2018

97^{HTA}: Isotopic niche partitioning among antagonistic pocket mice: how persistent is the ghost of competition past?

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Assessing mechanisms that allow species co-occurrence is key to understanding how abiotic and biotic factors drive range shifts. When species co-occur, interspecific competition can cause niche partitioning, allowing coexistence. When competitive pressure is released, however, whether niche partitioning persists as a legacy of competition past is less known. We analyzed ¹³C and ¹⁵N to compare dietary niche dynamics of two known competitors, *Perognathus mollipilosus* and *Perognathus longimembris*, within a framework of shifting co-occurrence patterns in two Great Basin mountain ranges over the last century. In the Toiyabe Range, co-occurrence models and elevational range data suggest these species were not segregated historically yet are today, with mostly non-overlapping elevational ranges. Isotopically, historical range overlap was associated with significant isotopic niche partitioning, however no strong legacy of this persists today; the isotopic niche of *P. longimembris* converged with *P. mollipilosus* as range overlap was reduced and thus competition lessened. In the Ruby Mountains, elevational ranges were mostly non-overlapping historically, and isotopic niches overlap, similar to the modern Toiyabes. Today in the Rubies, *P. longimembris* has been locally extirpated. Interestingly, *P. mollipilosus*' isotopic niche appears conserved across time periods and mountain ranges, suggesting it is the stronger competitor. Analyses of climate change over time suggest isotopic niche dynamics are not driven by abiotic factors, but instead reflect a primary role for biotic interactions.

98: Specialist and generalist herbivore strategies across scales in the fossil record

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Competition for resources shapes the realized niche, constraining species' biogeographic and evolutionary trajectories. A more diverse herbivore community composed of specialists (browsers, grazers) as well as generalists (mixed-feeders) existed during the Pleistocene in North America. If competition among herbivores was greater in the past, then specialists may have experienced competitive release where, and when, mixed-feeding was less common. We test this hypothesis with stable isotope analysis (SIA), using the ratio of the heavy and light isotopes of carbon in tooth enamel, represented as $\delta^{13}\text{C}$, as a diet proxy. We curated a database of $\delta^{13}\text{C}$ from tooth enamel of fossil mammals from the literature. We ask how regional herbivory has changed since the Early Pleistocene between feeding guilds in southern North America. Using a global dataset of serially sampled $\delta^{13}\text{C}$ tooth enamel spanning the Miocene through the Holocene, we look at dietary breadth of individuals and ask how that scales up to the species level. SIA reveals that grazers are consistent in their diets throughout the Pleistocene. Where mixed-feeders are abundant, in the eastern region of our study system, browsers exhibit lower dietary breadth. Browsers consume a greater breadth of resources in the absence of mixed-feeders. Species tend to be composed of individual specialists, regardless of feeding group, with breadth arising from how different individuals are. We find the greatest individual breadth, surprisingly, among grazers.

99^{E,HTA}: Using micromammal teeth to evaluate megafaunal extinction ecology

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During the terminal Pleistocene extinction (TPE) ~10,000-14,000 years ago, extinction of 100+ megafaunal species restructured New World ecosystems. Here, we examine the TPE's ecological consequences using a fine-grained age model and the exceptional small mammal fossil record at Hall's Cave in central Texas. We employ multiple paleoecological proxies to characterize the TPE's effects on body size, isotopic niche, and dental ecomorphology for 10 ecologically diverse small mammal taxa. We estimated body size from dental measurements, a suite of ecomorphological proxies from microCT-derived surfaces, and Bayesian isotopic niche ellipses from bone collagen carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) across 16 time intervals spanning 0-21,000 years ago. Extracting each proxy from the same individual specimens for each taxon and time interval, we evaluate ecological shifts and assess proxy performance alone and in combination. Preliminary results reveal strong shifts in rodent ecology post-TPE. In contrast to their modern, broad isotopic niches, *Peromyscus* deer mice occupied narrow C₃-dominant primary consumer niches, whereas

both *Reithrodontomys* harvest mice and *Sigmodon* cotton rats shifted to better exploit C₄ isospace post-TPE. We also find intriguing shifts in body size. For example, post-extinction *Onychomys* grasshopper mice increased ~150% in average mass, which correlated with higher δ¹⁵N values (range 7.4-12.5‰). MicroCT-derived ecomorphological proxies will further characterize potential shifts in *Onychomys* diet. Ultimately, we aim to elucidate best-paleoproxy practices and inform ecosystem consequences for modern megamammal extinctions.

100^E: Tracking trace minerals across trophic levels for mammal populations

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Storage of trace minerals affects reproduction and disease resistance in mammal populations, but trophic availability is difficult to assess. We tracked the correspondence of copper (Cu) and zinc (Zn) from soils to plants to mammals across 15 sites in Texas during summer. We collected hispid cotton rats (*Sigmodon hispidus*; $n = 73$) in late summer and white-tailed deer (*Odocoileus virginianus*; $n = 317$) in winter. Grass Cu (4 ± 2 ppm) was lower and less variable than browse Cu (6 ± 5 ppm), while grass Zn (28 ± 12 ppm) was higher and less variable than browse Zn (22 ± 16 ppm). Liver Cu in rats (10 ± 4 ppm) was lower and less variable than that of deer (145 ± 158 ppm). Conversely, liver Zn in rats (83 ± 15 ppm) was higher and less variable than that of deer (73 ± 31 ppm). Unlike deer, liver Cu and Zn in rats increased with soil Cu and Zn. Population density affected liver Cu and Zn in both rats and deer. Liver stores of Cu and Zn followed the primary food source of each species (i.e. rats: grass, deer: browse), but correspondence between trophic levels differed among minerals. Rats may provide a better index than deer of the trophic availability of Cu and Zn to herbivores.

101: Islands in the sky: diversity and endemism of mammals on tepuis in Guyana

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The isolated table-topped mountains of the Guiana Shield of northern South America conjure up images of dinosaurs and a lost world. But what is not fanciful are the endemic species of plants and animals found nowhere else in the world. Based on three expeditions to the highest tepuis in Guyana, the community ecology of small mammals is summarized for this poorly known fauna. In addition, DNA barcoding is analyzed to assess the genetic diversity in the Pantepui region, but also in comparison to across the Neotropics. The general pattern for species diversity and relative abundance of bats decreases with increasing elevation. By contrast, rodents and opossums have a pronounced mid-elevation increase in abundance, which is less obvious for species. Although not as diverse as other groups of organisms, nine of the 63 mammal species known from this highland region >1,500 meters in elevation are essentially restricted to the upland plateau >500 meters. This includes the discovery of an arboreal rice rat (*Oecomys*) from Guyana that is a putative new species to science. It has richer coloration and >12% sequence divergence from the sister species in the eastern lowland rainforests. The Pantepui of the Guianas is still one of the world's most remote and unknown frontiers. International collaboration is needed to consolidate our expertise and resources in exploring and studying this lost world.

102^{HTA}: Museum specimens offer historical perspectives on a declining kit fox population

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Loss of genetic diversity has serious conservation consequences (e.g., loss of adaptive potential, reduced population viability), but is difficult to evaluate without developing long-term, multigenerational datasets. Alternatively, historical samples can provide insights into changes in genetic diversity and effective population size (N_e). In the Great Basin Desert, kit foxes (*Vulpes macrotis*) have declined precipitously from historical levels, causing concern about population persistence. We analyzed genetic samples from museum specimens and contemporary scats to evaluate temporal changes in genetic diversity and N_e for kit foxes in western Utah. The N_e of kit foxes in western Utah has decreased substantially, but we found no significant decrease in genetic diversity associated with declining N_e . We detected evidence of low levels of immigration into the population and suspect genetic diversity may have been maintained by this

previously undescribed gene flow from adjacent populations. Low or intermittent immigration may serve to temper the potential short-term negative consequences of low N_e . We recommend that kit fox conservation efforts focus on evaluating and maintaining landscape connectivity. We demonstrate how historical specimens can provide a baseline of comparison for contemporary populations, highlighting the importance of natural history collections to conservation during a period of declining funding and support.

103^E: Evolutionary potential of endangered Ganges River dolphin in human-modified South Asian waterways: an integrative review

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The Ganga-Brahmaputra-Meghna and Karnaphuli (GBMK) river basin (GBMK) in Nepal, India, and Bangladesh is among the world's most biodiverse. However, human-induced habitat modification processes threaten the ecological structure of this river basin. Among the GBMK's diverse flora and fauna, the endemic Ganges River dolphin (*Platanista g. gangetica*, GRD) is one of the most charismatic species in this freshwater ecosystem. Though a > 50% population size reduction has occurred since 1957, researchers and decision makers often overlook the evolutionary potential of this species in a highly fragmented GBMK. After rapid declines in population size and distribution, here we review, describe, and discuss the evolutionary trap mechanisms in an integrative way that affect the dynamic and viability of GRD population. Six potential trap mechanisms have been detected, representing population demographics, behavioral ecology, and environmental -based factors that might affect in a discrete or combination of ways: 1) habitat modification; 2) finite and geographically restricted local populations; 3) declining effective population size ($N_e < 500$); 4) increasing risk of inbreeding depression in genetically isolated groups; 5) behavioral attributes; and 6) direct fisheries-dolphin interaction. As evolutionary traps appear most significant during low water season, it adversely affects demographic parameters that might reduce evolution potential. These traps have already caused some local extirpation; we recommended sustaining river flow and restoration and preservation of essential habitats as immediate conservation strategies.

104^E: Determining habitat requirement at multiple scales for the southeastern pocket gopher (*Geomys pinetis*)

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The southeastern pocket gopher (*Geomys pinetis*; SEPG) is a fossorial ecosystem engineer that provides vital services including soil aeration and nutrient cycling. The SEPG is of conservation concern across its range, but conservation is hindered by uncertainty about specific variables influencing its presence. We determined vegetation characteristics associated with SEPG distribution at the home-range and local-landscape scales. We conducted vegetation and presence/absence surveys at 177 sites during March-September, 2016-2017. We detected SEPG at 21.5% of sites. Occurrence of SEPGs at the local-landscape scale was best explained by understory structure and canopy closure. For every 1 in. increase in groundcover height, a site was 1.2 (1.1-1.3) times less likely to be occupied. Occupied sites occurred over a range of canopy closure, but the highest probability of occupancy was ~48% closure. At the home-range scale, variables related to food resources and canopy best explained SEPG occupancy. For every 1% increase in grasses, a plot was 1.01 (1.007-1.019) times as likely to be occupied. Similar to the local-landscape scale, the highest probability of occupancy was an intermediate level of canopy closure (~48%). Our results indicate that conservation efforts should aim for areas with intermediate canopy closure, low understory structure, and groundcover dominated by grasses and forbs. Restoration of SEPG habitat should explicitly include multiple spatial scales as occupancy was affected by different vegetation variables at our two scales.

105^{E,HTA}: Estimating densities of a patchily distributed, sagebrush specialist across the Great Basin

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Accurately estimating densities of populations and identifying variables that contribute to changes in these densities are vitally important for species conservation. A lack of information on population densities of pygmy rabbits (*Brachylagus idahoensis*), habitat and dietary specialists that only occur in sagebrush – one of the most imperiled ecosystems in North America, caused United States Fish and Wildlife Service to deny listing under the Endangered Species Act in 2010. To investigate how pygmy rabbit populations are changing across the Great Basin, we created a spatial capture-recapture (SCR) model within a Bayesian framework to estimate densities temporally (over 3 years; 5 sites), and spatially (14 sites), while correcting for patchy, non-uniform distributions across our study sites. Temporally, estimated densities decreased throughout the study at 4 sites and spatially varied from 15 to < 1 pygmy rabbits/Ha. Additionally, we investigated environmental variables that may have contributed to varying estimated population densities and burrow densities. We found that percent clay in soil and cumulative snowpack were significant variables in predicting burrow densities, and elevation and slope were significant variables in predicting population densities. We will soon use our SCR model and significant environmental variables to project estimated rabbit densities across occupied sites within our study areas. This novel modeling approach will be widely applicable to other burrowing and central-place foragers.

106^{HTA}: Heard but not seen: bioacoustic analysis of Bengal tiger vocalizations

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Development of new methods of remote monitoring is essential for a more efficient, minimally disruptive census of species where dense jungle prohibits visual confirmation. This is particularly important for *Panthera tigris* whose populations have declined over 50% within the past century. With the population decline of many other forest-dwelling species, it is important now more than ever, to establish an efficient census method for such landscapes. Framework laid by the field of bioacoustics has the potential to fill this niche by exploiting the vocalization patterns of forest dwelling species. In order to develop an acoustic monitoring method for *Panthera tigris*, we first determined what physical characteristics could be identified solely from an individual's long-distance vocalization. To answer this question, spectrogram outputs of 265 bouts from approximately 1,618 hours of recording were analyzed to determine vocal characteristics from eight female and nine male adult Bengal tigers residing in controlled, ex-situ conditions. We found a significant difference existed between sexes as well as among individuals. The apparent complexity of tiger vocalizations could potentially enable a vocal "fingerprint" to be assigned to individuals, which, in turn would allow for censusing when using microphone arrays placed strategically over tigers' home ranges.

107: Novel approaches to improve modeling of species distributions for climate-sensitive mammals

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Realized niches reflect constraints on species distributions by different factors over small spatial extents (e.g., lower- vs. upper-elevation edges of occupancy, within mountains); additionally, species-climate relationships may reflect clinal variability in local adaptation, ecological context, and climate. Ecological niche models framed on the different range-subdivision schemes provided vastly different predictions of currently suitable distribution of *Ochotona princeps*. Furthermore, different division schemes best explained relationships to climate depending on the spatial extent at which relationships were examined, reflecting differences between long- and short-term processes of climate accommodation and suggesting the influence of local versus broader-scale drivers of species-climate relationships. Although we hypothesized *a priori* that evolutionary history (i.e., subspecies designations) would perform best, we found that heterogeneity in species-climate relationships was typically best explained by the ecoregional scheme across all three classes of analyses, especially at longer time scales. In some cases, responses to some important climate variables changed sign depending on the unit of analysis (e.g., Sierran vs. other clades), even within the same division scheme. Elevational subdivisions performed worst, in nearly every analysis,

even though climatic variables often covary with elevation. In addition to revolutionizing the analysis of ENMs via our novel methods, this study holds great promise for informing climate-adaptation management actions because it identifies the particular mechanisms limiting a species' distribution at the local extents at which such actions are typically implemented.

108^{E,HTA}: Invasive predator activity does not influence native mammal population demography

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Invasive species are among the greatest threats to global biodiversity. Invasive predatory invertebrates can influence native species directly via depredation and indirectly via behavioral changes (i.e. foraging behavior and movements). The combination of these direct and indirect effects of invasive species on native prey may be expressed at the population level via a demographic response or individually through reproduction. We conducted a before-after-control-impact experiment to assess the influence of red imported fire ants (RIFA), an invasive predatory invertebrate, on native rodent demography in Newton, Georgia, USA. From 2012-2015 we live-trapped rodents seasonally (11 total sessions) on a 1.21-ha grid centered on six 10-ha plots. Seasonal ant foraging activity was measured on each grid, with a hotdog bait trap placed at every other grid intersection. We collected pre-treatment data from summer 2012 - spring 2013. In July 2013, we broadcasted Amdro[®], a granular insecticide, on half of the 10-ha plots to reduce RIFA density. We analyzed survival, recruitment, and capture rate of three small mammal species: cotton rats, cotton mice, and oldfield mice. Reducing RIFA foraging activity did not influence small mammal species demography. Additionally, the proportion of reproductively active adult female rodents did not vary by treatment. Although other studies documented small mammal behavioral changes in response to RIFA activity, our results suggest no demographic response to RIFA activity at the spatial scale measured.

109: Impacts of trespass *Cannabis* cultivation on public lands to small mammal populations

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Trespass cannabis cultivation (TCC) on public land is an emerging concern throughout California. The associated environmental impacts and degradation to the surrounding ecosystem and its wildlife is significant. Small mammals are intentionally poisoned by cultivators with rodenticides to prevent them from harming cannabis plants and cultivation infrastructure, and may become contaminated prey for predatory species such as fishers (*Martes pennanti*) and spotted owls (*Strix occidentalis*). We designed a mark-recapture study to determine the spatial and temporal extents of environmental impacts from rodenticides used at TCC sites on small mammals in California. Pesticides at TCC sites may be impacting the demography and physiology of small mammals. We investigated the effects of pesticides at TCC and control locations on population parameters, abundance, species diversity, sex ratios, and weights of small mammals. We found significant differences ($P < 0.05$) in both sex ratios and weights for selected small mammal species. Differences seen may be due to a wide array of demographic variables including differing male and female home ranges, behavioral risks associated with TCC pesticide and small mammal interactions, as well as sublethal impacts associated with rodenticides on an individual's fitness. This is an ongoing seven-year study that will continue into 2020 investigating the longevity of these effects associated with TCC sites across California.

110^E: Use of camera traps to detect southern flying squirrels, *Glaucomys volans*

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Many small mammal studies involve live trapping, even though this can be labor intensive, expensive, influences behavior, and results in some mortality. Camera traps are less invasive and can be used to assess presence and occupancy of species. We used camera traps with bait tubes to detect southern flying

squirrels (*Glaucomys volans*). We surveyed three sites using 10 to 25 cameras and bait tubes. We used program Presence to estimate detection probabilities and area occupied by flying squirrels and non-target species. Detection probabilities for flying squirrels were influenced significantly by non-target species, prompting us to modify the bait tube design. When portion of area occupied was high, detection probabilities for raccoons was highest on the first night and then decreased, whereas flying squirrel detection probabilities were highest after three nights. When portion of area occupied was smaller, this pattern was not apparent and there was no negative affect of raccoons on flying squirrel detections. Detection probabilities for flying squirrels were related to forest structure, presence of raccoons, and to a minor extent, bait used. The three sites differed significantly in terms of detection probabilities and portion of area occupied by flying squirrels. Our results demonstrate that camera traps used with bait tubes provide an efficient and statistically reliable means of assessing occupancy by flying squirrels without the risk of mortality or adverse effects on behavior.

111: Effects of net-gun capture on survival of mule deer

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Remote tracking devices such as radio collars are of great use for wildlife studies, but capture techniques to deploy such devices always risk mortality and injury to the animal. Capture-induced mortality not only affects population sizes, but also introduces bias in survival estimates based on data from captured animals. In recent years, a large-scale research and monitoring project in Utah has involved capturing and radio collaring hundreds of mule deer (*Odocoileus hemionus*), a species of great interest in large parts of North America. Our objective was to investigate how the survival rates of these mule deer were affected by capture and handling to place collars. We used Cox proportional hazard regression within a model selection framework to compare the survival rates of animals that were captured in a particular year to those of animals that were not captured but fitted with a GPS collar in a previous year. We found that capture directly affected deer survival for 2-3 weeks. However, captured animals also experienced higher mortality rates during the rest of the year, potentially due to a biased sample. We recommend caution with analyzing GPS data from recently captured animals, as demographic rates may be biased compared to the overall population.

112^{E,HTA}: Space use and movement based interactions of two sympatric mesopredators in the low Arctic

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Changes are occurring rapidly in northern ecosystems in response to global warming. As winters become shorter and milder, taiga species encroach onto the tundra, where they may compete with tundra dwellers. Ecologically and morphologically similar species have similar needs and thus are most likely to compete. In northern Manitoba, where tundra, taiga and marine ecosystems merge, red foxes recently increased their use of coastal tundra breeding dens that were historically occupied by Arctic foxes. However, little is known about habitat use of tundra red fox or possible interactions with the sympatric Arctic foxes. We deployed 12 satellite collars (Telonics Inc., USA) on 5 red and 7 Arctic foxes to compare their spatial behaviors in a context of sympatry, and understand interspecific interactions. Red fox home ranges were larger or similar compared to Arctic fox depending on the season. Both species underwent long-range movement during food shortage, but they used different habitats and red foxes mostly used this strategy after Arctic foxes. Independence of fox movements and extensive home range overlap between species in winter, averaging 11%, suggests that red foxes do not exclude Arctic foxes from resources when resources are scarcer. Exploitation competition may be more important than interference competition, and when resources become too limited, Arctic and red foxes apparently co-exist in this area of sympatry because of their behavioral flexibility.

113*: Genetic diversity and connectedness among *Peromyscus* populations in the Great Lakes Region**

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The ranges of small mammal species in the Great Lakes Region are shifting rapidly in response to increased temperatures. The white-footed mouse, *Peromyscus leucopus noveboracensis*, has recently colonized the Upper Peninsula of Michigan, expanding across a large area of patchy habitat over a short period of time, such that new populations would be expected to show strong founder effects. At the same time, the woodland deer mouse, *Peromyscus maniculatus gracilis*, has disappeared from most of its historic range in the Lower Peninsula, and the remaining populations are increasingly isolated, so that they would be expected to show losses in genetic diversity and connectedness. Instead, both species currently show high levels of genetic diversity and low differentiation between populations in Michigan, with little to no isolation by distance. These patterns are likely due to a combination of factors, including the population ecology of these species and anthropogenic effects. This research was supported by an American Society of Mammalogists Grant in Aid of Research awarded to Joseph Baumgartner in 2015.

114: Collect to protect: how past and present collecting promotes conservation

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Given the high rate of biodiversity loss, it is not unreasonable to ask how responsible continued active collecting is when we already have drawers and cases full of specimens. I will present the case that continued scientific collecting is not only a useful tool for biodiversity conservation but an imperative for understanding the ongoing impacts of anthropogenic environmental change. Museum specimens provide irreplaceable baselines for biological diversity at a given point in time and location, allowing us to assess changes in geographic range and demographic parameters. Collections allow reassessments of taxonomic and geographic boundaries among species and populations, permitting accurate evaluation of threat status when taxonomy changes or species are cryptic. Data gathered through collecting or from existing collections can provide critical insights into population trends, reproductive rates, and timing of reproduction, all important elements in modeling future population viability. By comparing genetic data from collections at different time points we are able to assess changes in gene flow and effective population size. Finally, collections allow us to track changes in environmental stressors, diet, and contaminants using novel techniques and approaches. Contributing to and curating museum collections allows us to address current challenges in biodiversity conservation and better prepares us to confront future conservation needs.

115: Integrating mammalian specimen archives, long-term research initiatives, and natural resource conservation

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Long-term datasets provide vital insight into processes of change occurring across ecological and microevolutionary timeframes. Yet, eco-evolutionary investigations of mammals in a broader context are often limited in the scope of available data through long-term sampling to the use of unverifiable catch-and-release measurements. Fundamentally, small mammal sampling without voucher representation precludes the ability to perform rigorous analyses of integrated functional change through time. We must look forward by merging collective resources from ecological and evolutionary initiatives for more efficient and effective conservation and management of biodiversity and associated natural resources. I will review the relative impact of specimen collecting on natural communities, based on statistical evidence, and provide empirical examples of an integrated specimen-based framework for investigating linkages among small mammal communities and their associated flora and fauna. Importantly, I will discuss the logistical hurdles of incorporating specimen voucher collection into ecological field work, and some options for reasonable expectations towards expanding research opportunities across the mammalogical and broader scientific community.

116: Madagascar's tenrecs exemplify the necessity of continued scientific collecting for the conservation of biodiversity

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Madagascar is renowned for its unique biota, much of which, including the entirety of its native mammal fauna, is found nowhere else on Earth. Like many tropical countries, Madagascar is undergoing a conservation crisis characterized by rapid anthropogenic habitat loss that threatens to outpace ongoing taxonomic discovery. Extensive biological surveys across the island over the past three decades have produced an unprecedented wealth of voucher specimens that have formed the basis of hundreds of newly described species while simultaneously illuminating Madagascar's ecological, evolutionary, and biogeographic history. Collectively, this information is critical to the prioritization of protected areas. However, vocal objections to continued scientific collecting on Madagascar have emerged based on a series of assertions. These include the purported obsolescence of both voucher specimens and traditional specimen-based data in the delineation of cryptic species, the attainment of sufficient knowledge of Madagascar's vertebrates, and the mischaracterization of the fundamental objectives of modern scientific collecting. Tenrecs, one of four terrestrial mammal radiations endemic to Madagascar, provide counterexamples to such claims, which we illustrate using museum specimen data. Furthermore, analyses of range sizes across all Malagasy terrestrial vertebrates as well as taxonomic accumulation curves over time confirm that the current rate of species discovery on Madagascar is unprecedented, shows no sign of dampening, and is heavily biased towards microendemics most at risk from habitat destruction.

117: The role of collection-based research in promoting the conservation of mammalian diversity in the Philippines

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Collections-based research has shown the Philippines to have one of the greatest concentrations of endemic mammals. Field surveys following standardized procedures for over 30 years—conducted by a network of collaborating foreign and national museums, conservation organizations, universities, and government agencies—have documented the abundance, habitat associations, reproductive patterns, distribution, and phylogenetic relationships of most of the 200+ species, including discovery of more than 40 previously undescribed species and many others awaiting formal description. Much of this work is only possible through specimen-based research. Field surveys often uncover areas of endemism, some smaller than 200 km² but containing more endemic species than in any country in continental Europe. These data have had a direct role in initiating or improving the conservation status of more than 20 protected areas, and provide the primary basis for assessing the conservation status of mammals by Philippine government agencies and the IUCN. They also have laid the foundation for future studies of Philippine mammals by a new generation of field biologists who participate in the annual meetings of the Biodiversity Conservation Society of the Philippines, which was established as one outcome of this project, and have sparked a rising sense of national pride in the natural patrimony of the nation.

118^E: Polyestry in Mt. Graham red squirrels (*Tamiasciurus fremonti grahamensis*) provides clues to *ex situ* propagation

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Female Mount Graham red squirrels (*Tamiasciurus fremonti grahamensis*), are known to be receptive to breeding for a single day each season and for perhaps only six hours during that season. This field observation of seasonal receptivity is believed to be true for each of the 25 *Tamiasciurus* sub-species. However, by tracking glucocorticoid estradiol levels in an *ex situ* managed population for two consecutive years, we discovered evidence of polyestrous females with an average cycle interval of approximately 15-25 days. With this insight, we developed a schedule for conducting behavioral assessments and established a breeding management strategy. These behavioral assessments have helped to identify a window for breeding introductions while minimizing the chance of animal injury. Additionally, this approach maintains essential sociality, and territorial responses, a critical component necessary for producing animals viable

for release into the wild. This work is part of an ongoing study to develop a consistent propagation release program for this endangered sub-species. We will continue to track metabolite hormones and refine the breeding management approach to determine the ideal timing for breeding introductions. We are also monitoring *ex situ* cortisol and testosterone levels and plan to examine *in situ* metabolite levels for comparison. Determining polyestry in Mt. Graham Red Squirrels is an important discovery for this sub-species and will facilitate increased likelihood for *ex situ* reproduction to occur.

119^{HTA}: A natural diet promotes retention of the native gut microbiota of *Neotoma albigula* in captivity

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Mammals brought into captivity experience drastic lifestyle changes resulting in perturbations to the host's gut microbiota; however, it is still unclear which factors related to captive conditions are drivers of microbial community shifts. We examined the effects of diet on the gut microbiota of captive white-throated woodrats (*Neotoma albigula*), and tested whether the intake of foods that are part of the natural diet facilitates retention of native microbial communities. Woodrats were live-trapped at Castle Valley, Utah and transferred to the laboratory. Individuals received either a natural diet of *Opuntia* cactus pads or a novel diet of commercial rabbit chow. Fecal samples were collected on 3, 7, 14 and 21 days after entering captivity. Microbial inventories from feces were generated from Illumina 16S rRNA sequencing. Provisioning woodrats with natural diets considerably mitigated alterations in their microbiota, promoting a 90% retention of native microbial communities. In contrast, the artificial diet significantly impacted microbial structure and function such that 38% of the natural microflora was lost. Moreover, the relative abundances of microbial families (Ruminococcaceae, Lachnospiraceae) associated with non-digestible carbohydrate degradation increased, relative abundances of microbes (S24-7) related to oxalate degradation decreased, and phylotypes considered core microbiota including *Bifidobacterium* and *Allobaculum* were lost from these animals. These results highlight the importance of supplementing natural foods to maintain native microbiomes of animals kept in captivity for scientific or conservation purposes.

120: How much energy and protein do female barren-ground caribou (*Rangifer tarandus granti*) require in summer?

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Caribou maintain and restore body mass for survival and reproduction through the next year in just 4 months of summer. We varied digestible energy (16 vs. 12 kJ/g) and protein (15.2 vs. 7.6%) content of diets for captive caribou to simulate foraging on forbs (high energy & protein) sedges (low energy & protein) and a forage mix (low energy high protein). We used the relationship between net change in body composition (i.e. fat and protein mass) and the average daily intake to estimate the intake of digestible energy and protein required for maintaining the body of females with one calf (n=14) and those without a calf (n=6). Lactating females consumed 25% more food than non-lactating females as intakes rose from the period of parturition (106 vs. 142 g·kg^{-0.75}·d⁻¹) to weaning at 116 days postpartum (148 vs. 184 g·kg^{-0.75}·d⁻¹). Mass gains were greater on the forb than the sedge rations for fat (6.0 vs. 3.1 kg) and protein (3.3 vs. 1.6 kg). Lactating caribou required 44% more energy (1501 vs. 2156 kJ·kg^{-0.75}·d⁻¹) and 65% more protein (8.43 vs. 14.25 g·kg^{-0.75}·d⁻¹) than non-lactating caribou. Food intakes (6 – 7 g·100kg⁻¹) and daily energy requirements of lactating caribou are greater than those of other Cervidae, which is consistent with the large foraging areas used by caribou herds in summer.

121^{E,HTA}: Behavioral thermoregulation via roost selection by bats**

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Physiological processes are temperature-dependent, so climatic warming is expected to alter or disrupt them. To offset such adverse impacts, animals can use “thermal refugia”—relatively cool areas of the landscape or microhabitats that facilitate maintenance of optimal body temperatures—to escape the heat. Bats are believed to use diurnal roosts as thermal refugia, but supporting evidence is scarce. To evaluate whether diurnal roosts serve as thermal refugia for bats, we tracked fringed myotis (*Myotis thysanodes*) to roosts using VHF telemetry and used data loggers to measure roost temperatures. We compared temperatures of roosts used by bats to available but unused roosts using generalized linear mixed models and tested whether physical characteristics of roosts were correlated with thermal characteristics. Aspect—but no other physical characteristic—was correlated with roost temperatures and the timing of temperature peaks, but neither physical characteristics nor thermal characteristics of roosts influenced roost selection. Bats appear to have little ability to reduce energetic costs via selection of thermally preferable roosts. Because bats use torpor to save energy during the day, and because the efficacy of torpor decreases with increasing temperatures, bats are likely to face energetic costs as climates warm. This research was supported by a ASM Grant-in-Aid of Research awarded to Jesse Alston in 2018 and an ASM Travel Award awarded in 2019.

122^F: Amino acid isotope analysis reveals gut microbial contribution to protein metabolism in wild small mammals

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The role of the mammalian gut microbiome in breaking down recalcitrant carbohydrates (cellulose) and plant toxins has been studied for decades, particularly in hindgut fermenters that efficiently convert cellulose into short-chained fatty acids. The gut microbiome’s potential role in supplying essential amino acids (AA_{ESS}) to their mammalian hosts, however, has received less attention despite the fact that herbivores and omnivores of all body sizes are often protein-limited. Small mammal communities provide a useful system for studying this phenomenon because species with different foraging strategies (e.g., granivores vs. insectivores) often co-occur in the same habitat, allowing for a comparative approach across diets that vary in protein content. We used carbon isotope ($\delta^{13}\text{C}$) analysis of AA_{ESS} in C₃ and C₄ plants ($n=55$) and small mammal red blood cells ($n=50$) to examine the role of the gut microbiome in the protein metabolism of five small mammal species, including three granivores in the genus *Dipodomys*, an omnivore (*Peromyscus*), and an insectivore (*Onychomys arenicola*) in the Chihuahuan Desert. Our analyses indicate *D. ordii* and *D. spectabilis* route a substantial proportion (~20–45%) of the AA_{ESS} they use to build tissues from gut microbes. In contrast, *Peromyscus* and *O. arenicola* obtain nearly all of their AA_{ESS} from insects that consume C₄ plants. Our results highlight an under-recognized but potentially ubiquitous functional role of the mammalian gut microbiome.

123^F: Ultraviolet fluorescence discovered in New World flying squirrels (*Glaucomys*)

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Fluorescence of visible wavelengths under ultraviolet (UV) light has been previously detected in a wide range of birds, reptiles, and amphibians and a few marsupial mammals. Here, we report the discovery of vivid UV fluorescence of the pelage in *Glaucomys*, the New World flying squirrels. Fluorescence in varying intensities of pink was observed in females and males of all extant species (*G. oregonensis*, *G. sabrinus*, and *G. volans*) across all sampled geographic areas in North and Central America and a temporal range of 130 years. We observed fluorescence in museum specimens ($n=109$) and wild individuals ($n=5$) on both dorsal and ventral surfaces. Museum specimens of three co-occurring, diurnal sciurid species (*Sciurus carolinensis*, *S. niger*, and *Tamiasciurus hudsonicus*) were also examined but did not fluoresce. The ecological significance of this trait in the nocturnal–crepuscular flying squirrels warrants further investigation and opens the door to a new world of scientific exploration.

124: Estimating energy expenditure by fishers using GPS telemetry data

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Energy budgets provide insight into animal food requirements and how environmental conditions affect animal lives. Direct measurement of energy expenditure by animals is difficult, making indirect measurements important. In the past, Powell measured the metabolic rates of fishers (*Pekania pennanti*) running on a treadmill inside a metabolic chamber. He used the treadmill data to complete a model for energy expenditure by fishers based on the time fishers spend resting and running. Powell used field telemetry and snow-tracking data for wild fishers in the model to estimate field energy expenditure of the tracked fishers. Telemetry using Global Positioning Systems (GPS) can provide data that, though not as precise or complete as snow-tracking data combined with telemetry, can be far more extensive and available in non-snow seasons. In the autumns of 2012-2017, we outfitted 10 fishers (3F; 5 M) in northern California, USA, with GPS telemetry collars programmed to locate the fishers every 5 to 8 minutes. We followed the fishers for 4.5 ± 2.9 days and collected 1800 ± 2000 GPS locations per individual. We identified resting bouts and their length by identifying clusters of GPS locations all within the distance of telemetry error. We estimated distances travelled by adjusting linear distances using a fit equation developed from the data. Our results provide an important comparison of fisher energetics in 2 places with different terrain, climate and forests.

125^F: Lord of the fleas: shedding light on nocturnal hosts and stress hormones

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Parasites often are highly costly towards their hosts, depleting energy reserves and forcing redistribution of resources. A common response to parasite presence in some host species is an increase in stress hormones (e.g., glucocorticoids). These hormones have been proposed as biomarkers of physiological state and exposure to an adverse stressor. There is very little research on mammalian stress hormones and their variation with parasite presence; therefore, the aim of this study is to determine how costs of parasitism are mediated through endocrine function in deer mice (*Peromyscus maniculatus*). Specifically, we tested whether host individuals respond to parasite presence by increasing glucocorticoid levels. Individuals were randomly assigned to a parasite removal treatment (application of Frontline Plus ®) or a control group. Fecal samples were collected from all host individuals, and glucocorticoids were measured using enzyme immunoassays. Glucocorticoid levels did increase with parasite presence, but not significantly. This suggests that deer mice may develop a tolerance to parasites as a strategy to reduce negative symptoms. Further research should examine the use of varying concentrations of insecticides in parasite removal and the effects of nest parasites.

126^F: Small mammal responses to local and landscape variables in a forest/agriculture mosaic

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How do local and landscape processes affect community assembly? The contribution of these two spatial scales has been investigated in several taxa, but most authors analyze only the most common species in the community and fail to account for bias introduced by detection error. Hierarchical abundance models address both of these problems. They correct for detection error by pooling information from across the community to estimate species-specific abundance and detection probabilities. Using small mammal communities in forests, old fields, and active farms in Vermont as a model system, I will construct a hierarchical abundance model to 1) estimate abundances while correcting for detection error, 2) use estimated abundances to calculate species richness and diversity, and 3) determine the environmental covariates that are most highly correlated with these community measures. Covariates associated with the local environment will explain more variation in community structure than covariates associated with the landscape. Preliminary tests of the hierarchical model with simulated data demonstrate that the model produces accurate estimates of small mammal abundance and covariate significance at high and variable detection probabilities. Model estimates are less accurate at lower detection probabilities, but are still an improvement over uncorrected data. These early findings suggest that the modeling framework will successfully reduce the bias in detection error and better estimate the relative contribution of local and landscape processes to small mammal communities.

127: Mammals of the Sierra Madre Occidental, Mexico

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The Sierra Madre Occidental (SMO) is the largest mountain range in Mexico, yet it remains one of the least studied regions of the country. Using records from museum specimens, direct observations, and literature data, we built a database with 9323 records of mammals. The objective of our work was to update the inventory, to examine general distribution patterns based on the most recent ecoregional classification, and to have a preliminary assessment of hot spots and collection gaps. We recorded 143 species of mammals in the SMO (29.5% of the Mexican terrestrial mammals). Thirty-two are endemic from Mexico, including 12 endemic to the SMO. The highest species richness was recorded at the Tropical ecoregion (T, 78 species), followed by Madrean south (MS, 69), and Madrean Xerophilous (MX, 68). In contrast, the number of endemic species is higher in MS (17), followed by Madrean central (MC), Madrean north (MN) and Madrean Tropical (MT, 13 species each). All species endemic to SMO occur in highlands (MN, MC, MS). Sampling efforts are scarce or nonexistent for more than half the SMO, including the Mezquital and Santiago river basins, the regions with the highest biodiversity and speciation potential. It is urgent to assess the condition of current protected areas to ascertain their effectiveness, as well as to continue inventory efforts, particularly in the south.

128: Genetic variation of the long-haired mouse *Abrothrix longipilis* (Sigmodontinae), a SNP based assessment

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Abrothrix longipilis is an endemic species of semi-arid and Mediterranean areas of central Chile. An assessment of cytochrome b gene variation shows that the species presents phylogeographic structure; haplotypes form three main clades that latitudinally replace each other. Here we further assessed the pattern of the geographic variation of *A. longipilis*, by analyzing a dataset of over 124 thousand SNPs retrieved from unigenes assembled from transcriptomes gathered via RNAseq. Sampling includes specimens from localities covering the three main mitochondrial haplogroups and the latitudinal distribution of the species. Ordination analyses of the SNP dataset show that, in spite of the relatively large area inhabited by the species, the genetic variation of *A. longipilis* is not geographically structured. This result is discussed in light of geological evidence and environmental variables. Financial support: FONDECYT 1180366

129: Stomach nematodes in cotton rats: parasites, commensals, or mutualists?

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Helminth endoparasites of mammals can be detrimental and even lethal. However, certain gut nematodes of rodents can have neutral or beneficial effects, upregulating host immune systems, influencing gut microbiomes, and altering host life histories. We determined presence and total mass of stomach nematodes, host body masses (BM), reproductive masses (RM), and litter sizes in > 1,100 cotton rats (*Sigmodon hispidus*) from 1987-1990 field samples from Virginia and Georgia (which each had parasitism rates around 25%), and an early-1980s sample from Virginia, which had an 80% parasitism rate and heavier parasite loads. BM and RM were highly significantly correlated with body length (surrogate for age) in each sex from each sample, so we used body length as a covariate in general linear models testing effects of worm presence and worm mass (parasite load). Parasite presence had either positive or neutral effects on BM and RM in both states' later samples; they had no effect on BM but negative effect on RM in the earlier Virginia sample. Parasite load in infested rats had no effect on BM or RM in either sex for any sample. For the Georgia and earlier Virginia samples, for which we had litter-size data, being parasitized had no effect on litter sizes in either sample, whereas increasing parasite load had no effect on Virginia litter sizes but positive effect on Georgia litter sizes.

130^E: How pathogen species limits correspond with mammal taxonomy: predicting species boundaries in *Pneumocystis*

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Although instances of perfectly cospeciating host-parasite assemblages are rare in nature, fungi in the genus *Pneumocystis* and their mammal hosts are a potential example. *Pneumocystis*, a group of mammalian lung parasites, are the only known obligate fungal parasites of animals. With no known environmental reservoirs and lab tests suggesting strict host specificity, *Pneumocystis* presents an interesting system with which to study the impact of host phylogeny on a group of parasites with limited host-switching potential. Researchers have predicted that there may be a single species of *Pneumocystis* for every mammal species, and thus far, *Pneumocystis* has been found in every mammal species that has been tested. However, ecological and taxonomic study of *Pneumocystis* has been slow, with only five species described and no new species descriptions published since 2006. Here, we identify potential undescribed *Pneumocystis* species using genetic species delimitation techniques. Results support the existence of many more *Pneumocystis* species than are currently known, but several are apparently capable of infecting many closely-related mammals (i.e. those in the same genus). Additionally, we predict that there may be 3,000 to 5,000 *Pneumocystis* species inhabiting the 6,399 currently recognized mammal species. Although crude, our prediction challenges the dominant perspective of strict specificity between mammals and *Pneumocystis*.

131^E: Migratory bats: stable population or compensatory immigration?

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Migratory animals continually face new human-made structures along their migratory pathways, and some can pose lethal dangers to the animals that interact with them. Partly due to interactions with wind turbines, hoary bats (*Lasiurus cinereus*) and silver-haired bats (*Lasionycteris noctivagans*) are thought to be in decline. We therefore hypothesized a similar trend in long-term capture data at a summer roosting site. We compiled available capture records over 19 years and corrected for variation between months and survey effort. Contrary to some other studies, our data did not support the hypothesis of a population decline for either species. This suggests the possibility that range-wide declines are less severe than previously thought. However, given the high quality and abundance of roosting habitat at our site, we caution that compensatory immigration could be stabilizing bat populations locally, despite overall declines at larger spatial scales.

132^{HTA}: Morphological variation of epipubic bones in didelphid marsupials: sexual dimorphism and locomotion

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Studies of skeleton morphology using linear morphometry allows us to assess size and shape influence in bone functions. Marsupials are the main vertebrate group that possess epipubic bones. There are two hypotheses for its function: reproduction and locomotion. The aim of this work was to study the morphological variation of these bones to understand its function in Didelphimorphia marsupials. We measured 371 skeletons (epipubic bones, pelvis, humerus, femur and tibia) from both sexes of nine species representing six genera with different locomotion habits, to test sexual dimorphism and its locomotion influence. We named epipubic bone structures which were undefined in literature. We demonstrated the sexual dimorphism in size through t-tests and qualitative osteological analysis. Females had longer and curved epipubic bones than males in all studied species. A principal component analysis (PCA) of epipubic bone and pelvis measurements generated groups consistent with the locomotion habits (semi-aquatic, arboreal, scansorial and cursorial), and the most important measures were the longest length and the base

width of the epipubic and the pubis length, where the epipubic articulates. This groups were also recovered in a PCA with appendicular skeleton measurements, in which the more important variable was the humerus. These results support both previous hypothesis: reproductive, with a longer bone, females can have more muscle attached to support the abdomen; locomotion, specific morphological features for each locomotor habit.

133: Energy expenditure of captive adult non-reproductive common marmosets (*Callithrix jacchus*) is below anthropoid primate norm

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The National Research Council (NRC) recommendation for maintenance energy requirement (kcal/day) of captive non-human primates is twice estimated metabolic rate or $140X(\text{body weight})^{0.75}$. This recommendation may be an overestimate of energy requirement for common marmosets due to the fact that marmosets reduce metabolic rate significantly during sleep. We present data on day- and night-time resting metabolic rate (RMR) and daily digestible energy intake (DEI) for 22 adult common marmosets of both sexes and body weights ranging from 322g to 618g. RMR was measured using open circuit respirometry with animals in a temperature controlled chamber set at 30°C, which is within marmoset thermal neutral zone. DEI was the average of two four-day digestion trails in which food intake and fecal output was measured and gross energy quantified with bomb calorimetry. DEI equals energy intake minus fecal energy loss. Mean body weight=435±16g; mean day-time RMR=31.3±1.3kcal/day and night-time RMR=26.3±2.1kcal/day; and mean DEI=52.5±2.4kcal/day. The mean value for day and night RMR was 83.5% and 70.1% of the NRC estimated RMR value for 435g primates (37.5kcal/day), respectively. Mean DEI was 1.7 times day RMR, twice night RMR, and only 70% of the NRC recommended value for 435g primates (75kcal/day). We suggest that the equation $100X(\text{body weight})^{0.75}$ provides a better target for daily maintenance energy intake for adult non-reproductive captive marmosets.

134: Road crossing patterns of ocelots in South Texas

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Once widespread throughout Texas, Louisiana, and Arkansas, the U.S. population of the federally endangered ocelot (*Leopardus pardalis*) is now restricted to the Lower Rio Grande Valley (LRGV) of South Texas. An estimated <80 individuals remain between two genetically isolated breeding populations. While the population decline is due to several factors, vehicle collisions have been found to be the contemporary leading proximate cause of ocelot mortality in the LRGV. Wildlife crossing structures may provide a viable mitigation strategy, but must be placed in locations that maximize likelihood of use by ocelots. To better understand ocelot movement patterns in relation to roads, we will analyze a telemetry dataset of 68 ocelots (30 female, 38 male) radio collared in and around Laguna Atascosa National Wildlife Refuge from 1982-2007. We will determine the frequency at which these animals crossed four types of roads - high traffic paved, low traffic paved, gravel, and dirt – and evaluate whether these crossing rates were influenced by sex or by density of each road type within the animal's home range. We will further evaluate land cover spatial distribution at locations where ocelots crossed paved roads to determine if there were patterns in crossing locations. This information will help the Texas Department of Transportation and other management entities in developing ocelot conservation strategies in this highly fragmented landscape.

135: Genomic tools to inform white-tailed deer management in Rhode Island

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The white-tailed deer (*Odocoileus virginianus*) is a keystone species and major game species for hunters. In parts of the U.S. and Canada, white-tailed deer have been infected with Chronic Wasting Disease (CWD), which could be a potential risk to human health. We used genomic tools to determine the potential risk of CWD spread in white-tailed deer in Rhode Island. In collaboration with the Rhode Island Department of Environmental Management Division of Fish and Wildlife, 206 ear samples were collected from deer check stations in Rhode Island from 2012 to 2013. The samples were located to city or town of origin and included samples from two islands, Block Island (n = 14) and Conanicut Island (n = 3). We expect island deer populations to have lower levels of genetic diversity than animals from the mainland. We used the double digest restriction-site associated DNA sequence method and next-generation sequencing to generate genomic data. The program STACKS was used to quality filter the data and identify single nucleotide polymorphisms. The data will be analyzed to determine the population structure of deer and the area that should be quarantined if CWD is detected. The data also will be used to determine if deer in Rhode Island should be managed as one or multiple management units. Genomic tools can readily be developed for non-model animals and greatly contribute to management decisions.

136: Chill out: microclimate use by small herbivores challenged with plant toxins and warmer temperatures

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Increasing ambient temperatures due to climate change pose a novel threat to herbivorous mammals. Ambient temperature interacts with mammalian physiology in such a way that toxic compounds become more potent at higher temperatures. This phenomenon is known as temperature-dependent toxicity (TDT). While the mechanism and effects of TDT have been previously documented, it remains unknown whether mammalian herbivores can behaviorally mitigate TDT. Here, we investigated use of cooler microclimates by desert woodrats (*Neotoma lepida*) from the Mojave Desert that feed on chemically defended leaves of creosote bush (*Larrea tridentata*). Utilization of cooler microclimates and the influence of microclimate access on food intake and body mass maintenance were determined in a lab-based experiment. We predicted that woodrats would use cooler microclimates when provided and would show improved performance compared to woodrats held at warmer temperatures. Woodrats did use cooler microclimates when provided, but there was no effect of diet on microclimate use. Access to cooler microclimates did not affect total food intake but did buffer against body mass loss compared to woodrats without access. Our results suggest that cooler microclimates could provide a means to mitigate TDT through improved body mass maintenance. Understanding how mammalian herbivores interact with their environment is imperative to advance the field of plant-herbivore interactions and to further elucidate impacts of climate change.

137: Lion-porcupine interactions in Africa, including impacts on lion predatory behavior

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In the 1600s, Jan van Riebeeck, Commander of the Cape for the Dutch East India Company, discussed in his personal journal, the first accounts of lion-porcupine interactions in sub-Saharan Africa. These might be the first accounts of relations between the two species. Although African crested porcupines *Hystrix* spp. typically represent less than 2% of lion kills, under certain circumstances this proportion can rise to 34%. Due to the small size of the prey, interactions between the two species are poorly documented. Here we review porcupine-lion interactions and their impact on lion behaviour, including: 1) lion predation on porcupines and the circumstances under which porcupine predation increases; 2) lions injured or killed by porcupine quills; and 3) a case of a lion severely injured by a porcupine quill. Porcupine quills can be effective weapons and sometimes seriously wound lions, resulting in death. Death from quills can be a slow process and under these circumstances, death may be the result of starvation or infection (septicemia).

138: Systematic revision of Peruvian forms of *Caenolestes caniventer* (Paucituberculata: Caenolestidae)

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The shrew opossum *Caenolestes caniventer* is a species widely distributed in mountain forests of southern Ecuador and northern Peru, and Huancabamba depression (HD) was suggested as barrier of distribution. Currently, this species is considered as monotypic due to lack of morphological differences between populations. We performed a phylogenetic analysis using cytochrome b for *caniventer* finding two different lineages: 1) populations from north of HD (*C. caniventer* "North"), and 2) populations south of HD and one close to the frontier with Ecuador (*C. caniventer* "South"). The genetic distance between them was 6.5%. Also, we examined 62 specimens assigned to *C. caniventer* from Peru, including new records south of HD, and compared with other species including *C. sangay*. Morphologically, these groups are almost similar. Principal component analysis using 12 meristic variables showed that most character variation was related to size (PC1: 80%) but the two groups were partially overlapped. We suggest that the "south" population is a candidate new species within the *caniventer* group, separated by the "north" population by the HD, likely a barrier and speciation driver in this group. The "south" population close to Ecuador probably indicates a secondary invasion or a case of sympatry not yet confirmed.

139^{HTA}: Phylogenomic systematics of rorqual whales: ultra-conserved elements support a novel Gulf of Mexico lineage

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Rorqual whale taxonomy is a work in progress. Ambiguity in the evolutionary relationships that form the basis for naming balaenopteroid whales (genera *Balaenoptera* + *Megaptera* + *Eschrichtius*) creates confusion for the naming and protection of these taxa. Genomic tools have the ability to help resolve these relationships and provide clarity for conservation. However, for balaenopteroid whales, previous genome-scale studies have had incomplete taxon sampling, particularly for the more cryptic medium-sized whales in the genus *Balaenoptera* (*B. edeni*, *B. brydei*, *B. borealis*, and *B. omurai*). In this study, we used a novel method to isolate and sequence 3080 ultra-conserved elements (UCEs) from throughout the nuclear genome of 57 samples representing 15 taxa, including all taxa within the clade Balaenopteroidea. From these data we identified 1.8 million polymorphic nucleotides for phylogenetic analyses. Importantly, our results support the unnamed Gulf of Mexico Bryde's whales (*Balaenoptera* cf. *B. edeni*) as a unique lineage outside of the clade that includes Eden's whales (*B. edeni edeni*) and Bryde's whales (*B. edeni brydei*). This novel taxon warrants a name and protection equivalent to that of an independent species. Furthermore, our results show the gray whale lineage (Eschrichtiidae) nested within the clade Balaenopteridae, resulting in paraphyly of Balaenopteridae. In addition, the clade Megaptera is nested within the clade Balaenoptera, making the latter paraphyletic. Based on these results, we propose several taxonomic revisions.

140^E: Ecogeographic skull variation across southwestern red squirrels (Genus *Tamiasciurus*)

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Multiple disjunct populations on mountaintops across the American Southwest have a predictable mammalian fauna. Unfortunately, we still know relatively little about geographic variation in ecological and evolutionary features and biogeographic history for many of these species. For example, recent phylogenetic analyses reveal phylogeographic structure among regional, disjunct southwestern populations of red squirrels (chickarees, genus *Tamiasciurus*) that mismatches with taxonomy. Despite size variability across the range of red squirrels, previous efforts to characterize craniodental variation have failed to detect clear geographic patterns, or associations between body size and environmental factors in this taxon. Here, we sampled 298 specimens of red squirrels to evaluate the relative support for major explanatory hypotheses of geographic body size variation including seasonality, productivity, heat conservation or dissipation, or a combination of ecogeographic processes. Results suggest that resource availability may

ultimately underlie observed spatial patterns in size and morphology of red squirrels among southwestern sky islands.

141: Black bears (*Ursus americanus*) recolonizing historic ranges: Indiana human-bear interactions

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Over a century after extirpation from Indiana, two American black bears (*Ursus americanus*) were confirmed in the state during the summers of 2015 and 2016. During 2015, the public and management agency were unaccustomed to living with large carnivores, which resulted in intentional and unintentional feedings, habituation, and ultimately its euthanasia of the bear. The following year a second black bear was confirmed in Indiana and the Department of Natural Resources deployed targeted education and outreach materials to the general public to try to minimize negative human-bear interactions. This time, the bear avoided negative human interactions and safely overwintered in Indiana, due in part to a more informed public. Expanded public education and an increase in preparedness of the State provided two different outcomes for the recent bears in the state. Habitat suitability models suggest that Indiana could potentially support bears in portions of the state. Natural range expansion in neighboring states suggest that Indiana will see more black bears in the future. These two bears highlighted the need for Indiana and other state agencies to have some preparations in place—especially related to public education—to respond to transient large carnivores that are moving through and eventually recolonizing long extirpated areas.

142^E: Characterizing diet of an endangered salt marsh endemic rodent with DNA metabarcoding

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Salt marsh harvest mouse (SMHM; *Reithrodontomys raviventris*) are a federally endangered species endemic to the San Francisco Estuary wetlands. Historically, SMHM were presumed to specialize on pickleweed (*Salicornia sp.*) for habitat and diet. However, recent data from cafeteria trials suggest a wider breadth of dietary resource use and potential preference for non-native plants commonly used in waterfowl management. Understanding the dietary resources utilized by SMHM and potential competitors is important for guiding restoration efforts in their historic range. We used high-throughput sequencing to identify plant DNA sequences in scats of SMHM, western harvest mouse (WHM; *R. megalotis*) and house mouse (*Mus musculus*). Scats were collected from Goodyear Slough in the Grizzly Island Wildlife Area during summer 2018. We amplified the ITS2 locus, a common barcode region for plants, in scats from 36 individuals from two sampling locations: tidal and managed wetlands, respectively. Nine plant genera were detected across 17 SMHM scats from the tidal wetland, where no competitors were sampled. Plant detection frequencies reflected their availability on the landscape. Twelve plant genera were detected in 12 SMHM, 3 WHM, and 4 house mouse scats from the managed wetland, six of which occurred in SMHM scats. Grasses (*Bromus*, *Festuca*, *Hordeum*, *Sonchus*) were detected in WHM scats but not SMHM scats, suggesting potential dietary partitioning by harvest mouse species. Additional sampling for spatiotemporal dietary patterns is ongoing.

143: Lek of the wrinkle-faced bat, *Centurio senex*

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The mating system called "lek" has rarely been documented in bats. This system consists of groups of males that are exhibited and selected by females to copulate. The males do not contribute more than genetic material. In 2018, we found a group of *Centurio senex* males (a species that presents sexual dimorphism with males that have chin folds to create skin masks) perched and performing visual and acoustic displays. During 13 visits, we characterized the perches of the males and conducted censuses.

We recorded the behaviors with an IR-sensitive camcorder synchronized with an UltraSoundGate device. A maximum of 56 males were observed during the same night, showing displays on perches with an average 2.35 m height. A total of 21 hours divided into 8 nights were filmed, where a total of 645 events were quantified and grouped into 11 behavior categories. The general display of the males was perching with the skin mask up. They moved their wing tips regularly and produced ultrasound. We recorded "encounters" when another bat approached the male, and the male began moving his wings quickly and varied vocalization with an audible beep at the end. The visitor almost never perched. We recorded 181 "encounters". On one occasion, the visitor hung next to the male and they copulated. At least 8 sonotypes were recognized in the different behaviors displayed.

144: A re-examination of the distributional range of the least weasel, *Mustela nivalis*, in the Nearctic

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The least weasel, *Mustela nivalis*, the smallest member of the Order Carnivora, has a circumboreal range throughout the Holarctic. In the Nearctic, many recent range extensions of *M. nivalis* have been reported. This poses the question as to whether these are actual range extensions or merely artifacts. To examine this question, I looked at factors including specifics of the range extensions reported, natural history traits, commercial trapping records, timing of emigration from the Old World, and how these factors relate to those of *M. frenata* and *M. erminea*. *Mustela nivalis* is a secretive species rarely found throughout their range because they are very infrequently trapped or otherwise found, vulnerable to extirpation during localized rodent declines, and populations tend to be unstable, highly mobile and locally ephemeral. Recent reported range extensions are almost all at the southern periphery of their distribution in the US, and all involve sympatry with only one other *Mustela* weasel species. None of the range extensions have been reported from the area of sympatry where all 3 *Mustela* weasel species co-occur in the Great Lakes region. The Nearctic range of *M. nivalis* likely is influenced by its rather late arrival into North America (late Pleistocene), local distribution of small rodents, interactions with *M. frenata* and *M. erminea*, and various abiotic factors.

145: Diversifying mammalogy by intentional interventions for undergraduates and beyond

Corey Welch

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The reality of 'minority becoming majority' and the current demographics of the American Society of Mammalogists demonstrates that multiple, intentional interventions must be made by the faculty, postdocs, and graduate students to retain the relevancy of mammalogy in the coming decades. Interventional actions will be highlighted to improve undergraduate retention in mammalogy from underrepresented populations (UR = minorities, women, low income, first generation, LGBTQ+, and people with disabilities). These actions include ways to 'decolonizing your syllabus', cultural awareness of specific barriers facing different UR-groups, and how to create UG-programs that succeed in retention & inclusion within the biological sciences. Some common myths about "why diversity recruitment and retention is difficult" will be highlighted. The talk will include a brief introduction/overview of the overall session, the 4 subsequent presentations, and the final extended question/answer period.

146: Mentoring and learning strategies to increase URM retention in STEM

Brett Woods

High Point University, High Point, NC, USA

Less than one third of underrepresented minority students planning to earn a STEM degree will complete their STEM degree within six years. Attrition from undergraduate STEM programs, rather than a lack of recruitment, interest or incoming academic credentials, largely accounts for the disproportionately low representation of minority students with STEM degrees. It is essential for educators, administrators, and institutions to implement practices that ensure the success of all students, especially as student populations become increasingly diverse. In an effort to increase URM retention in STEM, a program was created to address known barriers to URM success. Program participants showed significantly higher pass rates in two STEM courses and significantly increased retention rates to year two compared to non-participant

underrepresented minority students. Participants performed similarly or better than non-underrepresented minority students, supporting the program's effectiveness in reducing or eliminating the achievement gap. In this presentation, I focus on the mentoring aspects of the program and effective strategies that address habits of mind, implicit bias and student perspectives. Specifically, strategies faculty should employ to provide an environment that addresses challenges associated with being a URM student and thus increase URM retention in STEM.

147: Testing the “cherry-on-top” hypothesis: is evidence important in convincing TAs to use evidence-based teaching practices?

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Evidence-based teaching practices (EBTP), like inquiry-based learning, inclusive teaching, and active learning, have been shown to benefit all students, especially women, first-generation, and traditionally minoritized students in STEM. However, little research has focused on how best to train teaching assistants (TAs) to use EBTPs. Our previous work has shown that TAs who model EBTPs in a workshop find the practices more valuable and useful than TAs who are exposed to evidence for EBTPs' effectiveness while facilitators do the modeling. We hypothesized that if we experimentally manipulated workshop groups such that all TAs actively modeled teaching practices, but only one group was exposed to evidence, there would be no differences between the experimental groups. To test this hypothesis, we offered a workshop in which all TAs learned and modeled EBTPs. Participants in the Evidence group were exposed to evidence of EBTPs' effectiveness whereas Activity group participants were not. Using survey data, we found no differences between the groups at any time point. Our findings support the “cherry-on-top” hypothesis, whereby evidence is a nice, albeit non-critical, addition to TA training: modeling new teaching practices is the most effective component of training and exposure to evidence is helpful, but not enough to convince TAs to use EBTP. This outcome has broad implications for how we provide professional development sessions to TAs and potentially to faculty.

148: Building personal bridges: connecting your science to your communities

Danielle Lee

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I have built a scientific and extra-curricular professional career that includes a very strong emphasis of science outreach to traditionally under-served and under-represented communities. Traditional science communication includes journalists as information mediators between the science community and the information consumer public. Science communication in the 21st century has brought not only new technologies, but also a revised meaning of science engagements. Today, effective science outreach and communication requires authentic connections with audiences to attract participation and participation from wider demographics. Owning your identity and using that as your center is the key to connecting your science to wider, more diverse audiences and serving traditionally under-served groups.

149: A history of diversity, inclusion, and safety in the American Society of Mammalogists

Jessica Light

Texas A&M University, College Station, TX, USA

In this presentation, I will discuss how the American Society of Mammalogists (ASM) has worked to provide a safe and professional environment that promotes inclusion and encourages diversity. According to our Statement of Inclusion, ASM expects its members to maintain an environment free of discrimination, harassment, or bullying. In 1992, The Office of the Ombudsperson was established to address member concerns and complaints and help maintain a professional environment at all ASM sponsored events. Similarly, the Human Diversity Committee strives to increase the diversity of active ASM members by working to reduce barriers for participation by people from underrepresented groups in biology. The Human Diversity Committee was elevated to a standing committee in 1998 after being originally established as an *ad hoc* committee. ASM is proud to be an inaugural member of the Societies Consortium to Stop Sexual Harassment in STEMM (science, technology, engineering, mathematics, and medicine), and we continue

to strive to take necessary measures to provide a safe, welcoming, and inclusive environment for all ASM members.

150^F: Effects of land-use on the spatio-temporal ecology of two mongoose species in KwaZulu-Natal, South Africa

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The spatial ecology of the Herpestidae family remains relatively poorly studied across southern Africa. Small carnivore species, like mongoose, can provide models of how mesocarnivores persist with anthropogenic land-use change. We are investigating how this land-use change affects aspects of the ecology, especially spatial habitat and temporal use and movements of two co-inhabiting mongoose species (water: *Atilax paludinosus*, large grey: *Herpestes ichneumon*). Individuals of these two species were trapped, collared and tracked using Global Positioning System (GPS) - ultra high frequency (UHF) transmitters to study their activity, home range size and habitat use across a land-use gradient from the fragmented natural and farmland mosaic of the KwaZulu-Natal Midlands to urban areas of the greater eThekweni Durban Metropolitan Open Space System (D'MOSS). Home ranges and habitat use showed individual variation within and across species. Preliminary findings suggest that urban inhabiting mongooses have home range vastly reduced as compared to natural and farmland inhabiting mongooses. This highlights how the behavioral plasticity and generalist nature of these species contributes to their persistence in anthropogenically transformed landscapes

151: Risk, resources and information; how environmental cues impact small mammals' behavioral strategies

Sonny Bleicher

George Mason University, Fairfax, VA, USA. University of Jyväskylä, Jyväskylä, Finland

It is well established that animals adjust their behaviors based on cues they collect as they navigate the landscape. Meanwhile, scientists entrench themselves in opposing views on whether the cues are acute or chronic. The ecological implications of that distinction is whether animals act in predictive, preventing risk, manners or in a responsive, responding to a direct risk cue, thus minimizing impact in a direct exposure to the cue. In this presentation I intend to provide a framework to investigating this broad question and present a couple of examples to suggest that the evolutionary pressures resulted in a risk management strategy that includes both, but switches between them based on environmental, sequential and evolutionary circumstances. My examples include: (1) a study of voles' ability retain information on predator activity and (2) a study of convergent rodent populations applying divergent strategies to respond to variations in predation risk, based on the ghosts of predator past and the structure of their historical predator community structure.

152^F: Variation in play behavior among early- and late-born juvenile squirrels

Martha Monroy, Madelene Shehan, Scott Nunes

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Animals must allocate available energy according to priorities that ensure survival and maximize long-term reproductive success. Among seasonally breeding animals, young born at different times in the season may face different energetic constraints and may need to allocate energy differently. For example, young animals born later in summer may need to devote more energy to growth or fattening in preparation for winter and may thus have less energy to devote to behaviors such as exploration or play. We evaluated the play behavior of juvenile Belding's ground squirrels (*Uroditellus beldingi*) over a three-year period, during which the timing of the squirrels' active season and breeding interval varied substantially between years. The play behavior of juvenile squirrels varied significantly with both body mass and birth date. Juveniles with low body mass and juveniles born later in the year played at lower rates and had shorter-duration play bouts than did heavier juveniles and early-born juveniles. These results are consistent with the idea that the expression of play behavior in young animals is influenced by competing demands for energy. Play behavior can influence various aspects of juvenile development; thus, our results also raise

the possibility that in some animals, birth date may influence the trajectory of development via effects on the expression of play behavior.

153^F: Play behavior and the development of boldness and caution in juvenile ground squirrels

Madelene Shehan, Scott Nunes

University of San Francisco, San Francisco, CA, USA

We evaluated the relationship between play behavior and the development of boldness in juvenile Belding's ground squirrels (*Urocitellus beldingi*). We observed the play behavior of juvenile *U. beldingi* and conducted flight-initiation distance tests to measure boldness at the beginning and toward the end of the developmental period during which play primarily occurs. The age of mothers was a significant predictor of the outcome of initial tests. Juveniles with yearling mothers noticed and fled from intruders at greater distances than did juveniles with older mothers. This result suggests maternal influences on the development of boldness and caution, with young of less experienced mothers developing greater caution. Distances at which juveniles first noticed and fled from an intruder increased significantly over the play period, suggesting an increase in caution across the play interval. Rates of social play were significant predictors of increases in distances to notice and flee from an intruder, with juveniles who engaged in social play at the highest rates having the greatest increases. Other studies have indicated an association in some situations between social play and increased boldness rather than greater caution. Together with these studies, our results suggest that possible influences of play behavior on boldness may vary with the context in which an animal finds itself.

154^E: Space use patterns of the burrowing echimyid rodent, *Clyomys laticeps*

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Understanding the space use patterns of a population and its determinants may give insights about a species' ecology, social and mating systems. Although echimyid rodents display a variety of mating and social systems, movements of burrowing species are poorly studied due to their cryptic habits. Hence, in this study we evaluated the effects of body mass, sex, and palm fruit availability on space use patterns of the burrowing echimyid *Clyomys laticeps*, by measuring individuals' daily home range (DHR) and intensity of habitat use (IU). In nine months of study in a Cerrado site, we tracked 14 adults with the spool-and-line in a backpack method. Males had larger daily home range size than females, probably as a response to greater body mass and reproductive behavior. Furthermore, females had greater IU, presenting site fidelity, which can be due to offspring care as a response to non-seasonal reproduction observed in our study. *Allagoptera campestris* palm fruits had no influence on the space use patterns of *C. laticeps*. Shifts in proportion of consumed food items may explain the lack of this influence in our study. Our findings suggest that space use patterns of *C. laticeps* are mainly explained by behavioral and physiological differences between sexes, including body mass and reproductive strategies. Additionally, larger male movements and female site fidelity suggest a solitary behavior and a polygynous mating system.

155^{E,HTA}: The vocal repertoire of a highly social carnivore**

Kenna Lehmann, Kay Holekamp

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To understand the patterns of variation and diversity in animal signaling, we first need to understand the function and evolution of signals in a wide range of animal taxa. We must also determine how signals can be modified and adapted to new contexts and allow for the evolution of new signal types. To that aim, we have characterized the spotted hyena's (*Crocuta crocuta*) repertoire. The spotted hyena lives in a complex fission-fusion society with a linear dominance hierarchy and maternal rank inheritance. Group mates hunt cooperatively, defend a common territory, and even lead coordinated attacks on lions. Hyenas also possess a rich vocal repertoire that appears to facilitate their myriad social interactions. Despite this, the hyena repertoire is largely unstudied and has not been quantitatively described. Here we quantify the spotted hyena repertoire via clustering analysis on a large library of recordings. We then discuss how the spotted hyena repertoire demonstrates how signals can vary and then diverge to derive new signals that

can be applied to new contexts, expanding the repertoire in the process. This research was supported by a Grant-in-Aid of Research awarded to Kenna Lehmann in 2017

156^{HTA}: Bait-station use by non-target wildlife as a route of exposure of urban carnivores to rodenticides

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Anticoagulant rodenticides (ARs) are placed in tamper-resistant bait stations to control urban commensal rodent populations. Native rodents can be exposed to ARs directly, through consumption of AR baits, whereas carnivores, such as coyotes, can be exposed indirectly by eating AR-laden prey, which can eventually lead to death. The extent to which native wildlife visit AR bait stations, however, is unclear. We used Reconyx trail cameras to monitor use of commercial bait stations in 90 residential yards in Orange County, California. Two stations, baited but with no ARs, were monitored continuously in each yard for ~30 consecutive days during the dry and wet seasons. Based on dry-season results, most yards (84%) were visited by at least one wild mammal species (range = 0-6). Wild mesocarnivores were recorded in 52% of yards, with Virginia opossums and raccoons being the most common species (38% and 30%). Unlike other mesocarnivores, striped skunks were rare (4%). Native rodents, including ground squirrels, deer mice and woodrats, were only detected in 13% of yards. Larger carnivores were present at least once in 10% of all yards, with coyotes and bobcats present in 6% and 8% of yards, respectively. These results will be combined with wet-season results to examine the relative importance of local environmental features versus mapped, landscape-scale measurements of urbanization as predictors of risk of rodenticide exposure of native wildlife. This research was supported by a ASM Student Travel Award awarded to Christopher Burke in 2019

157: Ecological impacts of a population outbreak of the long-haired rat (*Rattus villosissimus*) in arid Australia

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The northern arid zone of Australia is notable because of the unpredictable rainfall patterns that it experiences. Sufficient rainfall results in pulses in primary productivity that can lead to population outbreaks of native rodents (Muridae). Not all species of rodent respond to each resource pulse. Perhaps the best example of this irregularity is the long-haired rat (*Rattus villosissimus*), the largest extant rodent in arid Australia (body mass: 150 g). The species is not resident in our study area in the western Simpson Desert, rather population outbreaks occur every 25-30 years. Such outbreaks have significant impacts on the biotic and abiotic environment. Here, we report on an outbreak that occurred from June 2010 to December 2012 and that resulted in a series of novel ecological interactions, specifically: 1) long-haired rat predation on smaller mammals (body mass <100 g); 2) invasion by the rats in to refuge habitat of the nationally vulnerable plains mouse (*Pseudomys australis*), and 3) feeding and associated damage to the nationally vulnerable keystone tree species (*Acacia peuce*). Further, the presence of rats produced a spike in rodent biomass that was over twice that during irruptions where the rat was absent. The sporadic occurrence of the long-haired rat and the intensity and spatial scale of the novel interactions lead us to consider it a disruptive factor in the functioning of the Simpson Desert ecosystem.

158^{HTA}: Signaling from below: rodents select for deeper fruiting truffles with stronger volatile emissions

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Truffles, the underground fruiting bodies of mycorrhizal fungi, have closely evolved with mammals for spore dispersal. Using four *Elaphomyces* truffle species we explored the role of fruiting depth, emissions of volatile organic compounds (VOC), and protein content in selection by five rodent species. Despite

presumably easier access to the shallow fruiting truffle species, *E. americanus* and *E. verruculosus* (1.5 and 3.6 cm below the soil surface, respectively), most rodents selected for *E. macrosporus* and *E. bartlettii* that fruited deeper in the soil (5.9 and 8.6 cm, respectively). These deeper fruiting species had distinct VOC profiles and produced significantly higher quantities of odiferous compounds. However, *Myodes gapperi* (southern red-backed vole), a fungal specialist, selected for the truffles with high levels of digestible protein, *E. verruculosus* and *E. macrosporus*. Our results highlight the importance of chemical signals in truffle selection by rodents and suggest that VOCs are under strong selective pressures relative to protein rewards. For truffles, strong chemical signals likely allow detection by rodents deep within the soil where fruiting conditions are less influenced by drought or freezing. Strong chemical signals of truffles likely increase detection and reduce foraging effort by rodents, irrespective of fruiting depth. However, for species that depend on fungi as a major food source, protein content may be more important than fruiting depth and VOC emissions.

159^{E,HTA}: Comparing ecosystem effects of native and non-native grazers in a North American shortgrass prairie

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Grasslands are deteriorating globally resulting in widespread biodiversity degradation so understanding impacts of loss, or replacement, of native megaherbivores remains a central challenge for grassland conservation, especially because of their disproportionately strong and unique functional roles. We compare native (bison) versus non-native (cattle) grazers in a shortgrass prairie from a multi-year experiment by sampling 875 unique vegetation locations in 3 habitat types (grassland, woodland, riparian) across 35 transects (14,000 trap-nights) and collecting >4,600 parasites from 327 small mammals. We report significant impacts for parasite assemblages despite few influences on vegetation structure and mammalian community composition. Bison plots have significantly less canopy cover and shrub cover compared to cattle plots and analogous mammalian diversity despite abundance and species occupancy differences. Across parasites, ticks maintain higher prevalence (sevenfold increase) on cattle plots and nematodes (twofold increase) on bison plots regardless of habitat type ($P \ll 0.05$ and $P = 0.015$, respectively). Lice prevalence is higher (sevenfold increase) in bison plots, but only in woodland habitats ($P = 0.015$). We failed to detect significant differences across treatment or habitats for fleas or cestodes. Taken together, these results have implications for wildlife disease because altered host and vector population abundances and composition are known key drivers of pathogen transmission. Moreover, these combined results differ from tallgrass prairies, so land managers should consider differing tactics to conserve distinct types of grasslands with different megaherbivores.

160: Virginia opossums are dominant scavengers of mammal carcasses and potential competitors with American burying beetles

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In this study we attempted to (1) identify potential competitors for carcasses, appropriately-sized for use by endangered American burying beetles (*Nicrophorus americanus*; hereafter ABB) and; (2) determine if ABB distribution or abundance might be impacted by competition with mammalian mesocarnivores. We used camera traps to identify potential competitors by placing ~100g brown rat (*Rattus norvegicus*) carcasses in two habitat types, forests and fields. Virginia opossums (*Didelphis virginiana*; hereafter opossums) were dominant scavengers at forest sites and crows (*Corvus spp.*) at field sites. A variety of mammalian, avian, and one reptile species scavenged carcasses. Rat carcasses persisted longer at field than forest sites (2193 vs. 1616 min) and cumulative carcass persistence times displayed a steeper removal curve at forest sites (KS D = 0.37, $P = 0.03$). Part 2 of the study occurred at a site in western Arkansas with a sustaining and annually monitored ABB population. We placed camera traps at ABB trapping locations to document mesocarnivore activity. Opossums made up 75% of total mesocarnivore captures and were most abundant in pine, developed, and shrubland habitats whereas ABBs were most abundant in the grassland/prairie habitat. ABB and opossum presence was negatively associated ($P = 0.06$) indicating ABBs may have avoided trap locations that had opossum activity. Management for ABB habitat should minimize attractiveness to opossums including limiting roads, edge habitats, and densely overgrown areas.

161: Conceptual reconstruction of large mammal communities on the Palaeo-Agulhas Plain

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Recent evidence indicates that the now-submerged continental shelf, the Palaeo-Agulhas Plain, in southern Africa, formed a novel ecosystem during periods of low sea level during the late Pleistocene. This terrestrial landscape potentially provided nutrient-rich forage and habitats to a variety of large herbivores and associated predators. This is in stark contrast to the faunal assemblage found in the present-day Cape Floristic Region, which is dominated by landscapes with nutrient-poor soils and unpalatable plants. The archaeological record for the region provides some clues on species occurrence of the region. Here we reconstruct species communities for the Palaeo-Agulhas Plain and investigate potential gaps in the record using Hutchinson's weight ratio theory. We then compare the results to modern occurrences of mammals on the Cape South Coast and the Serengeti (a comparable migratory system in East Africa) using an analysis of co-variance. Both sea-level and sampling effort (minimum number of individuals in archaeological records) influenced species numbers found during the last seven marine isotope stages. Large mammals showed an extraordinary resilience to extreme habitat loss caused by changing sea levels where, especially the large grazers, survived as refugee species during high sea levels and low habitat availability. However the combination of habitat loss and modern human weapons were the cause of severe extinction rates during the last 400 years.

162^{HTA}: Precipitation and prey abundance influence food habits of an invasive carnivore

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Invasive predators threaten biodiversity worldwide, with generalist predators being particularly impactful because of their broad diets. Prey abundance, prey preference, and weather can influence predation patterns, and understanding these relationships aids conservation of native species. We examined stomach contents from 2,882 feral cats (*Felis catus*) from San Clemente Island, California from 2000-2018 to assess annual and seasonal variability in diet, and how precipitation and prey abundance correlated with predation patterns. We found rodents in 95% of non-empty stomachs, and a positive relationship between rodent abundance and rodent consumption. The San Clemente deer mouse (*Peromyscus maniculatus clementis*) was the most prevalent prey species and was preferred to non-native rodents. In dry years, the proportion of cat stomachs containing rodents decreased while the proportion containing lizards increased. Endemic night lizards (*Xantusia riversiana reticulata*) were particularly affected, with prevalence in cat stomachs doubling in dry compared to normal rainfall years. Cats rarely consumed birds, but consumption peaked in spring, overlapping with the nesting season of two federally listed endemic avian subspecies. Even low predation rates could influence recovery of these subspecies. These results suggest cats use rodents as primary prey and lizards as secondary prey, particularly during droughts when rodent abundance is low. Understanding how weather affects predation patterns of invasive species will help conservation biologists predict and manage the effects of invasive species as climate change continues.

163: Resource availability and defense drive divergent home range dynamics in two ecologically similar tree squirrels

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Space use in animals is strongly tied to body size and energy requirements and these ties are reflected in the scaling of home range size with body mass and diet. The rate at which home range size increases with

body mass varies across taxa. Among species of similar trophic guild and body mass, differences in home range size can reflect extrinsic variables that exert divergent selective forces upon spacing behavior and social organization. We tested predictions about how social system and resource availability influence home range size and exclusivity in 2 ecologically similar tree squirrel species that differ in foraging strategy and social organization. We calculated home range area and intraspecific home range core overlap in the Mt. Graham red squirrel (*Tamiasciurus fremonti grahamensis*; Arizona USA; MGRS) and the Eurasian red squirrel (*Sciurus vulgaris*; Lombardy, Italy; ERS) as functions of species, sex, and season. Territorial MGRS evolved in a system of brief resource pulses and are larderhoarders, whereas ERS experience prolonged resource availability and are non-territorial scatterhoarders. MGRS home ranges were 3x smaller with higher core area exclusivity compared to ERS in all seasons. Home range comparisons between ecologically similar species highlight the divergent extrinsic factors shaping variability in body size – home range size scaling relationships. Timing in resource availability influenced the social evolution and space use in tree squirrels of similar body size.

164: Developing genomic tools for elephant health and conservation

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The ability to sequence whole genomes is revolutionizing our ability to manage animal populations, and is providing new approaches for understanding how animals adapt to their environment. These data are important because the success of captive management can be impacted by genetic factors. Zoo elephants are no exception, and management has been challenging because of poor reproduction and health issues resulting in non-sustaining populations for both species of elephants. This project has generated high coverage (30X-60X) genome sequences of African and Asian elephants, which will be used to enable genomics projects in elephants to address fundamental questions about individual and population health and species survival. We have completed whole genome sequencing and assembly of one male Asian elephant and are completing its annotation. Over the next year we will identify individuals with particular health problems and look for shared traits in their genome. These data will aid in the breeding and management of zoo elephants, and facilitate research on disease susceptibility and reproductive problems from a genetic perspective. Ultimately, our aim is to apply the knowledge gained from the *ex-situ* population to elephants in range countries that are experiencing increased human conflict, habitat loss, increased disease outbreaks and poor reproduction, possibly resulting in genomic variations that could impede the long-term survival of these fragile populations.

165: Connectivity in highly fragmented Atlantic Forest remnants of eastern Paraguay using graph theory

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Loss of habitat has been identified as one of the main contributors to biodiversity loss and extinction. This is especially true for tropical and subtropical rainforests, where forest fragmentation diminishes connectivity of formerly continuous habitats. The Atlantic Forest of eastern Paraguay has experienced extreme deforestation in the past ~60 years, resulting in only 8-12% of its original distribution. In this study, we used graph theory to identify important forest remnants in eastern Paraguay. We quantified structural connectivity for forest remnants at five nested spatial scales to encompass a range of wildlife dispersal abilities, with habitat networks ranging from those with remnants ≥ 5 ha ($n = 27,804$ remnants) up to ≥ 25 ha ($n = 7579$ remnants). We used eight graph theory metrics to assess aspects of network complexity, dispersal-route efficiency, and individual remnant importance in supporting connectivity. Patterns of connectivity varied, but all analyses revealed that the Atlantic Forest remnants of eastern Paraguay comprise a complex network with high path redundancy. Furthermore, we found that connectivity was constrained for organisms incapable of travelling at least 12 km. We also identify a few remnants that consistently served as valuable connectivity stepping-stones. Additionally, connectivity visualizations were valuable in identifying taxa that might be most affected by fragmentation patterns in this system. We conclude that structural connectivity metrics can be used to identify important forest remnants for conservation.

166: Landscape features associated with bat fatalities at wind energy facilities

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Currently, fatalities at wind energy facilities are the greatest known sources of mortality for migratory 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. Fatalities continue to occur, currently at a rate of ~400,000 annually, but increasing with the expansion of wind energy. Recent analyses 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 “low fatality risk” areas, 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, modelling based on fatality data from >50 wind energy facilities across Ontario, Canada suggest that fatality risk is correlated with landscape features, such as distance to forest and proportion of water and cropland, but this varies among species. This knowledge can be used in siting future developments, but also highlights that a one-size-fits-all approach to mitigation through siting is unlikely.

167: Forest habitat fragmentation and landscape barriers reduce genetic diversity in a small mammal

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Landscape genetics combines population genetics and landscape ecology with a fundamental goal to quantify the effects of landscape features on genetics, functional connectivity and gene-flow. Human activity is strongly implicated as a limit to gene-flow within the landscape, but functional effects of specific features is not well understood for most species. For example, while the effect of roads and railways is generally thought to inhibit dispersal in large mammals, effects on other species are less well studied. Here we used genetic data, 18 microsatellite markers from 706 individuals and landscape composition data to examine the influence of specific landscape features on population connectivity in a small woodland mammal, the hazel dormouse (*Muscardinus avellanarius*). We quantified the influence of landscape topography (slope, elevation and aspect), land cover and human activity (presence of roads, railways and vegetation) on shaping the level of genetic distance in relation to isolation-by-distance between populations. We identified that roads increase genetic differentiation and that this impact is higher with wide roads or motorways. Features such as hedgerows and vegetation structures actively promote dispersal, significantly decrease genetic distance, and may counteract the effect of barriers in the landscape. Land cover in combination with non-natural landscape features have the greatest effect on genetic diversity. Our results are relevant in the context of conservation in human-transformed woodland landscapes and connectivity for small mammal species.

168: Phylogenomic resolution of the cetacean tree of life using target sequence capture

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While the higher-level relationships among cetacean families have been largely settled, several aspects of the systematics within these groups remain unresolved. Problematic clades include the oceanic dolphins (37 spp.), which have experienced a recent rapid radiation, and the beaked whales (22 spp.), which have

not been investigated in detail using nuclear loci. The combined application of high-throughput sequencing with techniques that target specific genomic sequences provide a powerful means of rapidly generating orthologous sequence data for use in phylogenomic studies. To elucidate the phylogenetic relationships within the Cetacea, we used sequence capture to generate data for ~3200 protein-coding genes for 68 cetacean species and their close relatives. By combining data from >38,000 exons with existing sequences from 11 cetaceans and seven outgroup taxa, we produced the first comprehensive comparative genomic dataset for cetaceans, spanning 6,527,596 aligned base pairs and 89 taxa. Phylogenetic trees reconstructed with maximum likelihood and Bayesian inference of concatenated loci, as well as with coalescence analyses of individual gene trees, produced mostly concordant and well-supported trees. Our results completely resolve the relationships among beaked whales as well as the contentious relationships among ocean dolphins, especially the problematic subfamily Delphininae, which includes the common and bottlenose dolphins. In addition, we performed Bayesian estimation of species divergence times using MCMCTree, integrating recently described fossils as calibration points that have not been used before.

169^{E,HTA}: Bobcat gene flow in western Texas is influenced by land use at varying spatial scales

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Identifying the variables involved in structuring wildlife populations are challenging in highly mobile, generalist species. For many populations, gene flow is not limited by environmental features, resulting in populations that are often genetically panmictic, or follow a pattern of isolation by distance (IBD). However, these spatial patterns can be overestimated, which can result in erroneous conclusions about functional connectivity. Examinations that consider several landscape variables are necessary because the landscape processes that affect genetic diversity are often scale-dependent. In this study, we examined bobcat gene flow at two spatial scales across western Texas. Our objectives were to determine whether bobcats across western Texas comprise one panmictic population or are subdivided by landscape variables known to be ecologically relevant to the species. We genotyped 102 bobcats and found weak population structure separated by a latitudinal cline and IBD. We found strong spatial autocorrelation and evidence of philopatry among bobcats within a 5km distance class, and landscape genetic analysis identified significant associations with two rangeland types and agricultural land, but these results varied by spatial scale. Our approach of using ordination techniques to analyze spatial genetic relationships are especially useful in landscape genetics studies due to their ability to identify the combination of landscape variables that influence gene flow. These results demonstrate the importance of considering multiple spatial scales when assessing spatial genetic structure.

170: Non-invasive genotyping and sex determination of canid scat through improved hybridization capture

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Targeted genomics using hybridization capture has become one of the principal technologies in phylogenomics and conservation genomics. Hybridization capture utilizes sets of oligonucleotide “baits” to sequence only informative regions of interest, thereby greatly lowering sequencing effort and cost and permitting the analysis of low-quality DNA samples, such as those obtained non-invasively and from museum specimens. The development of these bait sets is non-trivial, but critical for successful experiments. Here, we describe recent improvements in the software package *BaitsTools* that facilitate the design of high-quality bait sets. We demonstrate these improvements on a set of unidentified canid scats deriving from coyotes (*Canis latrans*) and kit foxes (*Vulpes macrotis*). From our highly efficient capture experiment, we were able to identify scat species, the sex of the source individuals, and the number and kinship coefficients of unique animals that produced the scats.

171: Urbanization decreases genetic diversity of coyotes in Southern California

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Urbanization is increasing throughout the world, transforming natural habitats. The purpose of this study was to examine the effects of urbanization on the genetic diversity of coyotes (*Canis latrans*) in Southern California. We hypothesized that increasing urbanization would result in decreased genetic diversity due to a bottleneck effect. We analyzed 10 microsatellite genetic markers from 126 individual coyotes sampled across a spectrum of highly urban to highly natural areas in Southern California. We performed regression and rarefaction analyses to test for associations between genetic diversity and land cover or road density. At the population level, allelic richness is negatively associated with urban/suburban land cover and positively associated with the relative amount of natural vegetation. At the individual level, observed heterozygosity is negatively associated with local road density but not with highway density. This is likely because highways make up a minimal portion of coyote home ranges and, for coyotes living in very densely populated areas, local roads comprise a major portion of the usable land within their home range. These results indicate that a population bottleneck likely occurred during the extremely rapid expansion of the Los Angeles metropolitan area throughout the 1900s. Thus, urbanization reduces genetic diversity even in a generalist species thought to be minimally impacted by land development.

172^E: Ecology differentially influences genetic divergence of sympatric species

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There has been a push toward comparative studies in landscape and spatial genetics in order to better determine the generalizability of processes. For example, comparative studies of co-distributed species that differ in their ecology can provide insight into differences in response to historic isolation events. Our goal was to understand how geographic isolation, specifically insularization, influenced intra-specific genetic variation in sympatric populations of two distantly related rodents: the marsh rice rat (*Oryzomys palustris*) and hispid cotton rat (*Sigmodon hispidus*). Found throughout Florida, these species vary in their use of flooded environments. *Sigmodon hispidus*, while capable, is more averse to swimming than *O. palustris*, possibly resulting in different degrees of isolation with regard to aquatic barriers. We used 7,273 and 5,048 single nucleotide polymorphisms, respectively, to quantify divergence among two insular and four mainland *S. hispidus* and *O. palustris* populations. We calculated pairwise F_{st} between sampling locations as a measure of differentiation. We performed a discriminant analysis of principle components to determine the number of distinct populations sampled. We then compared observed patterns of divergence between species. We found that Sanibel Island, the most isolated location sampled, was distinctly divergent in both species, whereas Pine Island was only sufficiently isolated to result in *S. hispidus* divergence. These results suggest that ecology interacted with historic isolation events to influence contemporary genetic patterns.

173: Mapping species, splits, and synonyms in the Mammal Diversity Database and iNaturalist

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Species have an inherent spatial component. They are sets of organisms delimited by their genetic, ecological, and phenotypic coherency that interact in space. However, the formal process of defining species does not require taxonomists to indicate the spatial boundaries pertaining to a newly recognized species. Instead, this task of drawing 'expert range maps' is in many cases performed by third parties and then fed into conservation assessment processes for the IUCN Red List of Threatened Species. For the many species lacking population trend estimates, these polygonal maps form a substantial component of threatened status decisions under the B1a criterion (extent of occurrence + number of known localities). Thus, spatially delimiting species is an essential step in translating taxonomic revisions into conservation practice. Here we present ongoing work in the Mammal Diversity Database (mammaldiversity.org) and iNaturalist (inaturalist.org) to understand the spatial and taxonomic boundaries of mammalian species. These efforts have led to an updated list of 6,427 extant species (including at least 673 split and elevated subspecies) and 419,000+ observations of mammal species globally. We highlight recent examples in

Giraffa and *Semnopithecus* where the geography of species, subspecies, and synonyms has been consequential to understanding threatened status. We call for more attention from systematists and biodiversity stakeholders alike to the spatial dimension of mammalian species.

174: Taxonomy, nomenclature, and ZooBank

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Taxonomists long have conformed to standards for scientific nomenclature, formalized one century ago in Codes of nomenclature; the Code for animal names is managed by the International Commission on Zoological Nomenclature (ICZN). The current version of the Code (4th ed.), went in effect 1 January 2000. Since the first, mechanisms of scientific communication have transitioned from paper-printed books and journals to electronic publications. In 2012, the ICZN Code was amended to accommodate this shift, allowing new scientific names to become established through electronic publication. New rules include establishment of the “Official Register of Zoological Nomenclature” or, “ZooBank,” and registration of all electronically published works containing new names or nomenclatural acts. The Code and ZooBank maintain nomenclatural stability, a critical component of biological taxonomy, but represents only the core foundation. The Code is designed to avoid imposing rules regarding taxonomic judgement: rather as an operational taxonomic infrastructure. The only tangible links between name and taxonomic concept are type specimens. The Code provides a set of rules determining names to be used for taxa, but remains silent on establishment of taxon concepts and their boundaries. For the next edition of the Code, numerous questions remain regarding what role ZooBank will play in establishing new names and nomenclatural acts, and whether the role of ICZN and the Code should be expanded to govern taxonomy as well.

175: Cross-linking sequence records and specimens at NCBI

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The public sequence archive databases are challenged to find ways to make their records findable, accessible, interoperable and reusable. GenBank at the National Center for Biotechnology (NCBI) and the separately managed NCBI Taxonomy database have long played central roles in this regard. Creating links between specimen voucher data in GenBank records and their source collections enhances the research value of both the GenBank record and of the specimen, provides attribution to the source collection, and is a first step towards a future in which specimens and their derivatives are tracked accurately through the research pipeline. We will discuss various ways in which submitters can utilize longstanding, but under-utilized processes to accomplish this and also highlight more recent resources such as the newly public NCBI Biocollections Database.

176: Linking specimens to their data: a collaborative solution to integration and attribution

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Linking scientific investigations to museum voucher specimens allows replication, extension, and integration of systematic, behavioral, ecological, physiological, and evolutionary questions critical to an understanding of the distribution and conservation of global biodiversity. To link museum specimens to their extended data, museum databases must provide the tools to create and track relationships between museum specimens, specimen parts (e.g. tissues, embryos, parasites), and derivative data including gene/genome sequences, isotopic signatures, CT scans, digital media, permits, and publications. These tools must allow the attribution of derivative data and citations back to the specimen record, utilize updated taxonomy, map and track species status, and document regulatory compliance. The Arctos Collaborative Collection Management Solution (www.arctosdb.org) has developed the capacity to track relationships between cataloged specimens across collections, institutions, and databases. This system allows for reciprocal linkage between Arctos institutions and external data repositories including GenBank, MorphoSource, iDigBio, Global Biodiversity Information Facility, and soon, IsoBank. Arctos tracks

identification history and taxon status through integrated and external taxonomic services, tracks permits, accessions, and loan history, and emphasizes attribution, with linkages directly back to the museum specimen from publications and citations. Major challenges remain in facilitating the means for authors, publishers, and external data repositories to provide attribution back to museum specimens to improve interoperability of data, maximize the value of specimen-based research, and document the value of museum collections.

177: Taxonomic clarity and accurate spatial data are cornerstones of the IUCN Red List process

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The IUCN Red List is the global standard for the assessment of extinction risk. Over 96,500 species have been assessed with a goal to reach 160,000. Each Red List assessment contains valuable data on taxonomy, population trends, ranges, and diverse threats. The accuracy of the Red List is dependent upon the availability and quality of the data applied to the assessments. These data are used to inform and influence conservation planning and priority-setting, such as for the Convention on Biological Diversity, UNEP, and CITES among others. Correct and accurate spatial data and taxonomy are essential components of the Red List, and clarity and consistency both benefit meaningful conservation planning and action. There are several ways in which spatial data can be entered into species assessments, however many researchers do not understand differences between EOO and AOO and how to correctly record and interpret these data. In addition, the rate of description of new species has increased in recent years, but the quality of some revisions has resulted in mixed interpretations of which species require assessment by IUCN. Using case studies, we will review the differences among kinds of spatial data and provide suggestions for mammalogists to improve their quality. Finally, we will present examples of confusion in taxonomy and the importance of achieving taxonomic clarity in order to effectively advance mammalian conservation.

178: Double trouble building the Hitchhiker's Guide to Mammals

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Mammal biodiversity data often lives in disconnected repositories, with a critical tie-point around taxon names, which are the labels that connect together the content, and identifiers for physical and digital objects. The problem is that names are not stable, and that identifiers that could help manage linking content aren't either. These dual instabilities cause significant challenges in building linked open data systems instead of data silos. In this study, I first examine how well current identifiers work in providing an easy and unambiguous means to track from specimen records to genetic sequence records. I then examine challenges in linking content together based on taxon names and the significant issues associated with name instability when reassembling historical and even recent biodiversity record data. I demonstrate that the still commonly used identifier, the Darwin Core Triplet is often riddled with semantic and syntactic errors when deployed and curated in practice, despite specifications about how to construct them. And I show that name flux is higher than expected across the Tree of Life, and such flux means that special care needs to be taken when utilizing agnostically assembled biodiversity data from aggregators. Finally, I provide a set of potential solutions and next steps for building the linked biodiversity knowledge graph utopia.

179^{HTA}: Living on the (trailing) edge: The importance of climate to pika occupancy**

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Populations along the trailing edge of mammal species' ranges (either elevational or latitudinal) may show the strongest initial responses to climate warming, as they are positioned near the boundary of species' ecological limits. As climate has changed over the last century, American pikas (*Ochotona princeps*) have disappeared from parts of their range. This habitat specialist is an ideal indicator species for studying effects of climate change because its preferred habitat (talus) is largely spared the confounding effects of other

anthropogenic disturbances. Here, we examine which factors are most influential in determining *O. princeps* distribution at the southernmost limit of its range. We conducted extensive field surveys, documenting current or evidence of recent pika occupancy and used high-resolution spatial climate data to analyze determinants of occupancy. In this region, pika distribution was best characterized by low winter vapor pressure deficit (VPD, a measure of atmospheric moisture demand), higher total grass and forb cover, and greater talus patch size. At the southern limit of their range, pikas are more likely to have disappeared from sites with higher winter moisture stress (VPD), and warmer mean August within-talus temperatures. Our results indicate that anthropogenic climate change may limit pika distribution in a drier future and provide an example wherein abiotic factors appear to have a strong influence on species distribution at the trailing edge. This research was supported by a GIAR awarded to Marie L. Westover in 2018.

180^E: Habitat use by montane ground-dwelling squirrels over space and time

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High elevation species are thought to be particularly vulnerable to a warming climate, and this assumes that climate variables are directly or indirectly the primary drivers of current distribution. Factors determining species distributions are unique to each species, and likely vary at different spatial and temporal scales. Understanding the factors that determine current species distributions will allow more accurate forecasting of potential range shifts under changing environmental conditions. Therefore, we evaluated the niche space use and resource selection by three species of montane ground-dwelling squirrels in the Sierra Nevada, California; yellow-bellied marmot (*Marmota flaviventris*), Belding's ground squirrel (*Urocitellus beldingi*), and golden-mantled ground squirrel (*Callospermophilus lateralis*). This evaluation was conducted using five years of visual observations, collected along 21 10-kilometer (km) transects distributed across a latitudinal gradient of 320 km. We found that although the range of these species is sympatric within the study area, the niche space use by each of these species was unique. Even on a landscape scale, each species distribution is also determined by topographic and landcover types, not just climate variables. We also plan to evaluate resource use at the local and regional scale, as well as variation across the five years of the study.

181^E: Identifying genomic adaptations to diverse environments in the chisel-toothed kangaroo rat (*Dipodomys microps*)

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In the face of climate change, populations may stay and adjust, move to a different location (usually along latitudinal or altitudinal gradients), or face extinction. Many species exhibit plasticity in various traits which allows them to shift their realized niche and persist in place despite climate change. Though in some cases plasticity is an inadequate response to environmental changes across a species range. Individual populations of such species may exhibit signals of adaptation specific to their local environments. Understanding the role of plasticity and adaptation in species ability to withstand environmental change is critical to predict responses to current and future environmental changes. In this study we search for population-specific signals of adaptation in the genomes of the chisel-toothed kangaroo rat (*Dipodomys microps*), a species that occupies two distinct habitats and a wide range of climatic conditions throughout the Mojave and Great Basin deserts. We use double digest Restriction Site Associated DNA sequencing (ddRADseq) to perform genome-wide scans of 177 individuals from 27 populations distributed across the entire range of the species. We then use genotype-environment association (GEA) methods to identify adaptive loci based on correlations between allele frequencies and environmental variables.

182^{E,HTA}: Natural population variation may be masking the more-individuals hypothesis

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Species diversity and productivity are closely related at global and regional scales, but the mechanisms linking the two are inconclusive. The most commonly invoked mechanism, the more-individuals hypothesis (MIH), hypothesizes that productivity determines the quantity of available food resources which then regulates the number of individuals that can survive at a site. The number of species is then determined by the number of individuals, as species with low abundance are more likely to go locally extinct. Empirical evidence for the MIH remains mixed despite much investigation. This study used a simulation framework to determine the degree to which annual population variability (e.g. year-to-year fluctuations in rodent and shrew abundance) could be masking a “true” MIH relationship. In the simulations, fixed linear relationships between productivity, diversity, and a 50-year average abundance at each of 18-54 sites mimicked the MIH mechanism. Abundance was allowed to vary annually and sampled over various year spans. Linear regressions of diversity on sampled abundance assessed the probability of detecting the original fixed relationship. High population variability associated with small mammal populations, coupled with narrow sampling (1–3 years) led to poor detection of the MIH relationship. With a greater number of years sampled, relationships more closely mirrored the MIH relationship. Thus, empirical evidence of the MIH may be impeded by population variability, especially since resource constraints often preclude multi-year studies.

183: Elevational structuring of medium-large species of terrestrial mammals on Sumaco Volcano, Ecuador

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Assessing the occurrence, geographic distribution, and spatial and temporal activity patterns of species is essential for a full understanding of their ecology, biogeography and interactions with sympatric species. We report findings of camera trap studies of medium-large mammals on Sumaco Volcano, Ecuador, between 2010 and 2016. Sumaco Volcano lies in the heart of the Tropical Andes biodiversity hotspot and is noteworthy for having one of the most extensive, intact elevational habitat gradients in the Neotropics, ranging from the lowland rainforests of the western Amazon basin at 300m to páramo vegetation near the volcano's 3,800m peak. We characterize the medium-large mammal fauna at five elevational zones on Sumaco Volcano: one located in the lower montane rainforest at approximately 1350m, and four located in the cloud forest at approximately 1750m, 2200m, 2500m, and 2900m. We determined species diversity for each zone and species turnover between zones. Our major conclusions are 1) that species turnover between the 1750m and 2200m sites was the most pronounced; however, we also found substantial turnover among upper elevation sites, suggesting that elevational differences in mammalian communities within the cloud forest biome also can be surprisingly high; and 2) that several typical Amazonian lowland species occurred well up into the cloud forest (including 2900m, far above the rainforest-cloud forest ecotone); in stark contrast, no typical “Andean” species were found below this ecotone.

184^F: Unearthing proxy determinants of the subterranean niche for species distribution models

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A common objective in biogeographical studies is to determine which, and to what extent, environmental factors influence patterns of species diversity and distributions. Species distribution models (SDMs) have been used for this objective across numerous taxa occupying a variety of realized niches. Nevertheless, a unique perspective that is underrepresented in SDM literature is the subterranean niche, whose paucity of information is likely due to the inaccessible nature of direct predictors. When a suitable variable is unavailable, it becomes customary to incorporate efficient proxy variables to accurately envelop the distribution of a species. Here, we used three classes of environmental variables: historical, climate and habitat heterogeneity, spanning a stability-variability gradient, to model the subterranean niche of the pocket gopher *Geomys bursarius*. Within each environmental class, we assessed the explanatory power of each variable on species occurrence using generalized linear models. Significant variables were used to

construct overall species distribution models using Maxent. We compared this model to those that illustrate distributions of Merriam's kangaroo rat and the Southern Plains woodrat, two widespread rodents representing fossorial and non-fossorial lifestyles, respectively. We hypothesize that the environmental constancy captured by historical factors, namely geologic patterns, describes contemporary species distributions of subterranean rodents better than climate or aboveground habitat variables. Results from this study are essential for digging deeper into ecology and evolution of the understudied subterranean niche.

185^{E,HTA}: Area, isolation, and predators drive gigantism in island-inhabiting meadow voles

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Island rule is a pattern of body size change (dwarfism and gigantism) often observed across mammals, but the impacts of island effects remain incompletely characterized or evaluated for many systems. Here, using geometric morphometrics we report that voles (genus *Microtus*) have at least 4 island populations with significantly larger skulls consistent with expectations of island rule. We characterized craniodental variation (23 landmarks, $N = 615$) using Generalized Procrustes Analysis (GPA) and Principal Components Analysis (PCA) yielding skull centroid sizes (proxy for body size). Comparative analyses across eleven paired island and mainland populations of meadow voles (*M. pennsylvanicus* and congeners) revealed significantly larger skulls compared to mainland relatives for half of the Atlantic-island populations but no significant differences in skull sizes of Pacific-island populations. Information theoretic model selection revealed island area, isolation, and the presence of either a mammalian or reptilian predator as significant predictors of centroid size ($F_{6,104} = 11.91$, $R^2_{\text{adj}} = 0.3731$, $P < 0.0001$) with small, distant Atlantic islands lacking predators having the largest voles. Conversely, the large, proximal, predator-laden Alaskan Archipelago precluded a rejection of the null hypothesis of equivalent mainland-island skull sizes. Taken together, these results broadly support ecological release hypotheses with implications for anthropogenically altered island systems, especially those with introduced non-native predators (*i.e.*, domesticated cats).

186^F: In situ diversification of *Bunomys* (Muridae) on the isolated, topographically complex island of Sulawesi, Indonesia

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Sulawesi is the largest, most topographically complex island in the Wallacean biogeographic zone. The island has a rich fauna of endemic small mammals, dominated by murine rodents. The murine genus *Bunomys* is endemic to Sulawesi, and contains eight species, but our understanding of the systematics and biogeography of *Bunomys* is rudimentary. We explored the genetic and phenotypic diversity of *Bunomys* on the northern peninsula of Sulawesi to better understand the taxonomy, geographic ranges, and potential mechanisms of speciation within the group. We found that *B. fratrorum*, long thought to be endemic to the eastern half of the northern peninsula, is actually distributed more broadly across the peninsula. Phylogenetic analyses revealed Pleistocene divergences between *B. fratrorum* populations sampled at various points along the peninsula. Both Pleistocene sea level inundation and mountain habitat isolation may have facilitated allopatry and divergence among these populations. All three populations of *B. fratrorum* that we sampled are more closely related to other genera than to other species of *Bunomys*.

187: Delineating population structure and isolation among Allegheny woodrat metapopulations in Pennsylvania

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Allegheny woodrat (*Neotoma magister*) populations have experienced declines over the past 30 years throughout the northern part of their range and are listed as threatened or endangered in most of the states where they reside. They face a myriad of population pressures including habitat loss and fragmentation. They are particularly vulnerable to reductions in connectivity because they live in networks of small populations centered on exposed rock formations. Our study examined the genetic structure and landscape connectivity among the remaining metapopulations found throughout Pennsylvania. We collected tissue samples from 453 woodrats across 61 habitat sites. Based on microsatellite data analyzed using program STRUCTURE, we identified 5 genetic clusters, and 33 potential subpopulations. We then assessed heterozygosity levels among the subpopulations to identify populations at risk of inbreeding depression. We compared these locations to predicted landscape connectivity maps based on species distribution models generated using the Maxent program. By identifying genetically isolated populations, we hope to inform management actions that seek to reduce the inbreeding depression and improve productivity among at risk populations.

188: The use, characteristics and distribution of the drought refuges of a threatened desert rodent
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The response of irruptive desert rodents to extreme rainfall events is well documented. However, the population dynamics of these species during the prevailing dry periods are less well known. During these dry times it has been noted that some desert rodent species show marked habitat selection, or use of drought refuges. We aimed to understand the refuge use, characteristics and distribution of the threatened plains mouse (*Pseudomys australis*) during a period of low rainfall in arid Australia. We used trapping techniques to assess the dynamics of *P. australis* over the study area. To assess drivers of the occurrence of *P. australis* we measured four plant cover variables representing food resource availability and three variables representing shelter resource availability. The study population fluctuated in response to rainfall, showed a preference for cracking clay land types that weakened with increasing capture rate and was dependent on prior capture rate. The occurrence of *P. australis* across the study area was driven by shelter resource availability (soil cracks), as opposed to food resource availability. These findings informed the choice of remotely sensed mineralogical indices, which were combined with modelling techniques to predict *P. australis* occurrence across the study area. Understanding the distribution and dynamics of species when populations are most vulnerable to disturbance is vital for their conservation, particularly in light of altered rainfall regimes predicted under climate change.

189^{E}: Investigating the impacts of contemporary climate change using a space-for-time approach in montane systems**

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Contemporary climate change has been tied to shifts in species' phenology, behavior, and distribution, globally. Montane species may be particularly sensitive in their responses to climate change due to narrow ecotones, as well as varied levels of habitat connectivity. Here, we used a space-for-time substitution design to quantify the effects of aridity and other climatic factors on American pikas (*Ochotona princeps*), a small montane mammal. We documented current and historic pika evidence from 660 talus patches in the Northern Rocky Mountains of Idaho and Montana. We used an information-theoretic approach to evaluate hypothesized mechanisms by which climatic and non-climatic factors might influence occupancy and density, and upslope retraction of pikas. Our top-ranked model for occupancy included an interaction between mean summertime temperature and precipitation. Moreover, upslope range retractions were documented in 38 of 56 watersheds, and averaged 287 meters among those that retracted. Preliminary results suggest that increases in summer precipitation may partly counterbalance the negative effects of rising temperatures. Identifying the climatic variables that species are most vulnerable to, and the mechanisms by which they are responding, will be crucial for the implementation of effective conservation and management actions in the face of contemporary climate change. This research was supported by a Grant-In-Aid of Research awarded to Peter Billman in 2018.

190: Resource selection at den and rendezvous sites by canids in a wolf-coyote hybrid zone

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Resource selection by animals can influence the fitness of individuals and the growth of populations. We investigated factors influencing resource selection by wolves (*Canis lupus* and *Canis lycaon*), eastern coyotes (*Canis latrans*), and hybrids at den and rendezvous sites across a wolf-coyote hybrid zone in central Ontario, Canada. Specifically, we asked whether resource selection at homesites a) differed between den and rendezvous sites and b) varied across packs of varying wolf and eastern coyote ancestry. We also radio-tracked pups from a subset of packs which allowed us to investigate whether resource selection at homesites influenced pup survival. We found no support for differences in resource selection between den and rendezvous sites. Overall, we found that all canids strongly avoided paved roads and selected wetlands at den and rendezvous sites. Packs with greater wolf ancestry selected dirt roads/trails and wetlands more than packs with greater coyote ancestry. Finally, packs with better pup survival avoided paved roads marginally more than those with higher pup mortality. Our results support earlier findings indicating that roads increase mortality risk for canids and that variation in behavioral responses to roads can influence fitness. Our work contributes to understanding variation in resource use and ecological niches of wolves and coyotes in eastern North America. Our results also have implications for recovery efforts for eastern wolves, a federally threatened species in Canada.

191^E: Carnivore richness and diversity is driven by landscape change in shortgrass prairie ecosystems

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Landscape change in shortgrass prairie ecosystems (e.g., agriculture, energy development, Conservation Reserve Program [CRP] grasslands) is likely affecting native biodiversity. It is unclear, however, how these land-use changes structure native carnivore communities. During summer 2018, we assessed carnivore habitat use at sites across western Kansas, USA (n = 375; 7.16 million ha) using baited camera traps. We used generalized linear models and an information-theoretic approach to investigate how landscape composition and configuration affected native carnivore species richness and diversity. We documented 2,485 independent observations of 9 carnivore species over 10,470 trap nights. We detected ≥ 1 carnivore species at 332 sites (naïve carnivore occupancy = 0.89). Our most-supported model indicated that native carnivore richness was negatively associated with the proportion of hay pasture, sand-sage prairie, and CRP landcover surrounding sites. Additionally, native carnivore diversity was also negatively related to the proportion of sand-sage prairie and CRP landcover surrounding sites. Our results suggest that current biodiversity conservation efforts (e.g., CRP) may not benefit native carnivore communities. Additionally, our study highlights a complex relationship between native carnivore communities and contemporary landscape change in shortgrass prairie ecosystems.

192: Comparing the microbial communities of natural and supplemental nests of an endangered ecosystem engineer

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The endangered Key Largo woodrat (*Neotoma floridana smalli*) has long benefited from nest supplementation, but supplemental nests are enclosed and made from manufactured materials. Due to differences from natural nests, the microbial species to which Key Largo woodrats are exposed might be altered, which could negatively impact individual health and nutrient cycling at their nests. To test this hypothesis, we sampled the bacterial communities from inside natural and supplemental woodrat nests, as well as the forest floor in Key Largo, Florida. Furthermore, we sampled woodrat bodies to assess the microbiome of nest inhabitants. We observed distinct bacterial communities within Key Largo woodrat nests, relative to the forest environment; however, we could not differentiate between natural and

supplemental nests. Natural and supplemental nests had approximately the same relative abundance of rodent-associated pathogens, and we found them to occur at very low abundances. Where we expected to see an accumulation of pathogens, we instead observed high relative abundance of anti-microbial-producing bacterial families. The microbial biota of Key Largo woodrat individuals resembled those of their nests, in that we observed an accumulation of anti-microbial bacteria and low relative abundance of pathogens. Our results suggest that, although there is some microbial interaction between nests and nest inhabitants, there were no detectable differences in the diversity of bacteria to which they are exposed within natural and supplemental nest structures.

193^E: Seasonal effects on predator-prey spatial overlap

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Seasonal changes alter behavior in mammals due to variation in food availability, changes in daylight hours, and environmental constraints. The effects of seasonality can also influence predator-prey interactions, specifically on spatial overlap between predator and prey that can reduce prey availability. Previous work focuses on circadian rather than seasonal patterns of behavior, ignoring behavioral changes at larger temporal scales that are important for management. Our research aims to understand the variation in spatial overlap within predator-prey pairs across seasons in northern Michigan. Species of interest include coyote (*Canis latrans*) and its associated prey, white-tailed deer (*Odocoileus virginianus*), striped skunk (*Mephitis mephitis*), and lagomorphs (*Lepus americanus* and *Sylvilagus spp.*). We also explored relationships between the American black bear (*Ursus americanus*) and white-tailed deer and lagomorphs. We assessed activity of species pairs through an extensive three-year camera trap survey in all four seasons. A trigger history for each species was created using Rstudio. Kernel density values were then calculated from this data and re-entered into Rstudio for statistical analysis. Preliminary results from a linear regression indicate a negative relationship ($p=0.035$) between coyote and white-tailed deer during the summer season of 2018. The species investigated in this study are not only integral to proper ecosystem functioning, but are also of economic importance. Our findings contribute to the ecological knowledge required for proper management of these mammalian wildlife species.

194^E: Population performance of a large herbivore: effects of enhanced winter nutrition and climatic variation

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Population performance hinges on optimal allocation of available energy resources to competing life-history traits. Survival of adult female ungulates generally is high and stable, whereas recruitment of young is more variable. Nutritional condition and climate have the potential to influence demographic parameters that affect population growth. We focused on evaluating the effects of enhanced winter nutrition and environmental factors on survival of adult female and neonatal mule deer (*Odocoileus hemionus*). We evaluated the relative effects of those demographic parameters on the population growth rate (λ). We modeled survival of adult female mule deer from 2013-2018, and neonatal mule deer from 2014-2016. We identified and evaluated factors with the most influence on survival. We observed a strong negative effect of depth of snowpack on adult survival. We observed a substantial decline in adult survival in response to increased snow depths and winter severity resulting in negative population growth rates in 2017. We observed a strong effect of enhanced winter nutrition of pregnant females on survival of neonatal mule deer. Those effects resulted in substantial increases in survival of neonates to weaning. Declines in adult survival and λ observed in our study were attributed to nutritional carryover effects stemming from prolonged drought followed by a severe winter with above average snowpack.

195: An overview to the mammals of the Ecuadorean Andes: diversity and history of their knowledge

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Ecuador is one of the countries with the greatest biological diversity on the planet. This is mainly due to the presence of the Andes mountain range which crosses the country from north to south. In Ecuador (253,370 km²) almost 440 species of mammals are recognized, 297 of which inhabit the Ecuadorian Andes (over 1000 m in altitude), and more than 70 species inhabit an altitude higher than 3000 m and are considered high Andean species. This high species richness is related to the wide variety of geographical conditions that occur in the country; 8 biogeographical regions, 29 climatic zones, 25 life zones, and 46 different vegetation formations. The knowledge of the mammals of the Ecuadorian Andes begins with the naturalist explorer Alexander von Humboldt, who in 1802 visited Ecuador and years later described the first mammal species for the country: *Gulo quitensis* (*Conepatus semistriatus*). After half a century of silence, other writings appeared on the Andean mammals of Ecuador. Among the contributors were Robert F. Tomes and John E. Gray. However, the greatest contributor to information on Andean mammals, not only for Ecuador, was the British mammalogist Oldfield Thomas, who made numerous publications between 1880 and 1928; more than 60 referring to Ecuador. Thomas described more than a hundred new species of Andean mammals.

196: Geographic, geologic and phylogenetic analysis of the Andean cricetid rodents of Ecuador

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The Andes of Ecuador have some of the highest diversity of rodents found anywhere on Earth. This study compares cricetid rodent diversity, elevation, geology, and phylogenetic data from the Andes of Ecuador. We intergraded these data sets to get a picture of the geographic pattern of cricetid evolution in the Andes. Data were obtained from eleven month-long field studies in the Andes. The biogeography and natural history of high Andean rodents principally *Thomasomys*, *Microryzomys*, and *Akodon* was assessed in this study. These rodent groups tend to dominate the fauna of the páramo and high elevation temperate cloud forests and as such serve as good representatives of the high Andes taxa. These genera are phylogenetically interesting with many currently recognized taxa containing multiple lineages of cryptic species. The presence of these genera on Andean sky islands may lead to the identification of even more diversity. We will continue to investigate the ecology and phylogenetic structure of these and other Andean rodent taxa.

197: Origin and development of the South American montane mammal fauna by the Andean speciation engine

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Latitudinal and altitudinal species gradients hypotheses predict that as the former increase, species diversity decreases. In the Andes, altitudinal gradients are widely manifest among plants and animals. However, work on flora of the Páramos—grasslands $\geq 2,800$ m—showed lineage diversification rates higher than in other fast evolving hotspots. Páramo mammal species have not been shown to share the same explosive patterns of diversification. We argue that small mammals from both foothills and high elevations of the Andes have been systematically undersampled, and inadequately examined to accurately ascertain their taxonomic diversity. When such examinations are undertaken, they result in dislocation of existing taxonomy, with recognition of increased species diversity (as in cottontails, *Sylvilagus*). Species diversity in the Andes may increase with increasing elevation: in Ctenomyidae this has resulted in the hypothesis that the Andes constitute a “speciation engine,” with orographic barriers causing speciation by vicariance or ecological exclusion. Here, we show that the Andes constitute a more generalized speciation engine across mammal taxa: valley or hilltop taxa are conspecific over vast longitudinal spans, whereas geographically proximal taxa separated by altitude in contrast are distinct. The eastern Andes—“Central Andean Foldthrust Belt”—were uplifted eastward by crustal folding as the central Andes thrust east, creating isolated mountaintop habitats cut off by deep north-south valleys. Integrating geology with phylogeny better illuminates evolutionary processes in the Andes.

198: Exploring biodiversity with long-read barcodes and next generation sequencing.

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Cryptic biodiversity can be a difficult barrier to field collections in areas of high endemic diversity and low history of extensive study. Large collections may be sorted into "bins" based on the identification of one or two exemplars causing some taxa to be grouped artificially. Further, unknown taxa closely related to a common organism may be quickly identified as the common relative due to morphological similarities. These approaches can easily hide biodiversity, however alternative approaches may not be cost effective, especially if taxon group experts are not available. Recent advances in sequencing technology provide an opportunity for researchers to quickly sequence multiple individuals at the same time using longer reads more conducive to genes such as Cytochrome-b (Cytb). We took two field collections from Ecuador and used PacBio multiplexing and the Cytb gene to investigate the feasibility of identifying biodiversity in the collections. Using this approach, we identified at least one cryptic group, and are investigating 2 more. This method of identifying species is amenable to working with large groups of individuals (10k or more per run) and is cost effective with enough individuals. It does not replace important morphological techniques; however, it can provide a starting point for morphological based approaches.

199: Andean diversification in Phyllostomid bats

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The Andean mountain chain affects the distribution of several Neotropical bats, mostly by acting as a barrier that separate west and east populations, or creating ecological differentiation along the elevational gradient. In many cases, these geographic patterns result in distinct species whose study provides an exceptional insight into key evolutionary processes at this region. Phylogenetic studies for several of these taxa allow to look into these patterns and contrast that evidence with previous hypotheses. Here, I identify species or genera for which the Andes seem to delimit (allopatric or parapatric) populations representing divergent lineages, sometimes with nominal taxa representing that variation, and look into phylogenetic evidence for an Andean role in those processes. Using the most recent geographic patterns for this family, I identified 22 genera and over 150 species (representing nine out of the 11 subfamilies) that are suitable for these analyses. Morphological or molecular phylogenies exist for 107 species, allowing to test some of these biogeographic hypotheses. Because not all phylogenies include full taxonomic or geographic coverage, only preliminary insights are obtained. For most cases, however, a distinctive pattern was found in which events allegedly related to the Andes would promote that diversification. It is important to stress that biotic factors, such as direct interaction between populations (at a local or regional scale) are equally important for establishing these biogeographic patterns.

200: Current knowledge on Ecuadorian Andes mammals

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As in other South American countries, the Ecuadorian Andes have an important role for diverse biogeographical processes, acting sometimes as a North – South corridor for species adapted to inhabit certain elevations, as island-like refuges where species could differentiate and become endemic, and as barriers separating East and West populations promoting speciation. Although bats are not especially diverse in high lands, they occupy different elevational floors with distribution patterns that reflect those effects. In recent years niche modelling studies, and taxonomic assessments have been carried out at the Mammal Division of the Museum of Zoology that have revealed interesting distribution patterns, and new fauna added to the Ecuadorian mammal lists, as well as new conservation priorities for many species of bats. Results of various research projects will be presented as well as BioWeb, the new museum-based information platform on Ecuadorian diversity.

201^E: Seasonal changes in C3 and C4 plant consumption of ungulates in contrasting arid systems

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Ungulate diets are largely unknown in the arid and winter rainfall biomes of South Africa. We studied ungulate diets of 17 species, including ostrich (*Struthio camelus*) of the class Aves, in two contrasting arid biomes in South Africa, i.e. arid dwarf shrublands of the Nama Karoo and arid form of the Savanna biome. Ungulate fecal samples were collected from both biomes during three rainfall seasons and underwent stable carbon isotope analysis to determine relative proportions of C₄ and C₃ plant forms in their diets across seasons. The contribution of C₄ forage to the diets of species in the arid Savanna was generally higher than that in the Nama Karoo. Several species traditionally regarded as grazers included considerable amounts of C₃ forage in their diets. For example, mountain zebra (*Equus zebra*) diets consisted of 50% C₃ plant forms in the Nama Karoo, while in the arid Savanna they consumed almost exclusively C₄ plant forms. During the dry season (winter) C₃ intake was higher in the Nama Karoo than in the arid Savanna, reflecting C₃ plant growth (C₃ grasses and shrubs) and winter rainfall in the Nama Karoo. The plasticity of mixed feeders' (e.g. springbok, *Antidorcas marsupialis*) foraging habits allows them to exploit differences in relative C₄ and C₃ plant form abundance in the two ecosystems.

202^{HTA}: Fisher response to tree mortality in the southern Sierra Nevada

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In recent years, drought conditions followed by widespread beetle outbreaks have led to an unprecedented level of tree mortality in the southern Sierra Nevada. Tree mortality, particularly of conifers such as ponderosa pine (*Pinus ponderosa*) and sugar pine (*Pinus lambertiana*), has been extensive in areas known to be occupied by fishers (*Pekania pennanti*), but the impacts to this species and its habitat have not been quantified. Fishers in this region are of conservation concern and they rely on features of mature forest (e.g., dense canopy cover), thus these drastic changes to the landscape are concerning from a conservation perspective. To assess changes to fisher habitat and fisher use of forested landscapes with varying levels of tree mortality, we generated tree mortality maps for our study area in the Sierra National Forest and gathered data on fisher movement using GPS collars. We investigated 1) changes to habitat used by fishers prior to 2015 and 2) fisher use of habitat in a landscape altered by tree mortality. Preliminary findings indicate that conifer mortality has impacted significant portions of previously occupied fisher habitat and that large patches of live forest, particularly in riparian areas, may become increasingly important to support fisher populations in this region. We discuss implications for conservation of fishers and management of fisher habitat in the southern Sierra Nevada.

203^F: Bat box design affects microclimate and suitability as bat habitat

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Artificial roosts, called bat boxes, have become popular for conservation of bats, but we know little about how box design affects internal microclimate. Hot boxes (> 45°C) could be ecological traps. We assessed microclimate in 20 different box designs, modified by volume, insulation, shading, and airflow, measuring T_{internal} via 12 dataloggers in each box installed in close proximity in central Indiana (mid-May–mid-September 2018). We calculated and tested for differences in proportion unsuitable, maximum (T_{max}), minimum (T_{min}), and instantaneous range of temperatures (T_{range}). We also measured ambient temperature (T_a), global radiation (G), and wind speed (u) at the site. Boxes averaged 25.9°C (range 25.1–26.8°C), but varied from 11–54°C. Unsuitable conditions (>40°C) were mainly (97.3%) in the topmost portion of boxes. Changes to box volume produced the greatest differences in T_{max}, T_{min}, and T_{range}. A short box was 7°C cooler (P<0.001) and 7°C more stable than a long box (P<0.01), but the long box offered greater T_{range} (5.28±0.17°C vs. 1.58±0.06°C, P<0.001). Daily maximum T_a and G directly affected daily box T_{max}, T_{min}, and T_{range} while daily maximum u had an inverse effect (P<0.05). Box design and weather affect bat box microclimate, which has important implications for the use of bat boxes as mitigation tools.

204^{HTA}: On the ground and in the trees: A comparison of camera trap and line-transect surveys

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Monitoring trends in the occurrence or distribution of species over time is important for informing conservation plans and concurrent management actions. Understanding the effectiveness of field methodologies for collecting these data is crucial in order to have accurate and precise data and to optimize allocation of sampling effort. In this study, we compared mammalian species richness and detection probabilities between three field methodologies: line transects, and camera traps deployed on the ground and in trees in Nyungwe National Park, Rwanda. Using single-season occupancy models, we found that estimated species richness and detection probabilities for ground cameras and arboreal cameras were consistently higher than for line transect surveys. Estimates were similar between ground and arboreal cameras, but species composition differed. Our results suggest that ground and arboreal cameras used in conjunction provide the most effective approach to monitor the whole mammal community regardless of substrate use or activity period, which is particularly important in areas where species detection rates are very low. The combination of ground and arboreal camera traps can be used to improve species monitoring and management plans.

205^{E,HTA}: Ambient temperature influences winter torpor patterns of non-cave roosting 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). The stable temperatures of cave and mine hibernacula are ideal for extended torpor bouts and fungal infection from *Pseudogymnoascus destructans* (Pd). However, tri-colored bats use tree cavities, bridges, and foliage during winter throughout parts of their range and may experience variable roost temperatures. Our objective was to determine winter torpor patterns and skin temperatures (Tsk) of tri-colored bats using non-cave roosts and relate them to WNS susceptibility. From November to March 2017-2019 we measured Tsk of tri-colored bats in south-central South Carolina, an area devoid of caves or mines, using temperature-sensitive radio transmitters. In addition to three bridge roosts, we tracked individuals to 24 tree roosts. The median torpid Tsk of twelve bats ranged from 12.8°C to 18.8°C. Torpid bout duration varied from 3.5 hours to 9.6 days and decreased as mean ambient temperature (Ta) increased above 5°C. Normothermic bout duration varied from 15 minutes to 10.6 hours and increased as mean Ta increased above 10°C. Pd-susceptible bout duration (time Tsk <19.5°C) varied from 15 minutes to 8.9 days and decreased as mean Ta increased above 10°C. Our results indicate fluctuations of Ta in non-cave roosts influenced torpid, normothermic, and Pd-susceptible bout duration. Therefore, these tri-colored bats may be less susceptible to WNS than cave and mine populations.

206^E: Ocelot resource selection in a highly fragmented landscape

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Road networks are widespread and influence wildlife populations in profound ways. The ocelot (*Leopardus pardalis*) is an endangered felid in the United States, with an estimated remnant population of < 80 individuals in the Lower Rio Grande Valley of Texas. This area is one of the fastest growing population centers in the United States, resulting in high amounts of vehicle collisions and fragmentation of available habitat for ocelots. Despite the high amount of ocelot-vehicle collisions, it remains unclear how ocelots adjust their behavior relative to roads. We examined a preliminary subset of telemetry data to determine resource selection by ocelots (n=7; 3 males, 4 females) from 1982-1988 at the home range scale. We conducted a hierarchical modeling scheme to examine which aspects of woody cover ocelots were

selecting for and how roadways influence this selection. Preliminary results suggested patterns indicative of additive use and consistent selection for woody cover at the home range scale. Our top model included several aspects of woody cover as well as distance to roads ($\Delta AIC > 2$). This indicates that roads play a role in how ocelots select for resources at the home range scale and provides support for our hypothesis that ocelots avoid roads. This project aims to inform the placement of future road crossing structures to decrease ocelot-vehicle collisions and increase landscape permeability for this endangered species.

207^{E,HTA}: Ultrasonic acoustic deterrents reduce bat fatalities at wind turbines in south Texas

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The need for renewable energy resources to reduce climate change impacts has never been greater. Wind energy is a necessary component of the global renewable energy portfolio. However, wind turbines are known to cause bat fatalities worldwide, and, as a result, pose a risk for species extinction. Ultrasonic acoustic deterrents (hereafter deterrents), as a bat impact reduction strategy, are a promising solution; however, little field testing exists. Our research objective was to assess effectiveness of a newly developed deterrent for reducing bat fatalities at a wind energy facility in south Texas. We equipped 16 wind turbines with deterrents, and randomly assigned eight turbines as controls and eight as treatments on a nightly basis from 31 July through 30 October in 2017 and 2018. To quantify bat fatalities, we searched daily 100-m radius plots centered on each turbine, and assessed effectiveness of deterrents with generalized linear mixed models. We completed 2,560 wind turbine searches for both seasons combined, and identified 627 bat fatalities comprised of seven species. Our results indicate the deterrents significantly reduced overall bat fatalities with species-specific responses. Reductions were most pronounced for hoary bats (*Lasiurus cinereus*) and Brazilian free-tailed bats (*Tadarida brasiliensis*). Based on our results, deterrents represent a potential impact reduction strategy for some species of bats, but research is still warranted to improve the species-specific effectiveness of the technology.

208: A habitat suitability analysis for the red wolf (*Canis rufus*) across its historic range

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Red wolves (*Canis rufus*) are a critically endangered species endemic to the southeastern United States. Currently only a single, small wild population exists. Thus, it is imperative to identify potential sites that may be suitable for additional wild populations. We analyzed available data to identify and rank suitable habitat and sites across the historic range of the species. A geographic information system approach was used to develop habitat suitability models based on indices of landscape type and metrics such as distance to nearest road types and to human populations. A land use index was created based on information on habitat suitability, preference, and use extracted from the literature. We then incorporated human population measures and distances to major roads to create 12 models of ranked suitability throughout the range of the species. Modeled landscape suitability varied subtly as a function of parameter weights, but the 12 models could be reduced to three based on the similarities of results. These three models were used to further identify the suitability of large (>1000km²) areas of federally managed lands. Results suggest suitable habitat for population restoration is available across the historic range of the red wolf, with large areas of suitable lands occurring in several National Forests. These National Forests repeatedly ranked high independent of model choice and thus might represent appropriate localities for population restoration efforts.

209^E: Comparative phylogeography of *Sorex monticola* and relatives and Jemez Springs virus

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As intracellular parasites, the emergence of viruses is inherently tied to the evolutionary history of host organisms. Mammals are major reservoirs of zoonotic pathogens that have adverse effects on human health. Comparative phylogeography of host-pathogen systems provides valuable insight into the biotic and abiotic forces responsible for viral diversity and distributions. Jemez Springs virus (JMSV) is a widely distributed orthohantavirus harbored by the dusky shrew, *Sorex monticola*, and 4 close relatives: *S. vagrans*, *S. trowbridgii*, *S. palustris*, and *S. bairdi*. To examine the shared evolutionary and biogeographic histories of JMSV within this shrew complex, we sequenced the large, medium, and small genomic segments of JMSV and host mitochondrial cytochrome *b* gene for phylogenetic reconstruction and population demographic analyses. Orthohantaviruses showed a similar evolutionary history to their host species, with viral clades corresponding to host clades, which in turn were largely structured geographically. We detect initial divergence of JMSV in the Pacific Northwest coast consistent with codiversification and the Coastal Refugium Hypothesis, with the subsequent expansion of independent lineages following the Last Glacial Maximum. Connections between host ecology and evolutionary history impact pathogen diversity, essentially laying the groundwork for deeper understanding of pathogen evolutionary dynamics and disease emergence.

210: From RADSeq to whole genomes: phylogeographic history of the North American water vole (*Microtus richardsoni*)

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The North American water vole (*Microtus richardsoni*) exhibits a disjunct distribution in the Pacific Northwest, occupying habitat in both the Cascades and the Rockies, but not in the dry Columbia Basin in between. Recognized subspecies include *M. r. arvicolooides* in the Cascades, *M. r. macropus* in the U.S. Rockies, *M. r. richardsoni* in the Canadian Rockies, and *M. r. mylodonotus* in Utah. Previous studies in *M. richardsoni* using mitochondrial DNA (mtDNA) have suggested that a single refugial population persisted in the Cascades during the Last Glacial Maximum, which later separated into two Cascades populations, with the northern population subsequently colonizing the northern Rockies. However, the size of the species distribution offers the possibility of additional refugial populations and a more complex phylogeographic history than previously explored. Moreover, the use of mtDNA restricts the phylogeographic models that can be analyzed. Here we present preliminary research on the phylogeographic history of *M. richardsoni* using genomic scale data. First, we sequence and assemble a high-coverage genome using both linked-read and short-read sequencing. Next, we examine this genome using the Pairwise Sequentially Markovian Coalescent (PSMC) to estimate historical fluctuations in population size. Finally, we use this genome as a reference for calling SNPs, and perform phylogeographic model comparisons, including scenarios not testable using mtDNA. Future directions will be discussed, including increasing the sampling range and employing low-coverage genome sequencing.

211: Mighty Mouse: a high-elevation record for mammals (6,200 m) on Llullaillaco Volcano in the Andes

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Despite poor documentation, it has been widely reported that either the Himalayan yak or Himalayan pika holds the record for the highest elevation ever attained by a mammal. While this might apply to wandering individuals, here we report evidence of a sustained population of mice whose elevation exceeds that of all other known mammal communities. Expeditions to Llullaillaco (6,739 m), a dormant volcano on the edge of the Atacama Desert in Chile, on three occasions sighted mice at 6,200 m (20,340'). The first expedition photographed a mummified mouse, Sigmodontinae, and the second recorded a live animal on video. Visual inspection of the video provided a preliminary species identification but was not conclusive. A third expedition spotted a live mouse, and soil samples were taken from the hole it from which it emerged. Seven fragments of the cytochrome *b* gene were successfully sequenced from the soil samples. Each of the seven

regions independently corroborate the preliminary visual species identification, and place this population of mice robustly within a tightly prescribed haplotype group containing individuals the Atacama and nearby regions of Argentina. We also establish that this mouse occupies the greatest elevational range of any single species of mammal, from sea level to 6,200 m. Finally, we review the historical literature and show that several previously reported elevation records are equivocal or in error.

212: Phylogeography and taxonomy of the semi-aquatic African murine genera *Colomys* and *Nilopegamys*

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The forests of Sub-Saharan Africa have a rich diversity of endemic murine rodents, though many are poorly studied. The African wading rat (*Colomys goslingi*) is one such murine rodent from equatorial Africa. It forages by wading in shallow streams on stilt-like legs in search of aquatic prey. Despite its wide range in Sub-Saharan Africa extending from Liberia to Kenya, only a handful of studies have ever attempted to sequence DNA from this species. A potentially closely related taxon, the Ethiopian water mouse *Nilopegamys plumbeus*, is known only from the holotype collected in 1928 and is likely extinct. It has never been included in a molecular phylogeny. Thanks to recent collecting expeditions, many additional *C. goslingi* tissues are now available, allowing for an examination of the geographic structure of genetic diversity across its range. Our study also includes DNA sequences from old museum specimens, including the holotype of *Nilopegamys*. Here, we present intraspecific phylogenies from both mitochondrial and nuclear genes. Results show geographically structured genetic diversity and the possibility of more than one undescribed taxon and others in need of resurrection from synonymy. A molecular phylogeny demonstrates that *Nilopegamys* is sister to *Colomys*. We discuss patterns of genetic diversity in relation to the known disjunct distribution of populations within the species, and their proposed requirement of gallery forest along waterways in non-forested habitats.

213: Unraveling the evolutionary history of gray foxes with mitogenomes and UCEs derived from museum specimens

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The gray fox (*Urocyon cinereoargenteus*) is the only extant non-domestic canid with a widespread natural range that spans from the southern edge of central and eastern Canada to the northern part of Venezuela and Colombia. Most taxonomic studies are based on morphology, and only a few phylogeographic studies have been conducted to characterize the geographic patterns of genetic diversity but they are restricted to the United States. Sixteen morphological subspecies have been described, ten of which are distributed in Mesoamerica. In order to achieve a more comprehensive understanding of the evolutionary history of this species, it is necessary to conduct a robust phylogeographic analysis including representatives from Mexico and Central America. In this study, we sampled 200 museum specimens that represent all named subspecies. We combined in-solution DNA hybridization enrichment and high throughput sequencing protocols to obtain whole mitochondrial genomes and several thousand nuclear Ultraconserved Elements. Our phylogenetic results are discordant with taxonomic groupings based on morphology and suggest that the center of diversification of *U. cinereoargenteus* was in southeastern Mexico. We identified five main clades with genetic distances that range from 1.7% to 2.9%. Divergence time estimates showed that *Urocyon* diverged from other canids around 25.23 Mya. However, diversification within the species was much more recent, starting around 2.59 Mya.

214: Phylogeographic analysis of the Virginia opossum, a marsupial on the move**

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The Virginia opossum (*Didelphis virginiana*) is a generalist marsupial found across much of North America. Over the past two centuries, opossums have spread north into the Midwest, New England, and Ontario. Their contemporary range expansion provides an opportunity to evaluate microevolution in colder environments. However, to evaluate selection in current populations, we must first understand how they historically spread north out of Mesoamerica. *Didelphis* was part of the Great American Interchange, spreading into North America from South America 0.8 Mya. We extracted DNA from museum specimens and genotyped opossums from across their range using next-generation sequencing method ddRADSeq. We used > 20,000 quality-filtered single nucleotide polymorphisms (SNPs) to build a maximum likelihood phylogeny. Basal lineages were composed of specimens from Mesoamerica and Texas, suggesting a single initial expansion front out of Mesoamerica. Three northern lineages were identified: the Northeast (New England and Ontario), the lower Midwest (Kentucky, Ohio, and Michigan), and the Great Plains (Oklahoma through North Dakota), with the latter being the most divergent from the other two northern lineages. The Mississippi River and Appalachian Mountains may have served as barriers, creating distinct lineages as opossums moved northeast into temperate North America. These three northern lineages will be compared for shared signs of selection putatively associated with northward expansion. This research was supported by a Grant-in-Aid of Research awarded to Lisa L. Walsh in 2018.

215: Using museum specimens to investigate patterns & processes of phalangerid evolution in an emblematic biodiversity hotspot

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The island of Sulawesi has long been recognized for its highly distinctive endemic fauna; however, there has been historical confusion regarding the origin and diversification of these endemics. Uncertainty surrounding phylogenetic affinities and the difficulty of reconstructing the island's complex geotectonic history have contributed to this confusion. Advances in geotectonic modeling and phylogenetic analyses have provided insights into the formation of the island and its colonization. However, patterns of intra-island diversification are still unclear for many taxa that lack island-wide sampling. Here, we investigate the temporal and geographic patterns of colonization and intra-island diversification in the endemic marsupial subfamily Ailuropinae. We address three main questions: 1) What is the morphological and genetic diversity of the Ailuropinae? 2) Are diversification patterns consistent with hypotheses based on geotectonic models of Sulawesi's formation? 3) Are patterns of geographically distributed genetic diversity congruent with previously defined Areas of Endemism (AOEs)? By utilizing museum collections, we incorporate morphology with ancient DNA sequencing and phylogenomics. Our morphometric analyses suggest that there are several taxa undescribed under current taxonomy; however, preliminary analysis of mitochondrial genomes shows that lineages are only partially congruent with morphological groups. We also find that the geographic distribution of clades largely corresponds to AOEs. We will extend our dataset to include nuclear Ultraconserved element loci, and address the taxonomic and conservation implications of our results.

216^E: Modeling *Berylmys* (Rodentia: Muridae): species distributions past and present in Indochina

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Dramatic sea level drops from 2.6 million to 15,000 years before present BP resulted in exposure of the Southeast Asian continental shelf and formation of the landmass of Sundaland. At the height of the Last Glacial Maximum (LGM), a continuous tract of open savanna-woodland likely extended through central Sundaland and central Indochina as far as southern China. For many forest-dependent species, forest refugia linked by suitable dispersal corridors became important sources of genetic persistence as well as drivers of vicariance. Rapid diversification within the genus *Berylmys* (Rodentia: Muridae) during the last 2 million years was likely linked to these refugial landscapes. A dataset of fossil and current geographic localities for *Berylmys* was imported into DIVA-GIS v. 7.5 (Hijmans et al. 2005) with WorldClim v. 2 (Hijmans et al. 2001) climate data to model potential species ranges of *B. bowersi*, *B. berdmorei*, *B. mackenziei*, and *B. manipulus* at present and at LGM 21,000 BP. Models indicate potential refugia in southern Vietnam and

in northeast and northwest Indochina, linked through upland corridors. Favorable habitat for *B. bowersi* likely extended from southern Vietnam across the Sundanese shelf as far as East Malaysia, while little evidence of past range expansion was found in *B. manipulus*. Present day predicative models correspond well with known species distributions, except for *B. bowersi* in southern Vietnam and Hainan.

217: Systematics of Murinae and biogeography of an adaptive radiation

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Representing >10% of living mammals, the more than 700 species of murines (Old World rats and mice) arose over the last ~14 million years. The two most powerful mammalian model organisms (lab mouse and rat) emerged from this radiation, however, much of murine diversity remains unexplored. Since their origin, the Murinae repeatedly colonized Eurasia, Africa, and Indo-Australia with at least ten transitions across Wallace's line to reach Sulawesi, the Philippines and Sahul (Australia and New Guinea). Following these transitions, murine rodents adapted to a wide range of environments and ecomorphological niches. This history of repeated colonization and replicated radiations in murines provides an ideal scenario for testing the role of ecological selection in shaping diversification. For instance, on Sulawesi and the Philippines, shrew rats and their relatives, have evolved convergently extreme phenotypes through rapid rates of morphological evolution. In Australia, transitions between arid and mesic biomes occurred repeatedly in the phylogenetically-nested genus *Pseudomys*. We will provide a review of murine diversity and their biogeographic history with emphasis on their repeated radiations across the Indo-Australian Archipelago. Our systematic framework provides the foundation for pushing murines from a two-species genomic model to a 700-species adaptive radiation model with unusually rich genomic and phenotypic resources.

218: Convergences in the jaw muscle system among the independently derived worm-eating specialist murines

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Spectacular ecomorphological shifts are often associated with historical events that presumably opened ecological opportunities. One of the most spectacular ecomorphological changes is the repeated shift from omnivory to vermivory among Indo-Pacific rodents. Worm-eating murines are morphologically very distinctive, which led early taxonomists to group several genera in their own subfamily, the Rhynchomyinae. However, recent phylogenetic studies have demonstrated that these anomalous murines are convergently derived. We combined classical and contrast enhanced dissections to study the craniomandibular system of these unusual insular rodents. The dietary shift to vermivory involved major morphological changes of the craniomandibular system including elongated rostrum and jaw, loss or reduction of cheek teeth, a highly mobile jaw symphysis, and modifications of the alisphenoid region of the skull. A major reshaping of the mammalian craniomandibular muscle system also occurred with the reduction of the masseteric region indicating a loss of gnawing and chewing capacities. Notably, we found that these rodents have extremely large pterygoid muscles associated with high capacity for forward-back and medio-lateral jaw movements. These morphological changes likely allow these worm-eating rats to use their jaw like a precision tool to manipulate and ingest earthworms largely without chewing. The repeated origin of this suite of traits suggests that ecological opportunity is strong and/or potential developmental pathways are shared by murines that have been evolving independently for the last ~8 million years.

219^{E,HTA}: Adaptive evolution during the diversification of murine rodents revealed by whole exomes**

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Species that colonize novel environments are faced with unfamiliar assemblages of biotic and abiotic factors, to which they must adapt in order to survive. Changes in selective pressures during this process are expected to be measurable at the genomic level. Screening for differences in signatures of selection across genes and species, and how these associate with predicted gene function, can provide insight into the genetic basis of adaptive evolution. The rodent subfamily Murinae comprise greater than 11% of all mammal species, a diversity which has accumulated both recently and rapidly as they spread across the Old World. Murines are adept colonizers, and their diversification is typified by repeated colonization of new landmasses, islands and environments, especially in the Indo-Australian region. To examine the evolution of protein-coding genes during the colonization and diversification process, we sequenced whole-exomes from 47 species of murine rodents, primarily spanning the Indo-Australian Archipelago. Using a radiation-wide approach to detecting positive selection, we find genes associated with adaptation to novel environments, especially those that are likely involved in an evolutionary “arms-race” with pathogens, have been subject to pervasive diversifying selection. We additionally identify accelerated evolution in genes associated with lactation and bitter taste. Our results highlight both categories of genes, and specific genes, which may have played an integral role in the success of murine rodents in novel environments and ecological contexts. This research was supported by an ASM Grant-in-Aid of Research awarded to Emily Roycroft in 2017

220: The developmental basis of pigment pattern evolution in rodents

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Mammalian color patterns are among the most conspicuous characters found in nature and can have a profound impact on fitness. However, little is known about the mechanisms underlying their formation and subsequent evolution. We capitalized on the naturally occurring color pattern of the African striped mouse, *Rhabdomys pumilio*, to investigate the formation of periodic stripes, a common pattern in mammals. In striped mice, stripes result from underlying differences in melanocyte maturation, which give rise to spatial variation in hair color. Through transcriptomic analyses of the developing skin, we identified the transcription factor *Alx3* as a major hierarchical regulator. During striped mouse embryogenesis, patterned expression of *Alx3* precedes pigment stripes and acts to directly repress *Mitf*, a master regulator of melanocyte differentiation. Moreover, *Alx3* is also differentially expressed in the dorsal stripes of chipmunks, which have independently evolved a similar color pattern. Thus, differences in the spatial control of *Alx3* lead to striped patterns in rodents, revealing both a new factor regulating pigment cells and a previously unappreciated mechanism for modulating hair color. I'll end by discussing how my lab, through a variety of multidisciplinary approaches, uses stripe pattern formation as a model to uncover molecular mechanisms underlying the origin of evolutionary innovations.

221: Rats get dirty in the city: the impact of urbanization on rodents and rodent-borne diseases

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Urbanization is a global phenomenon that has led to a rapid increase in both the number of people living in cities and the proportion of land mass occupied by urban environments. Although the process of urbanization destroys and fragments natural habitats, it also creates new ecological niches and provides access to abundant resources, allowing some species to thrive. Rodents are among the most successful urban mammals, with several species distributed globally in cities (e.g., members of the genera *Mus* and *Rattus*), and many others persisting locally in urban and suburban areas. However, unlike many other species of urban wildlife, rodents often live closely with people and come into contact with many aspects of our food supply. As a result, people are often at risk from the pathogens carried by rodents. Our work seeks to understand how the ecological and environmental context of cities shapes the abundance and distribution of urban rodents and the pathogens they carry. Here, we explore how features of the urban environment influence human disease risk, and discuss how a One Health-based approach to urban rodent management can be used to ensure the continued and healthy coexistence of people and rodents in city environments.

222: Dietary and habitat specialization in woodrats (genus *Neotoma*) is associated with differences in caching behavior

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Woodrats, also known as packrats, display a range of interesting behaviors including, dietary specialization, food and object caching, and prolific building. We used four species of woodrats, *Neotoma albigula*, *N. bryanti*, *N. lepida*, and *N. stephensi* that differ in degree of dietary and habitat specialization, to investigate correlations between caching and building behavior, and diet and habitat selection. Animals were given the opportunity to cache food items, nesting items, non-essential items (jingle bells), and building items in both a lab and field setting. In the field, the two species *N. stephensi* and *N. bryanti*, from homogenous environments dominated by a single shrub species, had only 60% of the individuals studied take any of the items offered. The other two species *N. lepida* and *N. albigula*, from more heterogeneous environments, had all individuals studied take items offered. In the laboratory, the dietary specialists, *N. stephensi*, *N. lepida*, and *N. bryanti*, cached less food than the dietary generalist, *N. albigula*, when that foodstuff was not its naturally preferred food. All species readily cached sticks and nesting items in the lab, but caching of the non-essential items differed, because the strictest dietary and habitat specialist, *N. stephensi*, rarely cached jingle bells. We propose that dietary and habitat specialization in woodrats is correlated with a reduction in eclectic caching behavior.

223^{E,HTA}: Social thermoregulation in *Marmota caligata*: how group structure impacts thermoregulatory efficiency**

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Mammals at high latitudes rely on precise timing of energetically expensive life-history events to survive extreme winters with scarce resources. Hoary marmots (*Marmota caligata*) in interior Alaska exemplify this challenge. These highly social obligate hibernators rely solely on fat reserves to survive the long winters. We set out to determine if and to what extent these animals use social thermoregulation to survive this prolonged hibernation. Using body-temperature loggers implanted into eight marmots hibernating in two burrows, we documented hibernation timing and torpor-arousal cycles throughout the winter of 2016-2017. Within each burrow, body temperatures were highly synchronized, indicative of social thermoregulation. However, the burrows differed in social structure and extent of synchrony. The burrow with fewer individuals and a presumed monogamous social structure had higher synchrony than the burrow with more individuals and a presumed polygamous structure. Furthermore, the pattern of arousal leadership – an added cost of social thermoregulation – varied between burrows. The larger group shared this cost among individuals, whereas the smaller group showed much less reciprocity. Our results highlight the importance of understanding how social structure impacts group hibernation, not only through the total number of animals in a group, but also in how the burden of arousals is shared among group members. Questions remain regarding the relative advantage of higher synchrony versus fewer arousal initiations and which individuals will benefit the most. This research was supported by a Grants-in-Aid of Research awarded to Catherine E Rubin in 2015.

224^E: Pumas (*Puma concolor*) stabilize a community of competing meso-carnivores

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Competition is one of the greatest forces structuring carnivore communities. Interspecific co-existence is facilitated when a subordinate species minimizes niche overlap – in space, time or resources – with dominant competitors. To explore mechanisms behind carnivore niche partitioning, we studied a simple guild of strongly-interacting carnivore species in Patagonia: pumas (*Puma concolor*) and two species of foxes, culpeos (*Lycalopex culpaeus*) and South American gray foxes (*L. griseus*). Specifically, we established 46 random camera trap sites in and around Laguna Blanca National Park, Argentina (30,000 ha), during the winter of 2018 and collected vegetation, topographic, and human land-use data (e.g.,

horizontal cover, roughness, and distance to households). We estimated puma occurrence via a presence-only model from tracks, sign, and photos and employed multi-species occupancy models to analyze spatial co-existence between culpeos and gray foxes. Finally, we collected scat from each carnivore to estimate dietary overlap. Our preliminary findings indicate that foxes spatially avoid their predators, and that culpeos were positively correlated with distance to households whereas gray foxes utilized puma-associated habitat. Scat analyses indicated intermediate dietary overlap between carnivores. Our results suggest that, through competitive overlap, an apex predator can create spatial niche space for subordinates while facilitating the diet of intermediate guild members.

225^E: The mystery of movement and memory in mule deer

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Whether attempting to escape harsh environmental conditions or securing access to mates, animals move throughout their world to persist in environments where resources are heterogeneous in time and space. Seasonal migration, one of the most dramatic and widely observed forms of movement, can take animals across hundreds of kilometers of landscapes that they may see only twice a year. Consequently, migratory animals must possess the cognitive ability to manage massive amounts of spatial information to complete their journeys, yet how quickly animals develop such knowledge and their capacity to retain it remains a mystery. We observed a movement of a young mule deer (*Odocoileus hemionus*) that demonstrates an extraordinary capacity of navigation and memory that has been heretofore unrecognized and unexplored in migratory ungulates. Weeks after arriving on her summer range, this animal left her summer range and traveled 75 km across rugged, novel topography by herself, only to turn around and follow almost exactly the same route back to her summer range. This unguided movement through unfamiliar country suggests that mule deer – and ungulates more broadly – perhaps possess unappreciated cognitive spatial abilities that warrant future exploration.

226^{E}: Foraging site selection from GPS telemetry in a marine foraging bat**

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Habitat selection models can provide insight into how animals respond to their environment at multiple scales. Here we investigate GPS tracks of the Mexican fish-eating bat (*Myotis vivesi*) as it forages in the open ocean. The dynamic marine environment provides a challenge for animals attempting to reliably find prey as often the same location between nights will yield very different results. Our previous research found that fish-eating bat foraging areas are on average several kilometers apart over consecutive nights, suggesting that bats cannot reliably predict prey location. Playback experiments and on-board audio recordings revealed that these bats rely on social information to find ephemeral prey patches, yet there is consistency in the direction of their foraging flights suggesting habitat selection at some level. Here we ask if any of six environmental variables measured by remote sensing are associated with foraging at two spatial scales, (nightly path, foraging patch) to identify predictors of habitat selection by fish-eating bats. Preliminary results reveal that environmental variation fails to predict foraging patches, but at a larger scales bats choose to forage in areas with more dynamic regions (i.e. higher chlorophyll a, colder sea surface temperature, deeper ocean, and steeper ocean floor slopes), likely increasing the general presence of prey. Understanding how bats select foraging sites in a marine environment provides opportunities for comparison with strategies of other marine organisms. This research was supported by a Grant-in-Aid of Research awarded to Edward Hurme in 2016.

227: Hierarchical habitat use by raccoons *Procyon lotor* in the Prairie Potholes Region of Manitoba

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Habitat use by animals represents the integration of a series of hierarchical decisions made in response to multiple stimuli. Identifying the factors underlying individual decisions can illuminate not only how animals respond to their environment but also how multiple species might interact with each other. In the Prairie Potholes region of southwestern Manitoba, raccoons (*Procyon lotor*) are an important nest predator of waterfowl, but it is unclear how raccoons use this landscape during the waterfowl nesting season. We used high-resolution GPS telemetry to elucidate two hierarchical behaviors of raccoons near Minnedosa, MB, Canada. First, we evaluated the importance of proximity to pothole wetlands relative to other landscape features on third-order habitat selection using Random Forest models. Second, we determined which features contributed to variation in intensity of use of individual wetlands using GLMMs. We found that proximity to wetland and human-use sites were the most important predictors of habitat use by raccoons, with probability of use increasing with increasing proximity to these food-rich patches. Contrary to our expectations, proximity of a wetland to a human-use site was not a significant predictor of intensive wetland use. However, intensity of use did decrease with proximity to roads and increase with increasing tree cover around the wetland perimeter. These results can inform predator management in the prairie potholes, thereby enhancing conservation of waterfowl during the nesting season.

228: Fire and fawning in white-tailed deer

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Predators induce individual prey to express behavioral traits, but identifying when those traits influence population-level processes remains a challenge. Maternal investment is an intuitive link between predator-mediated traits of individuals and population-level processes, because maternal investment often decreases with predation risk, and influences processes such as recruitment. When safety and food resources are inversely related in space, prey face tradeoffs that could scale to population-level processes if selection of safer, but less productive areas represents a nutritional consequence during maternal investment. In frequently burned systems, ungulates typically move into recently burned areas to exploit increased forage quality, but the effect of the removal of cover on predation risk has received less attention. We examined effects of fire on spatial ecology of white-tailed deer and coyotes during fawning in a frequently burned pine savanna. Female deer selected forests with greater time since fire and avoided recently burned areas. Fawns selected bed sites that provided greater concealment cover. Adult female deer increased vigilance in more recently burned areas and habitat patches with lower concealment cover and a higher probability of use by coyotes. Our work describes fire-mediated foraging trade-offs in deer characterized by risk-averse behaviors, such as the avoidance of high quality forage in recently burned forests. Future work should examine if these anti-predator behaviors affect prey nutritional condition, demographic rates or density.

229^F: Behavioral plasticity in a short distance mule deer migration. To go or not to go?

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Migration maximizes accessibility of high-quality forage in variable systems. This ubiquitous behavior is found in taxa worldwide. Large herbivores in North America use long distance migrations to obtain seasonally productive forage. Mule deer (*Odocoileus hemionus*) and elk (*Cervus canadensis*) of the western US migrate to lower elevations when snow leaves high elevation forage inaccessible. A migratory herd of mule deer inhabiting the western slope of the Sierra Nevada Mountains in California show substantial variability in migration behavior. The average migration distance for this herd is 32 km, but in these migrations we see back and forth movement, termed exploratory movements, between habitat patches. These exploratory movements range from less than 1 km to more than 38 km. We hypothesize these individuals are testing forage quality in holdover locations and then deciding to continue with migration or move back to seasonal range. We have observed 95 migrations from 32 collared female deer. Individual variation in migration ranges from 2-141 days. These individuals vary among years in migratory pathways,

but show strong fidelity to stopover locations. Variability in migration behavior at individual and population levels allows for optimal use of high-quality forage and may be an adaptation to changing climate conditions.

230: Pathogens, colonization of new environments and migration: molecular evolution of immunity genes in cetaceans

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The radiation to different environments along cetacean evolution must have depicted distinct pathogenic challenges, which must have exerted intensified selection pressure on immunity genes. For example, abundance of pathogens tends to diminish with the increase of latitude, and tropical species are likely to be more exposed to this kind of threats than temperate species. As migrant cetaceans usually live both on temperate and tropical regions, they are exposed to different sets of pathogens. Hence, our aim was to investigate the molecular evolution of MHC loci, RAG1 and RAG2 genes, focusing on cetaceans. We analysed MHC genes on tropical and temperate species with different migration ranges and our results showed lower MHC diversity on migratory animals, possibly a trade-off between immune response and migration, as strong immune response can be metabolically expensive to migrating species. Regarding RAG genes, our analyses revealed a relaxation in the selection pressure in cetacean RAG1 compared to terrestrial groups, and evidence of positive selection occurring on few sites of cetacean RAG2 gene, probably as a response to the new pathogens found during early occupation of aquatic environment. Together these results contribute to understand host-pathogen interactions and how they may exert different selective pressures along habitats, which influences the molecular evolution of cetacean's immune system.

231^E: Pigmentation changes are (sort of) related to aging in chimpanzees

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Pigmentation loss, particularly of hair (greying), is a reliable marker for aging in humans. While hair greying in relation to aging is rare in other mammals, it can implicate other life history or behavioral traits, such as denoting sex-class in silverback gorillas or anxiety in dogs. Here, we examine the relationship between pigmentation changes of hair and skin in relation to chronological age, subspecies/population, and sex – for chimpanzees (*Pan troglodytes*). We used photographic data from two subspecies (and three populations) of various ages (1 – 52 years; N = 146 individuals). We scored chimpanzee hair greying on a scale of one [~100% pigmented] to six [~<10% pigmented], and facial pigment on a scale of one [~100% unpigmented] to four [~100% pigmented]. A significant positive relationship exists between hair greying and facial darkening with both age and population. However, the frequency of hair greying across ages exhibits substantial variation and average degree of greying remains relatively unchanged between all age-classes. Thus, chimpanzee hair greying is loosely related to age but is unlikely to be a reliable marker for chronological age—as it is for humans. In contrast, individuals exhibit consistent facial darkening (~50% pigmented or more) by middle age. Our results offer insights into pigmentation changes as a social cue in other mammals and calls attention to this lesser studied phenomenon in animal coloration studies.

232: Small but spiny: the evolution of antipredator defenses in Madagascar tenrecs

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Various mammalian taxa have evolved different morphological adaptations to aid in preventing death by predators, including spines, quills, dermal plates, and noxious chemical sprays. The development of these traits has previously been linked to intermediate body size, an openness of habitat, and smaller relative brain sizes, as well as a low metabolic rate and insectivorous diet. One family, Tenrecidae, contains several species that have evolved spines despite a small body size. We investigated the ecological factors that favored the evolution of spines within this group, focusing on conspicuousness to predators through body size and openness of habitat. We compiled hair and spine measurements along with natural history data and ran comparative phylogenetic analyses to study the morphological and ecological factors that favored

the evolution of these antipredator defenses. We show that as tenrecs evolved a larger body size and moved into a more open habitat, they were more likely to evolve spines, and as more robust spines evolved, relative brain size decreased. We discuss the suite of changes that occur during the transition from non-spiny forest dwelling tenrecs into larger spiny tenrecines with smaller brains and aposematic coloration.

233: Evolutionary implications of the high-protein milk of captive Xenarthrans

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The Xenarthra, the orders Cingulata (armadillos) and Pilosa (anteaters and sloths), probably evolved from an insectivorous ancestor. Based on other insectivore milks (e.g. armadillo, elephant shrew), milk of the common ancestor of living Xenarthrans was likely high-protein. Armadillos and anteaters remain insectivorous, but sloths evolved to become herbivores. Phylogeny and adult diet should both influence milk composition. This study explored whether the milk protein content of extant Xenarthrans reflects phylogeny or diet. Longitudinal milk samples collected from six nine-banded armadillos (*Dasypus novemcinctus*), two giant anteaters (*Myrmecophaga tridactyla*), and a single two-toed sloth (*Choloepus hoffmanni*) were assayed for water, fat, crude protein, total sugar, ash (total mineral), calcium, and phosphorus. Protein concentration was the highest of the milk solids for all species (9.8%, 6.0% and 7.1%, respectively) and contributed 47%, 58% and 40% of milk energy, respectively. Armadillo milk had high mineral content, increasing from 1% to 3%; calcium and phosphorus accounted for half the mineral content. Calcium and phosphorus in milk are bound in casein protein micelles. The high protein, calcium and phosphorus content of armadillo milk is consistent with growing their bony carapace. A high-protein milk may have been a preadaptation allowing the evolution of extensive osteoderm formation. The high protein content of sloth milk may represent phylogenetic constraint, but is also consistent with the moderate-protein, low metabolizable energy of the adult herbivorous diet.

234^{E,HTA}: Identifying environmental factors driving regional differences in patterns of distribution and diversification in *Peromyscus* mice

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Closely related species often compete over resources (e.g., food or shelter). Species can deal with this competition by niche partitioning that enables closely related, competing species to coexist within the same area. The number of competing species that can coexist within the same area seems to not be equally distributed across landscapes. *Peromyscus* mice can be found in most parts of North America. Currently, up to 11 species can coexist within the same area with the highest species richness in southern and southwestern desert and forest regions of North America. Other regions have fewer *Peromyscus* species. Are there certain environmental conditions that promote or hinder coexistence among these mice? To answer this question, we correlated the extent of overlap between pairs of *Peromyscus* species with the following environmental variables: temperature, precipitation, topographic complexity, climate velocity, and habitat heterogeneity. We hypothesized that overlap between species will be higher in areas with diverse resources that enable niche partitioning (e.g., areas with high habitat heterogeneity, high topographic complexity, or low velocity). Our multiple regression analyses suggest that environmental variables, especially topographic complexity and velocity, explain at least partly regional differences in species coexistence. However, the directionality of some variables, such as topographic complexity, is contrary to our predictions. We speculate that niche partitioning on different spatial scales (i.e., local versus regional) explains some of these unexpected results.

235^{E,HTA}: Opossums vs. vipers: molecular and functional characterization of a coevolving trait**

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Opossums in the clade Didelphini are among the few mammals resistant to pit-viper venoms, but the molecular basis of their resistance is unknown. A protein involved in blood clotting (von Willebrand Factor) has been found to have undergone rapid adaptive evolution in venom-resistant opossums. This protein is a known target for a subset of snake venom C-type lectins (CTLs). Several amino acid changes on vWF

unique to these opossums could explain their resistance; however, experimental evidence that these changes disrupt venom CTL binding was lacking. Using *E. coli* expressed opossum vWF and purified venom CTLs known to target vWF, we quantified binding affinity for vWFs from all Didelphini, their putatively venom-sensitive relatives, and their ancestors. Results demonstrate resistance to some but not all CTLs is mediated by vWF, and is modulated primarily by off-rates. CTL-resistant vWF was found to be wide spread in opossums both within and outside of clade Didelphini. Assays of *E. coli* expressed ancestors show that binding has been lost and regained several times tipward across nodes, suggesting a tit-for-tat coevolutionary dynamic. Ancestral data also show convergent loss of binding in opossum vWF via diverse binding disruption. These results reveal strong evidence for coevolution, widespread functional convergence, and suggest that an ecological relationship between opossums and vipers may be a broader driver of adaptive evolution across South American marsupials than previously thought. This research was supported by ASM Grant in Aids to Danielle Drabek in 2014 and 2017.

236^{E,HTA}: The genetics and persistence of a seemingly maladaptive trait in the hoary marmot species complex

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The hoary marmot (*Marmota caligata*) has a broad distribution in North America, but melanistic (black) individuals are known only in and around Glacier Bay National Park in SE Alaska. Melanistic individuals are much more visually conspicuous than their wildtype counterparts, and we hypothesize this might make them more vulnerable to predation. To determine if there is fitness effect of melanism in hoary marmots, we first sought to explain the genetic underpinnings of the trait. We identified a missense mutation in the melanocortin-1-receptor gene (*MC1R*) that is perfectly associated with melanism (n=10 melanistic and n=34 wildtype). The closest living relative of the hoary marmot, the Vancouver Island marmot, is completely fixed for a pelage phenotype highly similar to that of melanistic hoary marmots. Furthermore, the closest relative of these two species, the Olympic marmot, is sandy blond in the spring but molts into a melanistic coat in late summer. Variation in *MC1R* does not explain melanism in either of these two relatives, and it is unknown if and how melanism impacts fitness in either. Understanding the genetic causes of melanism in these species would shed light on how one trait evolved to become polymorphic, fixed, and plastic in three closely related species. We are leveraging recently sequenced marmot genomes and employing field experiments to further explore the evolutionary history and fitness consequences of melanism in marmots. This research was supported by an ASM GIAR awarded to Kendall Mills in 2018.

237^{HTA}: Genomic perspectives on chipmunk and pinworm codiversification**

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Mammalogists and parasitologists are advancing our knowledge of wild mammal and parasite interactions, but much about how these interactions shape diversification remains to be uncovered. Coevolution, when mammals and parasites impose selective pressures on each other, could be a force impacting diversification. A prerequisite to testing for coevolution is determining if the interacting species are codiversifying. Once these processes have been identified, genomic investigations can test for selection across the genomes of the interacting species. Unfortunately, genomic resources for resolving phylogenies and testing these dynamics are sparse for many mammalian parasites. We generated whole genome sequence data for two species of nematodes (Oxyurida) infecting western North American chipmunks (*Tamias*) to test for codiversification and build a foundation for investigating adaptive evolution in parasites. Our preliminary analyses of genes from across pinworm genomes yield different signals than phylogenies generated with a handful of loci, yet we found signals of chipmunk-pinworm codiversification. These signals suggest a complex history of chipmunk and pinworm associations influenced by past climate and geography. This approach will yield powerful tests of the role of parasitism in shaping chipmunk evolution because we are investigating two parasite species of the same hosts. Our findings have provided the baseline data to test for selection across pinworm genomes that, when paired with genomic investigation in chipmunks, will determine if the two groups are truly coevolving. This research was supported by an ASM Fellowship awarded to Kayce Bell in 2015.

238^E: The evolution of locomotory modes in North American shrews

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The clade comprising the soricid tribes *Blarinellini* and *Blarinini* is notable for the large proportion of species reported to exhibit semi-fossorial behavior, a proportion much higher than in the family Soricidae as a whole. To examine locomotor modes among species in these two tribes, we quantified locomotor adaptations by calculating 23 morphological indices from postcranial measurements obtained from museum specimens of *Blarina* and *Blarinella* and compared them with indices previously calculated for 16 species of *Cryptotis*. We then ranked relative ambulatory-fossorial function of each species based on scores from PCAs and on mean percentile rank analysis of the combined indices for each taxon. Species within the *Blarinellini-Blarinini* clade form a graded series of adaptations with four primary groupings that we classified as *ambulatory*, *intermediate*, *semi-fossorial*, and *fossorial*. To understand the evolution of locomotory modes, we mapped mean percentile ranks on a phylogeny of the clade and examined the resulting patterns. We found that the most recent common ancestor of the *Blarinellini-Blarinini* clade probably had either intermediate or semi-fossorial morphology. From that morphology, individual clades within the clade evolved either more ambulatory or more fossorial morphologies. Hence, evolution of locomotory adaptations within this clade is complex and shifts in modes are likely to have occurred multiple times within the clade.

239^E: A new species of *Cynomops* (Chiroptera: Molossidae) from the northwestern slope of the Andes

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The genus *Cynomops*, broadly distributed in Central and South America included six species until recently. However, various molecular studies have revealed a much higher diversity than previously thought, so that currently there are nine species described for the genus. From these reassessments, *C. abrasus* was further split into *C. mastivus* and *C. abrasus* (both distributed east of the Andes). Colombian specimens identified as *C. abrasus* from west of the Andes have yet to be included in any revisionary work. Preliminary analysis of mtDNA sequences (cytochrome b) indicated that these individuals are more closely related to specimens identified as *C. greenhalli* from the western side of the Andes in Ecuador. This result agrees with the difficulty to classify the individuals from Colombia as either *C. abrasus* or *C. mastivus* based only on morphological characters. With a combination of geographical distribution, mitochondrial and morphological data, we were able to determine that these individuals from western Colombia and Ecuador form a monophyletic clade that should be considered a different species. Our study serves as another example of the importance of including molecular data to solve taxonomic questions and the implications it can have on our understanding of the evolutionary history of a clade.

240^{E,HTA}: Impacts of beaver activity on small mammal communities in the central Adirondack Mountains, NY

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Beavers (*Castor canadensis*) are 'ecosystem engineers', altering waterways and forest structure through damming and tree-felling. Existing research on beaver largely focuses on their effects on forests and aquatic systems, but their effects on small mammals have not been well-studied. Small mammals function as important links in many trophic chains, supporting a diverse and healthy predator assemblage and consuming seeds and forest pests. However, these taxa remain understudied and their distributions unknown in much of the region. This study aims to determine the effects of beaver on small mammal assemblages compared to proximate beaver-free reference sites. This project is the first in the region to directly compare the small mammal communities of beaver and beaver-free reference sites. Live-trapping was conducted summer 2018 at two college-managed properties in the central Adirondacks. Six sites each

of beaver-impacted, beaver-free riparian, and non-riparian, beaver-free types were sampled. One site of each type was sampled simultaneously, and such sites were located at such proximity as to minimize confounding factors. Sites were sampled in two sessions, with 21 traps, for a sampling effort of 105 trap-nights per site and 1890 trap-nights for the study. Analyses using dissimilarity indices and mixed-effect linear regression indicates that beaver-impacted small mammal communities differ significantly from beaver-free reference sites, and differences were observed in the relative abundance of some focal species between beaver and beaver-free sites.

241: The rise and fall of small mammals: what's affecting communities at Hawk Mountain (PA)?

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Small mammal populations were monitored from 2003 to 2018 at Hawk Mountain Sanctuary (PA). Habitat consists of hardwood deciduous forest dominated by oaks (red, white, and chestnut) and hickory. Sampling began with 3, 6 X 6-grids (2 large Sherman traps per station, 20-m station interval) and was expanded to 6 grids (≥ 1 km between grids) in 2005, with grids trapped 3-5 times per year (from early spring to late fall). A line of pitfall traps (~10-m spacing) was placed diagonally across all grids except during 2011-2013. Small mammals experienced large population fluctuations at Hawk Mountain, with moderately high densities at all sites in 2006-2007 that then diminished, before showing tremendous population growth in 2010 that peaked in 2011. Only with these large rodent populations were a significant number of weasels caught. Following such a high capture rate, each grid was converted to 8x8 array (15-m station interval) to more effectively monitor high densities. However, in 2012, populations crashed. Despite the increased trap effort (36%), 2012 captures were less than 10% of 2011. Small mammals have declined even further in subsequent years (2013-2018). Such low densities defied explanation, especially given past responses to acorn abundance. A cicada emergence in 2013 and high mast year in 2012 failed to increase numbers. We discuss factors preventing population recovery but attribute the initial driver to intensive weasel predation.

242: Between-island divergence in the Philippine murine rodent *Rattus everetti*

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The Philippine archipelago is an ideal backdrop for studying patterns of diversification. Its dynamic geological history has produced a diverse fauna, exemplified by the murine rodents, which make up approximately one-third of native Philippine mammal species. Though prior work has clarified some aspects of Philippine murine diversification, other questions, including species limits, remain. Notably, Musser (1982) questioned whether variation among island populations of *Rattus everetti* represents a single widespread species or multiple, island-specific species. We collected phenotypic and genetic data from a broad geographic sample of *R. everetti* to assess this question. We inferred a phylogeny from cytochrome b sequences of *R. everetti* collected from multiple islands and conducted a Generalized Mixed Yule Coalescent analysis to delimit putative species for this assemblage. Each of the identified "species" clusters was monophyletic within a single island or small group of islands; however, Luzon—the largest island—contained two separate "species". We used two-dimensional geometric morphometrics of the crania from a subset of these specimens to examine whether the genetic differences between the suspected species extend to differences in morphology. Significant differences in cranium shape were found between specimens from the islands represented, though the two Luzon "species" showed no difference in cranium shape. These results suggest that species diversity of Philippine rodents is far greater than currently recognized and is driven by dispersal across islands.

243^F: Walking over wildlife: the effect of hiking trails on small and meso-mammals

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Hiking trails are found in many natural areas, including those managed for the preservation and conservation of wildlife. These human-made trails can potentially serve as a disturbance in a natural setting by altering the physical landscape due to trampling or facilitating the presence of humans in higher frequencies or intensities. Trails have been shown to decrease the abundance of some large mammals such as apex predators and megafauna, but few, if any, studies have examined the relationship hiking trails play on small and meso-mammal diversity and abundance. Using trail cameras set 0, 15, 30, and 45 meters from hiking trails at a nature preserve in southwest Michigan, we captured and analyzed over 120,000 photos. We found a significantly lower diversity of small and meso-mammals directly at the trail (0 meters) than at the further distances, though no significant differences were found in diversity among distances 15, 30, or 45 meters from the trail. Furthermore, frequency of trail use did not play a significant role in the diversity of small and meso-mammals in the affected areas. Our research suggests that trails may play a role in small and meso-mammal diversity, but the spatial impact is relatively localized, confined to a corridor no wider than 15 meters on either side of a hiking trail.

244^{HTA}: Geometric morphometric variation in *Abrothrix olivacea* (Waterhouse, 1837) (Rodentia, Sigmodontinae) in the Patagonian-Fuegian region

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The olive grass mouse, *A. olivacea*, has a wide distribution range in Andean South America, occupying diverse environments between 18°S and 56°S. Phylogeographic studies in the southern portion of its distribution uncovered differentiation between continental populations and the Big Island of Tierra del Fuego, as well as moderate differentiation between the Patagonian steppe and the temperate Valdivian rainforest. It is postulated that genetic and phenotypic diversity in the southernmost portion of this species distribution was originated from Pleistocene refugia located in these two areas, and another one in southern Tierra del Fuego. We studied cranial morphology of *A. olivacea* to test whether morphological variation parallels genetic divergence. Results obtained analyzing the weight matrices acquired by means of multivariate analyses revealed significant geographical variation in cranial morphology. Morphological divergence is largest between Andean forests and the Patagonian steppe, as well as between areas in the Andean forest biome. Relative to these, the divergence of Tierra del Fuego from populations in the southern continental steppe is limited. In sum, morphological variation appears to combine latitudinal divergence and separation between major biomes, thus showing limited consistency with phylogeographic analyses. Multilocus analyses are needed to fully examine these apparent discrepancies.

245: Dog activity in protected area: behavioral affects on mesocarnivores and impacts of a top predator

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Free-ranging dogs (*Canis familiaris*) negatively impact wildlife worldwide. Yet despite being members of the order Carnivora we have relatively little information on the role that dogs play in carnivore communities. To evaluate if activity patterns of wild carnivores are influenced by the activity of dogs and if the activity pattern of dogs is influenced by the activity of puma (*Puma concolor*), we placed camera traps in 14 protected areas in the São Paulo and Rio de Janeiro states, Brazil. From 2011 to 2017, we obtained 551 photo-captures of dogs in 17,210 trap nights in 12 of the 14 protected areas. Dogs were active primarily during the day and overlapped mainly with diurnal carnivores, such as the tayra (*Eira barbara*) and the coati (*Nasua nasua*). Mesocarnivores did not appear affected by activity of dogs, since the activity pattern of tayras, coatis, maned-wolves (*Chrysocyon brachyurus*) and ocelots (*Leopardus pardalis*) were similar in areas with and without dogs. Also, the activity of dogs did not seem influenced by puma activity, and the activity pattern of dogs in areas with pumas and without pumas showed 84% overlap. We hypothesize that dogs that use protected areas are provisioned by humans, and therefore their activity patterns may be more related to their owners than to the presence of native carnivore species.

246: Winter torpor patterns of tree-roosting southeastern myotis: implications for white-nose syndrome susceptibility

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Southeastern myotis (*Myotis austroriparius*) are one of 11 species of cave-hibernating bats that have been diagnosed with white-nose syndrome (WNS). However, it is not known whether tree-roosting populations of southeastern myotis are susceptible to the disease. Our objective was to determine the winter torpor patterns of southeastern myotis in the Upper Coastal Plain of South Carolina to assess whether they will be susceptible to WNS if they come into contact with the fungal agent (*Pseudogymnoascus destructans*) that causes the disease. We obtained skin temperature (Tsk) data from 17 southeastern myotis that roosted in basal cavities or canopies of large tupelos (*Nyssa* spp.), sweetgums (*Liquidambar styraciflua*), and oaks (*Quercus*) between November and March 2015-16 and 2016-17. We defined torpor as Tsk <32°C based on the Willis index and defined the WNS-susceptible zone (WNS-Zone) as (Tsk <19.8°C). Fifteen of the 17 bats exhibited at least one torpor bout. Mean torpor bout length was 10.5 ± 1.5 hours and only 8.3% of torpor bouts lasted for >1 day; most bats left the roost at least once during the night. Mean Tsk during torpor was 22.8°C and mean time in the WNS-Zone was 6.6 ± 1.3 hours. Our data suggest that tree-roosting southeastern myotis may not be susceptible to WNS due to their relatively high skin temperatures during torpor and their tendencies to arouse on a nightly basis.

247: Evaluation of introgression and incomplete lineages sorting among tuco-tucos (genus *Ctenomys*) using transcriptomes

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Incomplete lineage sorting (ILS) and introgression have been increasingly recognized as important components of biological differentiation. Both processes result in incongruences between gene trees and species trees, consequently causing difficulties in phylogenetic reconstruction. This is particularly the case in rapid, recent radiations, as short internodal distances and incomplete reproductive isolation increase the likelihood of ILS and introgression, respectively. Estimation of the relative frequency of these processes requires assessments across a large number of genomic regions. We use transcriptomics to test for introgression and estimate the frequency of ILS in a set of closely related, geographically adjacent, species of South American tuco-tucos (*Ctenomys*), a genus comprising about 70 species resulting from recent, rapid speciation. After stringent cleaning and filtering, 1,524 orthologous genes and 135,611 variable sites strongly support a sister taxon relationship between *C. pearsoni* and a sample from Villa Serrana (putatively representing *C. brasiliensis*). In line with earlier phylogenetic work, we find that the *C. pearsoni*-Villa Serrana pair is closely related to *C. torquatus*, whereas *C. rionegrensis* is more distantly related to them. Patterson's D-statistic rejects introgression between *C. torquatus* and *C. pearsoni* or Villa Serrana. Discordances between gene tree and species tree are symmetrical, as expected for ILS, which is estimated to have involved about 10% of the loci. In sum, ILS represents a significant process in the incipient diversification of tuco-tucos.

248^E: Using electrophoresis to differentiate between white-footed and deer mice in Minnesota prairie and woodland habitats

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White-footed mice (*Peromyscus leucopus*) and deer mice (*P. maniculatus*) are two morphologically similar species commonly found in Minnesota. These species are important indicators of climate and habitat instability, as well as carriers of diseases, making it important to track their habitat use and range shifts. Previous researchers have documented ecological replacement of deer mice by white-footed mice in neighboring states. Historically, researchers have used morphological measurements to differentiate these species, but measurement overlap makes these methods unreliable. Cellulose acetate electrophoresis of

specific salivary amylase allozymes is an accurate and reliable method to differentiate these species. We collected saliva samples from restored and remnant prairies, and woodlands in Minnesota from 2004 to 2018. We used cellulose acetate electrophoresis of salivary amylase to identify species. Densities of the two species fluctuated year to year, particularly in the forest, which could indicate vulnerability to ecological replacement. However, while the percentages of total captures of both species show some variability, there is no evidence that ecological replacement is currently occurring in Minnesota. Monitoring shifts in species distribution is important as it will affect the potential disease distribution and may serve as an indicator of how climate change is affecting woodland and prairie habitats in Minnesota. Continued research is necessary to document and understand the impact of the shifting distributions of *Peromyscus*.

249^{HTA}: The National Museum of Natural History's Division of Mammals: genetics-driven change in transaction management

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Technological advances in utilization of DNA from museum specimens transformed mammalogical research in the mid-1990's by broadly opening historic collections to genetic analysis. While the impacts of the genetic revolution on research are undeniable, the impacts on museum collection staff deserve equal attention. To characterize that impact on a single museum collection we analyze the set of all papers published in the Journal of Mammalogy from 1994 to the present which cite or acknowledge the use of specimens from the National Museum of Natural History's (USNM) Division of Mammals, as well as all outgoing loans transacted by the Division during the same time period. Using linear regression models we show that studies including a genetic analysis component have driven growth in the overall number of publications citing USNM specimens. We also show that as the raw number of loans transacted by museum staff has decreased over a 25 year span, the proportion of those loans consisting of genetic samples has increased. We examine several of the possible reasons for observed changes in transaction management trends and suggest that although we now transact fewer loans to the mammalogical community, those loans have greater impact in contributing to published research.

250: Melanism in hoary marmots and the critically endangered Vancouver Island marmot

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The critically endangered Vancouver Island marmot (*Marmota vancouverensis*) is characterized by its conspicuous melanistic (dark) pelage, and conservationists have expressed concern that this trait may negatively impact fitness. The hoary marmot (*M. caligata*) is the closest living relative of *M. vancouverensis*, and a SE Alaskan population contains individuals with a similar melanistic phenotype. Because there are no light-colored *M. vancouverensis*, the melanistic population of hoary marmots provides an opportunity to investigate the fitness effects of melanistic pelage relative to lighter-colored conspecifics. However, the structural basis of melanism has not been investigated in either species. Using museum study skins, we quantified and compared hair banding patterns between 155 melanistic and 300 wildtype hoary marmot hairs sampled along a dorsal transect. Most hoary marmot dorsal hairs are characterized by three bands, with one light-colored band between two darker layers. Melanistic hairs derive their darker color from proportionally shorter light bands, especially on the anterior region or the dorsum. We will perform the same analysis on Vancouver Island marmot study skins and expand the study to include spectrophotometric analysis of individual hairs, which will ultimately provide a better comparative context for investigating the consequences of a seemingly maladaptive trait.

251: Dentary shape of North American bears: Are polar bears (*Ursus maritimus*) in an evolutionary cul-de-sac?

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Climate change at high latitudes has the potential to exert significant selective forces on the feeding ecology of North American bears. Because polar bears (*Ursus maritimus*) are dietary specialists feeding primarily on seals, they are likely to be strongly affected by selection, perhaps for smaller size and use of other food

sources. This selection may place unique demands on jaw mechanics. If selection favors smaller size in polar bears, the allometric trajectory of dentary shape may result in jaw mechanics that are poorly suited to a different diet. In this project we explore shape variation in the dentaries of black (*U. americanus*), brown (*U. arctos*) and polar bears, and regress geometric shape variation against size for each species. We then compare these allometric trajectories across species to determine if they are equivalent. If so, selection for small size in polar bears would enable them to exploit omnivorous diets similar to other bears. We use canonical variates analysis of Procrustes coordinates to assess shape differences between the three species, and then regress these shape scores against centroid size. The results suggest that the allometric trajectories of polar bears differ from those of the other species.

252^E: Diversity and demography of hard ticks in the small mammal community of Michigan's Upper Peninsula

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In recent decades, a trend toward increasing abundance of ticks in Michigan's Upper Peninsula has been observed. This trend is concerning due to potential for ticks to transmit pathogens such as *Borrelia burgdorferi* and *Rickettsia rickettsii*. To establish a baseline for documenting future changes in tick diversity and abundance in the Upper Peninsula, we surveyed ectoparasites collected from small mammals (rodents, soricomorphs, lagomorphs) and archived in the Northern Museum of Zoology at Northern Michigan University. We recovered four tick species (*Dermacentor variabilis*, *Ixodes scapularis*, *Ixodes cookei*, *Haemaphysalis leporispalustris*), the most common of which was the American dog tick (*D. variabilis*). To investigate the geographic origins and demographic history of Upper Peninsula *D. variabilis*, we conducted a phylogeographic analysis that compared local populations to a previously published genetic dataset representing broader sampling across North America. We show that the Upper Peninsula *D. variabilis* specimens belong to an eastern clade that is widely distributed from Colorado to Maine and that the effective population size of *D. variabilis* has expanded historically, likely due to warming environmental conditions that followed the last glacial period. Prior work on diverse species suggests a history of post-glacial expansion from refugia in southeastern North America, and this study indicates that the distribution of ectoparasites of mammals may reflect a similar history.

253: Stable isotopes reveal dietary differences of urban and wild raccoons in the Florida Keys

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Various studies have shown that increased availability of anthropogenic food has impacted communities and food webs throughout history. Although recent research suggests that anthropogenic subsidies cause hyperglycemia and obesity in urban raccoons (*Procyon lotor*), little research has been conducted examining the differences in raccoon diets along urban-wild gradients. It remains unknown how differences in urban raccoon diets leads to ecosystem-level effects due to prey shifting, particularly in areas where they co-occur with endangered species. We collected hair samples from the tails of road-killed animals in undeveloped natural areas in Key Largo, highly developed areas in Big Pine Key, and from raccoons in a trapping array from natural areas on Big Pine Key for analyses of Carbon and Nitrogen stable isotope ratios. We observed little variation in ¹⁵N ratios across the three different raccoon groups, suggesting they mostly consume fruits and vegetation in the Keys, but we did note slightly higher ¹⁵N in wild raccoons from natural areas on Big Pine Key, suggesting more predatory behavior. However, we observed marked differences in the ¹³C ratios of wild raccoons from natural areas in Key Largo and Big Pine as compared to road-killed individuals occurring in highly developed parts of Big Pine Key. These Carbon signatures correspond with human foods derived from corn. We observed that raccoons in developed areas likely benefit from the consumption of human-derived subsidies.

254^E: Paternity analysis of a genetically-depauperate endangered species

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Understanding the reproductive and mating strategies of vulnerable species is often critical to their conservation. Genetic techniques can play an important role in uncovering the reproductive behaviors of species which are difficult to study in nature; however, these techniques are difficult to implement for species with low genetic diversity. We sought to understand paternity in black-footed ferrets (*Mustela nigripes*). This species is genetically depauperate and undergoes carefully controlled breeding in captivity, but little is known about their reproductive patterns in their natural environment. The recent effort to sequence the entire ferret genome allowed us to test ten newly identified microsatellite markers for polymorphisms. We found nine of ten markers to be polymorphic with two to five alleles each. We used these nine microsatellites, as well as seven previously known biallelic markers, to assess the feasibility of a paternity analysis in black-footed ferrets. Using the program CERVUS, we were able to correctly assign paternity to 18 of 25 kits from the captive colony with known parentage. Of the remaining seven kits, the correct father was the second-most likely candidate in five cases. Factors impacting correct assignment included null alleles at some loci and the lack of known mothers for some individuals. As such, before parentage analyses can be fully realized in the captive colony or in wild ferret kits, additional polymorphic loci need to be tested.

255^E: Characterizing Texas desert bighorn sheep: population structure, connectivity, genetic variation, and health using genomics

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Texas desert bighorn sheep (*Ovis canadensis texianus*), described by Vernon Bailey in 1912, were extirpated in the 1960's due to a variety of issues, including over-harvesting for meat and horns, competition and diseases from domestic sheep and goats, and the impact of netwire fencing that supported the domestic sheep and goat industry in the region. Restoration and translocation efforts by Texas Parks and Wildlife Department (TPWD) have reestablished bighorn populations to 11 previously occupied mountain ranges, totaling >1,500 individuals by 2018. Of immediate concern is bighorn competition with aoudad (*Ammotragus lervia*). These species compete for food, and perhaps most importantly, water resources in the Trans-Pecos region and it may be that aoudad can transmit diseases to bighorn. Aoudad, which are native to Northern Africa, were introduced to the Texas Panhandle in 1957 and flourished in West Texas habitats, increasing in population size (> 5,000) and extending their range in Texas over the last 60 years. Both species provide a unique opportunity to examine genetic profiles of reintroduced (bighorn) and introduced (aoudad) populations in Texas. This research will provide baseline information relevant for management and conservation purposes to assess inbreeding and "genetic health", optimize future translocation efforts, and develop parameters for tracking genotype fitness. Preliminary mitochondrial DNA analyses, utilizing cytochrome-*b* and displacement loop markers, indicate low levels of variation within bighorn and aoudad populations.

256^E: Influence of moon-phase on daily movement and habitat use of ocelots and bobcats

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Habitat selection and movement of wildlife are influenced by landscape and environmental factors. For nocturnal animals, visibility is greatly influenced by moon phase and, as such, the phase of the moon may influence activity and habitat selection of these species. However, effects of varying moon stage differ across taxa. Prey species often reduce activity during highly visible periods of night while predators may increase activity or alter their habitat use. Ocelots (*Leopardus pardalis*) and bobcats (*Lynx rufus*), two nocturnal predatory felids that coexist in southern Texas, may also alter their behavior in response to the phase of the moon. We predicted that ocelots would increase use of dense thornshrub to reduce visibility during a full moon. However, as bobcats are habitat generalists and are more active during crepuscular periods, we predicted less influence of moon phase on activity. To examine the effect of moon phase on movement and habitat selection, we collared 8 ocelots and 6 bobcats on the East Foundation's El Sauz

Ranch in southern Texas from 2013 to 2017. We will use logistic regression models to examine differences in movement rates. We will evaluate habitat selection, using resource selection functions to compare land use during periods of high luminosity compared to low luminosity. Understanding how environmental factors influence activity and habitat selection is instrumental for conservation of ocelots and other threatened species.

257^E: Patterns in the ontogeny of salivary hormones in juvenile spotted hyenas (*Crocuta crocuta*)

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Glucocorticoids (GCs) are steroid hormones that mediate responses to environmental conditions, such as limited food availability or inter- and intra-specific competition, and may also mediate adaptive life history tradeoffs. Non-invasive measures of GCs and GC metabolites in saliva and feces provide a valuable means of exploring relationships between these hormones and variation in phenotypic traits such as sex, age, and degree of anthropogenic disturbance of habitats. Previous analyses of GC levels in free-living spotted hyenas (*Crocuta crocuta*) in the Masai Mara region of Kenya have revealed that adult males and females differ in their GC responses to environmental stressors. Specifically, while variation in prey availability and anthropogenic disturbance affected GC levels in males, GC levels in females only varied with reproductive condition. No relationship was found between GCs and social rank in either sex. To explore the ontogeny of these differences in response, we assessed GC levels in juvenile (<2 years old) hyenas to determine if responses to environmental challenges are similar to those documented among adults. Using ELISA analyses of >300 saliva samples collected from individually identified juvenile spotted hyenas between 2015 and 2018, we examined variation in GC levels in relation to age, social rank, inter-litter dominance, and clan membership.

258^E: Linking foraging strategies and ear morphology in bat species of the Northern Great Plains

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For species inhabiting a wide geographic distribution, it is likely that the availability and diversity of food resources will differ across their range, leading to differential dietary preferences, foraging behavior, and associated morphological structures. Bats are an important group for studying the link between dietary flexibility and associated impacts on foraging behavior and morphology of individuals from different populations. Because different habitats generally have unique insect communities associated with variation in temperature and precipitation, populations of a species will likely be adapted for most effective foraging in their local environment. Such differences in foraging behavior involve specific flight patterns and prey detection methods, yet little is known about how locally-adapted foraging strategies have impacted the evolution of morphological structures. This project aims to investigate the diet and associated foraging strategies of the eleven species of bats found in North Dakota and South Dakota while examining ear and tragus morphology of one species, *Myotis lucifugus* (little brown bat), to see how these structures covary with observed foraging strategy. We expect intraspecific variation in dietary preferences and associated foraging strategies will covary with population-level differentiation in ear and tragus morphology. However, if *M. lucifugus* populations are found to be eating non-aerial prey and do not exhibit shifts in ear and tragus morphology, we can conclude these traits are not differentiated, due to plasticity or local genetic adaptation.

259: San Diego County Mammal Atlas

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In one of the most biodiverse regions in the United States, the 122 species of mammals of San Diego County, California, are threatened by urbanization and climate change. A collaboration of over 40

specialists has now addressed their natural history and conservation challenges in the San Diego County Mammal Atlas. Introductory chapters encompass an overview of mammals as a class, a history of mammalogy in San Diego County, and a review of regional conservation issues. Species accounts cover identification, distribution, habitats, and aspects of biology such as diet, reproduction, space use, activity patterns, predators, and behavior. They address conservation issues such as urbanization, habitat fragmentation, and the increase of wildfire. Techniques for detecting or surveying the species in the field are outlined and needs for future research are highlighted. A list of fossil mammals known from San Diego County puts the current mammal fauna in its evolutionary context. Maps depict localities of preserved specimens and the observations of experienced biologists. Though San Diego has served as a natural laboratory for the study of the effects of habitat fragmentation and fire, an understanding of mammals' response to these forces remains uneven. More study of these topics as well as the basic biology of many species is needed before the conservation of mammals in southern California with its large and growing human population can be considered secure.

260: A comparison of progesterone concentrations and pregnancies in Steller sea lions and northern fur seals

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Despite extensive management efforts, the endangered Western Distinct Population Segment (WDPS) of Steller sea lions (*Eumetopias jubatus*; SSLs) has failed to recover, unlike its Eastern DPS counterpart. One possible explanation for the discrepancy is reduced birth rates in the WDPS relative to what is possible. Northern fur seals (*Callorhinus ursinus*; NFSs), a sympatric otariid, has not experienced a similar population decline and may serve as a model for reproductive ability. We compared the two otariids to determine if birth rates were different in wild populations by analyzing progesterone concentration in serial sections of whiskers from both species. Whiskers were harvested from 31 individuals (21 SSLs, 10 NFSs) in eastern Russia. The number of pregnancies and reproductive stages (ovulation, implantation, gestation, and diapause) were estimated based on progesterone levels and the time span associated with each whisker. Average progesterone concentrations were found for each reproductive stage. Based on an average whisker length of 15.6 cm for NFSs and 18.1 for SSLs, the time span was estimated to be 13 months and 15 months, respectively. Eight of 21 SSLs and one of 10 NFS exhibited no pregnancies. We found NFSs had a significantly higher number of pregnancies per individual (average = 0.90) than SSLs (average = 0.76). Our results suggest that birth rates in SSLs are reduced relative to what is physiologically possible for otariids in the WDPS.

261^{E,HTA}: How competitive are iconic competitors? Testing resource partitioning in Great Basin chipmunks

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Competitive exclusion is a key concept in ecology describing the exclusion of one species by another from access to a limited resource. Competitive interactions between chipmunk species in the Great Basin, documented by James Brown in 1971, are often used as a textbook example of competitive exclusion. Whether competitive interactions and resource partitioning among the Cliff Chipmunk (*Tamias dorsalis*), the Uinta Chipmunk (*Tamias umbrinus*), and the Least Chipmunk (*Tamias minimus*) have remained stable across space and time is unknown, however. We addressed this question by analyzing $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values in hair for these three chipmunks along elevation gradients within three mountain ranges in the Great Basin, The Ruby Mountains, Toiyabe Range, and Snake Range. These gradients represent historical resurveys, thus we also evaluated isotopic change within and across species over the last century. We found that isotopes reflect a signal of resource partitioning among these species that is consistent across space and stable through time, despite changes in the resource base, climate, and composition of the small mammal community. Furthermore, species have shifted in isotopic space towards more negative $\delta^{13}\text{C}$ values (even after Seuss correction), and a broader range in $\delta^{15}\text{N}$ values over the last century. Their relative position in isotopic space has been maintained, however, suggesting an important and persistent role for competitive interactions.

262: Squirt-gun surveys: a novel mark-resight example for campus cottontails

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Iowa State University prides itself on the beauty of its campus but assumed locally high abundance of cottontail rabbits (*Sylvilagus floridanus*) presents an ongoing challenge to landscape management. Campus facilities requested help in determining the population size of rabbits on campus in the pursuit of an effective management plan. Rabbits can be difficult to census with precision. Methods that work well across larger scales do not lend themselves to counts on smaller scales. Distance counts are constrained by buildings and a highly heterogeneous landscape. Mark-recapture studies require significant time and effort and may not be acceptable on a campus. However, as capture is not strictly needed to mark and resight animals, we developed a method similar to that used in aerial paintball marking of large herbivores. Small groups of students methodically worked across campus flushing, cornering, and marking rabbits with livestock paint from squirt guns. This sample period was followed by a second survey two days later in which campus was again surveyed intensively and sighted rabbits noted as being marked or unmarked. A population estimate was derived from a Lincoln-Peterson model. This method proved efficient in both cost and personnel time and yielded a number with high precision. The method has the added benefit of involving students in data collection and analysis, with an aim to better their understanding of both theory and technique.

263: Small mammal survey in the Napo river basin, Ecuador

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The Napo river basin of Amazonian Eastern Ecuador, with its mosaic of seasonally flooded banks and evergreen forest, is known as one of the world's last high-biodiversity wilderness areas. The region harbors a high level of megafauna diversity, but very few surveys targeting small mammals have been conducted. Herein, we report the results of the first small mammal study from the southeastern part of the Napo river basin, the Rio Curaray basin. A hundred traps per night of combined Museum Special and Sherman traps were set to collect non-volant small mammals. For bats, we used mist netting of 120 meters per night during eight nights. Our results recorded four families of mammals, including 30 species of bats, two species of rodents, and two species of marsupials. Among the most outstanding results, we report new country records in the genera *Artibeus*, *Carollia*, and *Lichonycteris*.

264: Population estimate and herd demographics of Luangwa valley giraffe (*Giraffa tippelskirchi*)

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Giraffe populations in sub-Saharan Africa have been in decline for the past forty years. Recent studies call attention to the giraffe population declines and note that conservation efforts often lack basic population estimates and descriptions of demographic parameters such as sex and age-specific growth and survival. This project aims to address those research needs for an isolated population of Masai giraffe (*Giraffa tippelskirchi*) found in South Luangwa National Park (SLNP), Zambia. Collaborators studying carnivore species in SLNP opportunistically collect photographs in conjunction with geographical and affiliate data of these giraffes. Given that each individual giraffe has a unique spotting pattern in its coat, a photo inventory for each individual animal was created using photographs taken of animals in this population during the period 2016 to 2018. The photos are annotated with dates, sex, age class, location, and other metadata which are used to 1) develop a mark-recapture based population estimate for the giraffes living in South Luangwa National Park, and 2) estimate annual survival and growth for the population. This database will form the backbone for future studies of demographic changes in the population, mortality estimation, habitat associations, and social behavior.

265: Assessing environmental covariates associated with fisher (*Pekania pennanti*) occupancy in Southeast Alaska

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Fisher (*Pekania pennanti*) are mammalian carnivores that have been naturally expanding their range in areas across North America, potentially as a result of climate warming in winter. Fisher have been documented in Northern Canada for decades, but have recently expanded their range into the coastal temperate rainforest of Southeast Alaska (SEAK). Fisher range and winter movement is limited by the presence of deep, soft snow, and decreased snow accumulation in SEAK may be contributing to their colonization in the area. We examined the status and ecological requirements of this novel fisher population by investigating environmental covariates associated with fisher occupancy in Juneau, Alaska during the winter of 2018. Using data collected from 25 remote camera stations and Alaska IfSAR datasets, we conducted single-species occupancy analyses at both site (local) and grid (broad) scales. There were 17 fisher detections across the study season at seven stations. We found evidence that snow density and elevation have positive effects on fisher occupancy at the site scale, whereas vegetation height has a positive effect on fisher occupancy at the grid scale. Results from our research provided an initial assessment of important environmental characteristics associated with fisher occupancy in SEAK. This research contributed to a more thorough understanding of an expanding mesocarnivore species that can be used to highlight the effects of shifting species ranges associated with global environmental change.

266: New records of *Promops* from a high Andean urban landscape

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The constant growth of human population and advance of urban environments can affect mammal populations at different levels. Bats are a special group that can suffer greatly from habitat loss but can also adapt to urban environments. The Distrito Metropolitano de Quito (DMQ) is a fast-growing city that has lost most of the green areas in the urban cone, leaving patches of Andean forest where the bat fauna has not been studied. Bat diversity in DMQ is currently represented by 30 species in the families Phyllostomidae and Vespertilionidae. The bat genus *Promops*: Molossidae is known from both sides of the Andes in Ecuador. Herein, we report for the first time the presence of individuals of this genus in DQM over 2,800 m above the sea level, based on two bat recordings made in free flight in an urban park. Additional voucher specimens deposited at the Escuela Politécnica Nacional del Ecuador support the presence of this species in DMQ. Our findings suggest that high Andean urban landscapes, such as DMQ, still harbor poorly-studied faunas that need to be surveyed, analyzed, and protected.

267: Four new species of the *Hylomyscus anselli* group (Rodentia) from DR Congo and Tanzania

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In concert with many other small mammal groups from the Afrotropics, the number of species recognized within the genus *Hylomyscus* has increased significantly over the past dozen years. The last comprehensive review of the genus recognized eight species. Since that time, nine additional species have been elevated from synonymy ($n = 4$) or described as new ($n = 5$). Here we describe four additional new species within the genus, all collected by the late William Stanley. Two of the new taxa are sympatric and come from the poorly known left bank of the Congo River. One of these (*Hylomyscus* sp. nov. 1) is easily recognized as it is tiny and significantly smaller than any known species of the genus; the second new species (*Hylomyscus* sp. nov. 2) is also small and syntopic with the first. The third new species, from the SW corner of Tanzania, is quite large and had been previously included within the hypodign of *Hylomyscus anselli* following its resurrection from the synonymy of *Hylomyscus denniae*. The fourth new species is from Mahale Mountains National Park, western Tanzania, known for its well-studied chimpanzee population. These last two forms were first recognized following a genetic review of the group.

268^F: Increased prescribed fire reduces landscape-level prevalence of rodent-associated ticks in pine-oak woodlands

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Because ticks (Ixodoidea) are vectors for both inter- and intraspecific pathogen transmission with a high probability of influencing zoonoses, understanding community structure and host associations is expected to improve management of wildlife diseases. Ticks are likely to display distinct patterns of population dynamics due to their host relationships and interactions, coupled with other abiotic and biotic factors, so landscape-level disturbance (i.e., prescribed fire) is expected to reshape tick population structure. Here, using data from our field manipulation study on the Cumberland Plateau of Tennessee, we show that small mammal abundance (15,840 trap nights) is greatest with intermediate treatments but diversity corresponds with increased management activity. To evaluate how intensity of forestry management alters parasitic ticks, we evaluated competing hypotheses using generalized linear models (GLMs) and applied information theoretic approaches to decouple how tick intensity, prevalence, and demography (age) is optimally predicted by host age or gender, site (treatment) or season, or the interaction of site with other predictors. We find that tick prevalence is influenced by site and host gender and intensity is influenced by treatment effects with intermediate management. Therefore, taken together, these results suggest that mammal abundance and diversity, tick intensity and prevalence, and tick-borne diseases can be directly mitigated with forestry management and habitat restoration programs.

269: Wild lemurs in America: feeding behaviors in free-ranging *Lemur catta* (St. Catherines Island, GA)

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Lemurs are among the most vulnerable primates, with ~71% of species endangered or critically endangered and 21% classified as vulnerable (IUCN). The current rate of decline in Madagascar will be unable to support these species in the long-term, reaching a point where re-introduction of captive sub-populations may be the only hope for the survival of these primates in the wild. St. Catherines Island is a mixed forested-coastal environment along the Georgia coast. In 1985, captive-born *Lemur catta* were introduced onto the island as part of a “re-introduction” training program with the hopes of re-stocking populations in Madagascar. The lemur feeding adaptations to the native flora has been an important source of research, though lemurs receive daily provisioned meals. Full-day focal animal follows of 18 adults across 5 groups were conducted in November 2018 and February-March 2019. Daily traveling distances ranged between 0.32–3.22 km, with the two largest groups ($n = 6; 7$) venturing further from their provisioned feeding sites than the smaller groups ($n = 4-5$). In addition to the provisioned diets, food parts from 9 species of naturally occurring plants were actively foraged, including leaves, berries, bark, acorns, and Spanish Moss; geophagia and insect consumption was also frequently observed. The foraging abilities of this population resemble those of their wild conspecifics, suggesting hope for future re-introduction attempts.

270: Climate vulnerability assessments of mammals within Sierra Nevada forests, San Joaquin Desert, and rangelands

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Responding to a need to understand climate change vulnerability within areas of conservation priority for The Nature Conservancy, we assessed key mammals within three ecoregions of California: Sierra Nevada forest, San Joaquin Desert, and rangelands. Within each ecoregion, five focal species were selected based on either conservation interest or composite value. We used two climate models that represent the bookends of potential future climate: CNRM-CM5 predicts a warmer, wetter future and MIROC-ESM predicts a much warmer, drier future. Using the Climate Change Vulnerability Index (CCVI) developed by

NatureServe, the vulnerability of each species was scored based on life history attributes and climate change projected within its distribution. We found that our focal species within Sierra Nevada forests ranged from less to moderately vulnerable, except for the Sierra Nevada red fox, which scored as extremely vulnerable under the more extreme MIROC model. In contrast, all species within the San Joaquin Desert scored as highly or extremely vulnerable under both climate models. Rangeland species fell along the spectrum from less to highly vulnerable. Our findings suggest that climate change exacerbates current conservation challenges, where species experiencing on-going habitat loss and fragmentation appear considerably more at risk to changing climate, particularly where dispersal capabilities are limited. In addition to helping inform conservation priorities, these assessments highlight particular gaps in knowledge needed to understand the impacts of climate change.

271: Filling gaps in the range of two free-tailed bats in Costa Rica

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Bats (Order Chiroptera) face numerous conservation challenges, and basic information on geographic range, distribution, and biology are crucial to the development of appropriate conservation actions. Numerous gaps exist in geographic range maps for several free-tailed bat species (Family Molossidae) in the Neotropics, and these gaps could indicate this family of bats is limited in distribution, and perhaps rare and potentially in need of special protection. However, free-tailed bats as a group generally are difficult to capture with traditional methods employed to study bats, and these gaps may instead indicate gaps in field observations rather than true gaps in species geographic range. Recent survey results have provided additional information on the biology, range, and distribution of several little-known species of molossids, and here we provide new records of two species, *Nyctinomops laticaudatus* (É. Geoffroy St.-Hilaire 1805) and *Molossus currentium* (Thomas 1900), in areas of Costa Rica where neither species was previously reported. This information continues to fill in the gaps in knowledge on the geographic range and distribution for these species and provides the basis for future evaluation of conservation needs for molossids in the Neotropics.

272: Morphometrics of Chilean blue whales, *Balaenoptera musculus*, collected via UAS (drones) indicate possible unique subspecies

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Intraspecific taxonomy of blue whales (*Balaenoptera musculus*) is unresolved. Currently, there are two recognized blue whale subspecies in the Southern Hemisphere. The subspecific identity of the Chilean blue whale population is unknown, but genetic information suggests that it may be a unique lineage. Whaling records place Chilean whales intermediate in total body length to the smaller pygmy blue whales (*B. m. breviceuda*) and the larger Antarctic blue whales (*B. m. intermedia*). For this study, we collected measurements from free-swimming Chilean blue whales using unoccupied aerial systems (UAS; a.k.a. drones). We measured 24 whales over the course of two field seasons and report comparisons between the total body length and relative head and tail lengths with the two named Southern Hemisphere subspecies. Statistical tests confirm that the total body length of Chilean blue whales is intermediate; however, our data show overlap in relative tail length with the pygmy blue whale data (non-significant T-test). Relative head length showed no difference among the three subspecies. Overall, we conclude that the Chilean blue whale population is distinct from the Antarctic subspecies, but may be closely related to the pygmy blue whale subspecies. This study provides an example of how UAS can provide a safe and inexpensive tool for gathering morphological data *in situ* to answer questions of systematic relationships in cetaceans.

273^F: Removal of pinyon-juniper woodlands in the Toiyabe Range: population-level effects on mule deer

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Populations of mule deer (*Odocoileus hemionus*) are declining across their range for a multitude of reasons, including competition from wild and domestic herbivores, energy and urban development, and expansion of woody plants. In the Great Basin, expansion of woodlands into sagebrush habitat has caused declines of many sagebrush obligate species, including mule deer. The Toiyabe Range in Nevada is home to one of the most prolific populations of mule deer in the state. Habitat on winter range is primarily composed of woodlands containing single-leaf pinyon pine (*Pinus monophylla*) and Utah juniper (*Juniperus occidentalis*). These woodlands provide minimal nutritional value to mule deer while outcompeting herbaceous understory vegetation; therefore we are investigating how the removal of these trees on winter ranges affects this mule deer population. Roughly 1,050 hectares of pinyon-juniper were removed and will be compared with a designated control area. We have collared 36 adult female mule deer to determine the response of the population to that treatment. We will assess the effect of this removal on adult survival during winter, as well as the effects on home range size, resource selection, and movement patterns. We hypothesize that adult survival will increase, winter home range sizes will contract, and release of water from pinyon-juniper removal will improve the nutritional quality of herbaceous vegetation throughout mule deer winter range, resulting in higher adult body condition.

274: Simulating the *Journal of Mammalogy* experience in the classroom: southern red-backed vole (*Myodes gapperi*) phylogeography

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The peer-reviewed publication represents the standard across science, but its implementation into curricula can be challenging. In order to comprehend the process, students should gather and analyze data, write a manuscript involving novel findings, knowledgeably participate in the review process, incorporate changes, and see the manuscript in print. I report the experience and research findings of OSU-Lima Mammalogy students who focused on the phylogeography of southern red-backed voles (*Myodes gapperi*). Existing and easily obtainable data allow for small yet novel projects combining phylogeography with numerous aspects of Mammalogy. Each student was provided with the *Cytb* dataset from Runck and Cook (2005), alongside a unique but overlapping set of sequences from GenBank and unpublished data. Students analyzed these data and other relevant data in the context of their chosen topic and participated in a peer-review process designed to mimic the *Journal of Mammalogy* experience. Among other findings, students detected significant differences in body size between *Myodes gapperi* from major *Cytb* clades and between animals within and outside a hybrid zone. Fossil records from LGM are poorly matched to predictions based on ecological niche modeling. Likewise, observed phylogeographic patterns do not match fisher and snowshoe hare, but do align with meadow vole. The project culminated in a compiled pseudojournal, the *OSU-Lima Journal of Mammalogy*, and changes in student attitudes toward science were evaluated.

275: Animal sightings in Glacier National Park in comparison to park attendance

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Ecotourism is an expanding field, and more people are following the trend of vacationing in more natural areas, resulting in yearly increases in visitations to protected areas. The increase of interest in ecotourism provides an economic advantage; however, the influx of visitors can influence the animals in the park. Animals may respond negatively to human disturbance by avoiding areas with human activity which in turn can cause habitat fragmentation, or animals can react positively by habituating to human disturbance. This study focused on Glacier National Park during 1960-1979. During this time period the visitor attendance increased by 930,000. Animal sightings were counted from Glacier's Wildlife Observation Reports for the summer months of visitation, and the number of sightings for grizzly bear (*Ursus arctos*), black bear (*Ursus americanus*), mountain lion (*Puma concolor*), coyote (*Canis latrans*), elk (*Cervus elaphus*), moose (*Alces alces*), and mule deer (*Odocoileus hemionus*) were recorded. Regression analysis was done comparing

the total amount of sightings of a species each year to the total visitor attendance for the corresponding year. We only found a significant positive relationship for coyotes during 1960-1966, leading to the conclusion that overall the animals in Glacier National Park were not disturbed by the influx of visitors during 1960-1979.

276: Behavioral implications of relative brain size in the extinct dwarf Tapir, *Tapirus polkensis*

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Extant tapirs (*Tapirus* spp.) are typically nocturnal and solitary with occasional territory overlap, exhibiting no preference for relatedness and inflexible behavior in captivity. Consequently, similar behaviors have been assumed for extinct fossil taxa. Here, we present an investigation of sociality not otherwise observed in extant tapirs. Originally, the extinct dwarf tapir, *Tapirus polkensis*, was known from only fragmentary material, but now the taxon is represented by at least 150 individuals (including many articulated specimens) from the Gray Fossil Site of northeast Tennessee (~5 Ma). Number and age distribution of the individuals strongly supports the existence of a large tapir population at the site during deposition, implying some level of social interaction. To assess the potential social system, CT scans of extant tapirs and three fossil skulls, representing an ontogenetic sequence, are used to generate cranial endocasts. Relative brain sizes and encephalization quotients (EQs) are calculated using body mass estimations from palatal width measurements. Initial results show that the relative brain size of *T. polkensis* falls within the variation of extant tapirs. Therefore, instead of being driven by greater information processing ability, dwarf tapir intraspecific interactions are the coincidental result of some other bias (e.g., concentrated resources, simple predator detection, etc.). Future work includes investigating differences in primary sensory modalities during ontogeny using landmark-based 3D geometric morphometrics to identify regional volumetric changes within the brain.

277^F: Influence of human presence on feeding behavior of small mammals

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Most animals expose themselves to predators during feeding. Therefore, they must evaluate the likelihood of encountering a predator or being attacked before exposing themselves. Hiking trails increase the presence of humans, which likely impacts non-human mammal behavior. Using 40 trail cameras at a nature reserve in southwest Michigan, we evaluated the effects of humans on eastern gray squirrel (*Sciurus carolinensis*), fox squirrel (*Sciurus niger*) and eastern chipmunk (*Tamias striatus*) feeding behavior. Cameras were placed adjacent to trails and food was applied twice per week and return time for each species was recorded relative to the presence of a human. Gray squirrels were observed 1.3 times more often than chipmunks, and 3.0 times more often than fox squirrels. We found an inverse relationship between body size and the likelihood of being the first species to return to the food site, after controlling for relative abundance. However, this finding was contingent upon time; no relationship was found after the food pile experienced more than two days of depletion. Additionally, we found that the species utilizing the food did not significantly influence the use of the food by the other species; the next species visiting the food was observed to follow the relative abundance of each species.

278: Differentiating tracks of sympatric rodents in coastal dunes: implications for threatened and endangered beach mice

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Identifying techniques to conduct frequent, effective, and inexpensive monitoring of small mammals can be challenging. Approaches such as live-trapping can be laborious, harmful, and ineffective. Passive

approaches such as tracking have been shown to lessen these burdens, but the reliability of species identification from footprints can be subjective. As a result, tracking remains an uncommon method of monitoring small mammal populations. To address the need for a more accurate method for identifying small mammals from tracks, we measured footprints (N = 6,996) from live-captured animals (N = 542) of 8 species, and developed a classification tree to distinguish between species by footprint widths. We live-trapped rodents within and near the coastal dunes of Florida with a focus on areas occupied by threatened and endangered beach mice (*Peromyscus polionotus* ssp.), whose populations warrant regular monitoring but whose tracks are not easily distinguished from some sympatric species. The overall accuracy of our classification tree was 80.3% and was achieved using only the front footprint width. We were most successful in identifying beach mice: 94% of individual beach mice were correctly identified, while < 6% were misclassified as house mice (*Mus musculus*) and < 1% as cotton mice (*P. gossypinus*). Our study demonstrates that sympatric rodent species in coastal dune communities, and likely other systems, can be reliably identified from tracks using quantitative classification based on footprint width.

279^F: Comparing five analytical approaches to quantify habitat preferences of fawns from camera trap data

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Studying juvenile mammals helps understand population dynamics to inform management decisions. However, collecting data on juvenile mammals is often difficult due to short time windows between birth and adulthood, their small size, cryptic coloration or behavior patterns, and lack of mobility. Camera trapping can provide data on juveniles, as well as their potential competitors and predators. We are comparing five analytical approaches for camera trap data to evaluate impacts of different environmental covariates, deer, and predator abundance on fawns. As part of the North Carolina Candid Critter project, we worked with citizens and wildlife agency staff to conduct camera trap surveys in 748 camera sites across 10 counties from August to November of 2017-2018. In 12,909 camera nights we obtained a total of 13,681 detections of white-tailed deer (*Odocoileus virginianus*) including 1,975 fawns and 7,468 of does. We identified individual fawns for a subset of cameras, finding 36% of detections to be of sufficient quantity. The fawn/doe ratio index is calculated to represent fecundity but we find the index insufficient in accounting for deer abundance. We evaluated the potential for mark-recapture analysis, but found no individual fawn recaptures, showing that our >200m camera spacing is too wide for using this approach with fawns. A relative abundance model looks promising due to a strong correlation between fawn detection and number of individuals at a site.

280: Morphometric analysis of craniodental variation between *Neotoma macrotis* and *N. fuscipes* in the Sierra Nevada

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Craniodental variation has played a central role in our understanding of the drivers of mammalian ecological adaptation. Craniodental traits evolve in response to both abiotic and biotic factors and can provide insight into how mammals respond to environmental variation. At the edges of species ranges, we have a unique opportunity to examine how populations respond to changes in both abiotic factors, but also important biotic factors, especially when the range boundary of one species abuts that of a close congener. Here, we examine how these factors contribute to changes in craniodental variation where the ranges of *Neotoma fuscipes* and *N. macrotis* meet in the central Sierra Nevada. We use 3D landmark analysis to quantify craniodental variation in adults of both species collected from both sides of the range boundary. Our analyses suggest that the species differ in both size and shape. In particular, the species differ from one another most in dental and rostral morphology. Variation in these traits could be the result of several different factors, but may, in part, be the result of adaptation or phenotypic plasticity in response to dietary differences between the species. Dietary shifts in areas of secondary contact between closely related lineages of woodrats have been observed before and may be one of many responses to the ecological selective forces that occur at the edges of species ranges.

281^E: Coyote and deer interactions in South Carolina using concurrent GPS collars

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In the last 50 years coyotes (*Canis latrans*) have expanded their range and now occupy nearly the entire eastern United States. Managers want to know how coyotes are impacting other wildlife, particularly white-tailed deer (*Odocoileus virginianus*), which are a popular game species. At the regional level, efforts to control coyotes have not been effective, so finding ways to best manage both species is paramount. There is evidence that coyotes can be an additive source of mortality for white-tailed deer fawns in the southeastern United States, but this impact may depend on deer density and habitat. To better understand the effect of coyotes on deer populations in the piedmont region of South Carolina, we deployed GPS collars on coyotes, does, and their fawns to evaluate simultaneous movement patterns of each and quantify drivers of fawn mortality. To date, we have captured and placed GPS collars on 23 coyotes, of which 6 have died during the first 3 months of the study. We will present data from the first 6 months of this study including potential changes in fine-scale coyote movement patterns during fawning season, and fawn mortality investigations. In addition, we will highlight other facets of this long-term study currently being investigated related to coyote diet, survival, resource use in relation to deer feeders and carcasses, and coyote-mesocarnivore interactions.

282^E: Acoustic activity of *Tadarida brasiliensis* during fall at wind turbines in South Texas

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Tadarida brasiliensis incurs high fatalities at wind turbines. Despite their high abundance in Texas, the largest producer of wind energy in the U.S., there is little knowledge on their activity patterns and behavior at wind turbines. Such knowledge is important for designing species-specific impact reduction strategies. Our objective was to identify patterns in *T. brasiliensis* activity and high-risk periods at wind turbines. From 7 August to 28 October 2017, we monitored activity at three wind turbines in Starr County, Texas. We deployed an acoustic detector on each turbine and conducted weekly fatality searches. We recorded 64,939 total bat passes for an average of 281 bat passes per detector night, with the greatest activity occurring on 4 September (1,338 average passes per detector night). We classified 27% of total bat passes as *T. brasiliensis*, and 44% to a low frequency species group that includes *T. brasiliensis*. We documented differences in bat activity among turbines and assessed weather covariates. Bat activity was positively associated with increasing Julian date, absolute humidity, and temperature, and negatively associated with increasing wind speed (all p-values <0.001). Nightly bat activity was unimodal, primarily occurring from 2200 to 0400 hrs. In addition, acoustic activity reflected fatality patterns at the site. These results provide information on *T. brasiliensis* activity and behavior at wind turbines in a region with little publicly available data.

283^E: Microbiological survey of *Procyon lotor* intestines in South Texas for identification of pathogens

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We conducted a microbiological survey of northern raccoon, *Procyon lotor*, intestines from south Texas. Raccoons pose a unique health risk to humans. Their predilection to washing their food in water before ingesting and easily adapting to a diverse array of environments make them a key species in the identification of pathogens that can be potentially harmful to humans. Identifying a pathogen and how it is transmitted is crucial to the control of infectious outbreaks. Previous studies have shown raccoons to be an asymptomatic carrier of many zoonotic pathogens, such as *Salmonella* species. As raccoons are frequently found living in close proximity with humans, we sought to determine the types of microbes they might be

harboring, and what type of risk this might pose to human health. Further, we sought to identify if there were any antibiotic resistant bacteria that could potentially spread resistance through horizontal transmission to other bacteria. To better understand the bacteria in these animals, we enriched and selectively cultured gastrointestinal tract samples for *Salmonella*, *Escherichia*, and *Enterococcus* species. Culture samples from the gastrointestinal tract were taken from each species and positively identified at the species level to determine pathogens with a potential risk to human health. All three genera were discovered in nearly all samples. Testing for antibiotic resistance continues to be a work in progress.

284: Alignment of selection, plasticity, and among-individual covariances: a test of theoretical predictions with *Peromyscus maniculatus*

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Theory predicts that the direction in which selection acts should correlate with the direction in which both genetic variation and plasticity are expressed. Unfortunately, this prediction has rarely been empirically tested. Phenotypic covariance matrices can be divided into among- and within-individual matrices and the among-individual covariances subsume genetic and permanent environmental covariances, acting as a proxy for the additive genetic covariance matrix. Simultaneously, the within-individual (co)variances represent reversible phenotypic plasticity. If the two matrices align in multivariate space, phenotypic plasticity is expressed in the same direction as is genetic variation, making populations more responsive to selection. Here (co)variances among three different behaviors (activity, aggression, and anti-predator response) were estimated along with selection in a natural population of deer mice (*Peromyscus maniculatus*). The among- and within-individual matrices were estimated using multi-response mixed effects models and the angle between plasticity and among-individual covariances was 63°, demonstrating that reversible plasticity and additive genetic variance did not align. Simultaneously, the direction of selection on the three behaviors was misaligned with both among-individual covariances (77°) and plasticity (62°), suggesting that neither the expression of genetic variation nor plasticity are adaptive in this population.

285: Estimating levels of cryptic diversity within class Mammalia

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Barcoding gene sequences, while prevalent in public databases, are underutilized for assessment of species diversity. In order to estimate levels of cryptic diversity in mammals, we downloaded all available DNA barcoding sequences for five large groups of mammals including Rodentia, Eulipotyphla, Chiroptera, Carnivora, and Primata. Collectively, these five groups represent over 80% of described species richness in Class Mammalia. We then utilize two methods of automated species delimitation in order to estimate the number of cryptic species present within each group, and apply machine learning using geographic, environmental, morphological, and life history traits in an attempt to identify characteristics of clades that are likely to contain cryptic diversity. Our approach is intended to supplement, rather than replace traditional taxonomic work. Our results demonstrate that publicly available genetic data can be used to estimate levels of cryptic diversity and may represent an important resource for the prioritization of clades where taxonomic research is most needed. Because the identification of species boundaries is fundamental to basic research in both ecology and evolution, the accurate identification of such boundaries is critical to a wide range of biological disciplines.

286^E: Genetic diversity of Central American brocket deer (*Mazama temama*). Are we dealing with cryptic species?

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Mazama temama has a broad distribution occupying Mesoamerican humid tropical forests from NE Mexico to N Colombia; however, little is known about its biology and evolutionary history. Their populations have been severely diminished as its habitat is vanishing at an accelerated rate. Our main goal is to determine the genetic diversity and to identify if a phylogeographic pattern occurs within this species based on mtDNA markers. We obtained bone and skin samples from scientific collections from Mexico and USA to amplify fragments of mtDNA genes *Cytb* and *ND2*. We estimated nucleotide and haplotype diversity as well as demographic history parameters. A high haplotype ($Hd=0.93$) but low nucleotide diversity ($\pi=0.01$) is present within Central American brocket deer. The haplotype network shows two well-differentiated groups, one including individuals from Mexico and Guatemala and other by individuals from Honduras, Costa Rica and Panama. Genetic distance between these haplogroups are large enough to consider them as separate species but additional information is required to confirm this hypothesis. *Mazama temama* probably diverged in the humid tropical forests of southern Central America with posterior dispersal events along its current northern distribution. These events are relatively recent (<2 MYA) and Chiapas Highlands probably play a relevant role in the distinctiveness of the two haplogroups detected in this study.

287: Bat diversity in the Colombian Orinoquía is high, but heterogeneously distributed in composition and diversity

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The Colombian Orinoquía region comprises savanna and forests ecosystems. Unfortunately, the anthropogenic transformation of this region has increased in the last decades. The distributional patterns of biodiversity in the region are still unknown, but understanding these patterns is important to develop conservation strategies. We evaluated the variation of bat diversity in 14 sites with different plant physiognomies, as well as environmental factors that could explain such diversity and bat assemblage dynamics (e.g., forest cover percentage, precipitation). We analyzed the alpha diversity patterns through true diversity index, variation in the composition and diversity of species in relation to landscape and bioclimatic characteristics among sites. We registered a total of 104 bat species with an average of 34 species per assemblage. The local richness did not show significant differences among sites; however, bat assemblages of riparian forests from savanna ecosystems were more diverse than other assemblages. Additionally, the dissimilarity in bat composition and structure was high among all assemblages. Our results show that the regional bat fauna of the Orinoquía presents a high diversity, but local assemblages contain only 30% of the species pool of this region; thus, this local fauna can be composed of mixed faunas from the nearest regions. Possibly, annual disturbance in the precipitation patterns (e.g., decrease in rainfall and excessive drought) is a constraint that keeps these communities from reaching equilibrium.

288: How mice sing & why it matters: the ecology & evolution of sound production in vocal rodents

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Acoustic signaling is a fundamental mode of animal communication, yet we lack an integrated understanding of how ecology and physiology interact to shape signal evolution. Muroid rodents are celebrated for their rich diversity of social systems and a growing body of literature suggests that vocalizations mediate critical social interactions, including advertisement to mates and rivals. In other taxa, social structure and spatial organization are critical factors shaping vocal evolution. While most mice produce ultrasonic vocalizations using an aerodynamic whistle mechanism, at least one clade (grasshopper mice- *Onychomys*) has evolved the ability to produce sonic long-distance signals using airflow-induced vocal fold vibrations. Here, we report on the physiological mechanisms underlying sound production in relation to social organization and space use across a subset of ecologically diverse rodents. Integration of functional and mechanistic perspectives in senders, receivers, and the environment promises to provide important insight into the evolution of acoustic communication in relation to variation in social organization.

289^F: Distribution of parasitic tissue-dwelling nematodes in white-tailed deer of the Great Lakes Region

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Cervids serve as primary hosts for many species of tissue-dwelling nematodes in the family Protostrongylidae. Protostrongylid species of the genus *Parelaphostrongylus* are common parasites of deer in North America, and can be pathogenic to non-target hosts. Over the past half century, range expansion by white-tailed deer (*Odocoileus virginianus*) has increased transmission of *Parelaphostrongylus tenuis* from white-tailed deer to moose (*Alces alces*) contributing to declines in moose abundance in northern Minnesota. Despite concern regarding the threat of *P. tenuis* infection, the geographic distribution of the parasite is not well-documented. To evaluate the geographic distribution of *P. tenuis* in the Great Lakes Region, we used genetic methods to confirm the identities of sampled larvae. We collected deer feces along a transect from Grand Marais, Minnesota to the northern Lower Peninsula of Michigan. Larvae were isolated using the beaker-Baerman method. We sequenced the ITS-2 nuclear locus and 12s mitochondrial DNA to identify species and to characterize genetic variation within and between species. Our findings show an extensive geographic overlap between *P. tenuis* and *Parelaphostrongylus andersoni*, highlighting the necessity of using molecular methods to confirm species occurrence. The range of *P. tenuis* overlaps the distribution of moose in the northern and western Upper Peninsula. These results cast doubt on reports of *P. tenuis* that are based solely on visual inspection of larvae extracted from deer feces.

290: Cross-scale interactions shape the spatial distribution of a wetland-obligate species

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Landscape configuration and composition can influence the spatial distribution of species. Potential cross-scale interactions may exist when multi-scale effects interplay to shape distribution patterns of species. We used two years of presence-absence data (2015-2016) from 71 wetland sites (2 ha) in Minnesota, USA to quantify multi-season distribution patterns of muskrats (*Ondatra zibethicus*). We used an occupancy modeling framework to examine the influence of local resource characteristics (water depth, open water, vegetation composition) on initial site occupancy and turnover. We also assessed how fetch, the unobstructed distance wind can travel across water, influenced fine-scale habitat use by muskrats. As expected, sites with greater coverage of *T. x glauca* (a rapidly establishing invasive-hybrid cattail species), shallower water depths, and less open water had greater initial occupancy probabilities. Our most-supported colonization model revealed an interaction between the amount of *T. x glauca* present at sites and fetch. Muskrats were more likely to colonize fetch-impacted sites only if there were also greater coverages of *T. x glauca* present. Our results suggest that widespread establishment of invasive-hybrid *T. x glauca* populations may facilitate distribution expansions of muskrats into otherwise unsuitable habitats.

291^F: Changes along the trail: Shifting mammal communities along an elevational gradient on Mt. Kenya

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Studies of biodiversity patterns along elevation gradients, focusing on small mammal or bird species, have documented a drop off in species richness from mid elevations to higher elevations. This has been attributed to more habitat types being available at mid elevations due to a range of potential microclimates resulting from diverse localized environmental conditions. Due to challenges in data collection, similar studies of large mammal communities along elevational gradients have not been conducted in equal scope. Here we report on a study of medium- to large-sized mammals sampled with a camera trap transect covering a 2300m gradient up the western slope of Mt. Kenya. We found that the mid-elevation natural habitats (old growth forest) had the highest biodiversity and abundance of medium- to large-sized mammalian wildlife and that both of these metrics decreased steadily as elevation increased. Our calculations of mammal community relatedness show that the biggest difference in mammal communities

was between protected areas and forestry areas managed for timber plantations and small-scale farming, followed by more subtle step-wise differences in natural habitats due to elevation. Herbivore communities show more species replacement over elevation than carnivore communities. Understanding the impacts of land-use change and climate change on large mammal communities can help conservation managers prepare sensitive ecosystems, like Mt. Kenya, for an uncertain future.

292: Comparative genomics of mustelid species to investigate the evolution of embryonic diapause

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North American river otters (*Lontra canadensis*) undergo delayed implantation in which the fertilized embryo sits dormant inside the maternal uterus until a later time when it implants and begins to gestate. In spite of one of the largest longitudinal ranges among mustelids, from boreal Canada to southern Mexico, it has narrow mating and birthing periods. This pattern fits the constraints of living in the far north, when it would be critically important to give birth and raise nurslings only during the short warm season. Embryonic diapause is widespread in Mustelidae, but not found in some closely related species whose ranges are more extensive, such as the Eurasian otter (*Lutra lutra*). We obtained genomic libraries with next generation sequencing from *L. canadensis*, *L. lutra*, the African clawless otter (*Aonyx capensis*), and a wild American mink (*Neovison vison*). *Aonyx capensis* does not undergo diapause. We used hybrid *de novo* - reference-guided assemblies of these species to compare genomic content and structure, as well as candidate genes involved in implantation among these four species and other available mustelid genomes. The domesticated ferret, *Mustela putorius furo*, was used as a reference genome. No obvious large genomic variation was found among these similar-sized genomes. Some uterine environment genes show minor structural differences between diapausing and non-diapausing mustelids that could reflect functional differences.

293: Mitochondrial DNA sequences support recognition of several cryptic species within *Reithrodontomys fulvescens*

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Reithrodontomys fulvescens has a broad geographic and altitudinal distribution (~0-2,500 m) in the United States, Mexico and Central America. Evolutionary relationships among populations and the taxonomic integrity of the 15 recognized subspecies remain controversial. Results of allozyme studies indicated at least two species-level lineages within this taxon. We examined the evolutionary relationships among populations of *R. fulvescens* using cytochrome-b sequences and up-to-date methodologies to delimit species within a phylogeographic framework. Our results supported recognition of four species-level clades that last shared a common ancestor ~4.2 million years ago. We hypothesize that the ancestral range of this complex encompassed the mountains of western and northern Oaxaca. The most widespread clade (I) ranges from the USA southward to the Trans-Mexican Volcanic Belt and Veracruz, Mexico. Clade-II occupies Chihuahua and Sinaloa, Mexico; clade-III occurs in western and northern Oaxaca, Mexico; and clade-IV is found in eastern Oaxaca and Chiapas, Mexico. Average Kumura 2-parameter genetic distances among these four clades ranges from 6.9% to 10.4%. The fact that three of the four species-level clades are restricted to Mexico underscores the fact that Mexico is a megadiverse country.

294^E: Determining vertebrate host communities of a Relapsing Fever vector (*Ornithodorosturicata*) in Central TX

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Soft ticks have been greatly understudied even though they are vectors of veterinary and human health importance. Tick-borne relapsing fever reported cases have increased in North America. *Ornithodoros turicata* is the known soft tick vector of *Borrelia turicatae*, the causative agent for relapsing fever in the southern United States. The role of sylvatic mammal species in the transmission and spread of this pathogen has yet to be established, thus research that focuses on host-tick-pathogen interactions clearly is important. This study seeks to evaluate potential host exposure at 12 caves in central TX and determine seasonality effects on both host visitation and tick abundance. The presence of *O. turicata* was confirmed at surveyed sites and caves were monitored from February 2016 to May 2018 via game cameras. To estimate tick abundance, CO₂ traps, and capture-mark-recapture techniques were used. Partial analyses indicate a total of 19 vertebrate species as cave visitors with over 1,000 events analyzed so far. The most frequent vertebrate visitors were black vultures, porcupines, and opossums. Abundance estimates for soft ticks vary seasonally from 87 to 4,721 individuals. Quantifying host visits in soft tick habitats to determine potential exposure can elucidate vector-host interactions. Seasonal fluctuations of vector and host communities have potential to effect exposure rates. Gathered information will lead to more effective management strategies to reduce overall risk of infection.

295: Mammals of five protected areas from the Colombian Eastern Cordillera

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The Colombian Eastern Cordillera is a biodiversity hotspot (high endemism and high biodiversity); however, it is under constant habitat loss. Currently, there are a few studies about mammal biodiversity, and some of the impacts that these species are suffering are still unknown. Although there are protected areas, there is no a deep knowledge about which species are being protected. This study examined richness, diversity and similarity of mammal assemblages from five different protected areas in the Colombian Eastern Cordillera. We recorded 61 species, 8 orders and 16 families. Bats were the most representative order with 49% of the species, followed by Rodentia, Carnivora and Didelphimorphia. The protected area with the highest species richness was the one located in the lower altitude (31 spp), followed by the Andean forests above 2000 meters (25 spp, 18 spp and 12 spp) and the area above 3000 meters (7 spp). The species richness was associated to the altitude and the degree of intervention of each area, a high turnover of species among areas was also evidenced. We emphasize the record of eight mammal species with restricted distribution, two of them endemic for Colombia, and two mammal species in a global category of threat. This scheme of protected areas includes a high species representation; however, it is necessary to explore other aspects related to functional and ecological characteristics of these species.

296: Using stable isotopes to assess range of the Brazilian free-tailed bat (*Tadarida brasiliensis*)

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Brazilian free-tailed bats (*Tadarida brasiliensis*) are one of the most abundant, wide ranging mammals in North America, and along with other insectivorous bats, the value of ecosystem services they provide to agriculture is estimated at \$3.7 billion annually. Recent documentation of the northward expansion of their wintering range in Texas has not explored whether these individuals are northern migrants indicating a corresponding shift in summer range, or summer residents. This study sought to predict summer origins of individuals by assessing stable hydrogen isotopes (δD) of bat hair (δD_H) in comparison to δD in precipitation (δD_P). We obtained bat hair from carcasses at a wind energy facility in south Texas during fall and winter of 2017 and 2018, as well as live individuals from Bracken cave in central Texas in 2017. We made comparisons of isotopic ratios among four sex and age categories: adult, sub-adult, female, and male using an ANOVA. There was a significant difference in δD between age classes ($p= 0.04$) with juveniles δD signature averaging 19.25 ‰ higher than adults, while there were no significant differences in sex ($p= 0.91$). Also, we compared results of δD_H to grid maps of δD_P and geographic assignment of individuals were made with the IsoMAP cyber-GIS system. This study is crucial in determining whether these bats are extending their range northward or not migrating back south.

297^E: Evaluating allometric variation in sea otter (*Enhydra lutris*) bacula

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The baculum, or os penis, is found in several mammalian taxa and can serve as a valuable diagnostic tool, aiding in taxonomic identification (e.g., order Chiroptera) and assessment of age or developmental stage (e.g., *Procyon* species). The National Museum of Natural History houses the G. S. Morgan Comparative Baculum Collection, which provides an opportunity to assess morphological variation within taxa. We used this collection to investigate the relationship between baculum size (length by mid-shaft width) and skull size in sea otters (*Enhydra lutris*). We measured 168 bacula collected from the Alaskan Aleutian Islands between 1948 and 1962. We expected bacula measurements to be normally distributed, reflecting a representatively collected sample set. However, both length and width datasets displayed a bimodal distribution and failed the Shapiro-Wilk normality test ($p=2.71 \times 10^{-13}$ and 1.165×10^{-12} , respectively). We found a strong positive correlation between length and width (Spearman correlation=0.93, $p=2.2 \times 10^{-16}$); both results suggest bacula size is related to growth. Among bacula with associated crania, we collected eight measurements from 60 specimens. Among these measurements, six displayed a strong positive correlation (defined here as Spearman correlation ≥ 0.8) with baculum length and six a strong positive correlation with baculum width. Therefore, our sample falls into two distinct size groups, with bacula and skull size positively correlated. These findings shed light on the allometric relationships between bacula and cranial size in sea otters.

298^E: Gut microbial variation of howler monkeys (*Alouatta palliata*) on a small island in Panamá

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Animals are hosts to a wide array of microorganisms that influence overall fitness. Using wild primates to investigate these relationships potentially offers improved noninvasive methods for monitoring threatened species. This research is an exploration into the diversity of gut microbes present in howler monkeys in Barro Colorado Island, Panamá and how that diversity is affected by anthropogenic pressures. During June 2017, we followed randomly chosen groups of howler monkeys each day for six days a week. We collected fecal samples ($n = 88$), determined the sex and age class of the individuals, and estimated group size. We then extracted RNA and performed high throughput sequencing of the 16S rRNA gene. As expected, Bacteroidetes and Firmicutes were the predominant phyla of bacteria present in the samples. Group identity was the only demographic factor that explained some of the observed variation (~20%) in microbial communities ($F_{9, 36} = 2.01$, $p < 0.001$). This could possibly be a result of variation in territory, perhaps due differences in habitat quality or other environmental pressures. Statistical analyses are underway to elucidate other factors, such as parasite load and environmental pollutants, that may better describe the observed variation within this data. Understanding how specific communities of gut microbes are associated with environmental exposures and specific health outcomes will potentially provide novel methods for monitoring and identifying at-risk wildlife populations.

299^E: Variation in collared peccary (*Pecari tajacu*) vigilance and group size across La Selva, Costa Rica

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Neotropical rainforests are among the most biologically diverse ecosystems in the world. However, the decline of apex predators has led to the apparent population expansion of collared peccaries (*Pecari tajacu*) in La Selva, Costa Rica, which may pose a threat to various taxa. Peccaries are habituated to human activity at the research station and we examined if their activities were reflective of the human-shield, in which prey use human areas to avoid predation. If peccaries use humans as a predator shield, we hypothesized that peccary vigilance would increase as the distance from the station's lab clearing increases and human foot traffic declines. We deployed camera traps across 70 sites along a gradient away from the lab clearing and detected peccaries at 48 (68%) of the sites. We scored the vigilance behavior of individual

collared peccaries and counted the group sizes in all photos and videos and used generalized linear models and model selection to examine the factors associated with each response. The top-supported models suggested that forest age affects peccary behavior more than human factors, with peccaries exhibiting higher vigilance and smaller group sizes in mature forest. Although we found limited support for the human-shield hypothesis, our results suggest that peccary vigilance and grouping behavior likely are affected by predation pressure in mature forest where cover is more limited than in dense secondary growth.

300^E: Mammal activity patterns along an urban to wild gradient

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Urbanization is rapidly growing across the eastern United States. Recent studies have suggested that many mammal species adapt to urbanization by shifting their diel activity patterns. These temporal changes could therefore affect species interactions with potential ecosystem-level impacts. We used camera traps to monitor mammal populations along an urban to wild gradient from the Washington D.C. metro to the Shenandoah National Park along the Blue Ridge region of Virginia. We examined data from six common mammals to estimate the diel activity patterns and the degree of overlap across the gradient both within and between species. Our results suggest that general activity patterns correspond with the natural history (e.g., nocturnal, crepuscular, or diurnal) of each species, with peaks in activity matching across the gradient of development. However, in the highly urban environments, we observed differences in dispersion of these activity peaks. For example, white-tailed deer (*Odocoileus virginianus*) are crepuscular, but exhibit more cathemeral behavior with heightened activity throughout the day and night in the urban sites. We suggest that these differences may be a consequence of hunting pressure in rural areas, whereas deer are habituated to humans in Washington D.C. where hunting is absent. Similar patterns prevail for other species that we examined, suggesting that habituation to humans in the urban environment may make some species bolder to anthropogenic activity and thereby shift their temporal cycle.

301^E: Collaborations with citizen science to update species distributions: case study with *Ursus americanus* in Texas

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Given the decline in collection efforts worldwide, data from citizen science initiatives and natural history collections will be instrumental in better understanding species distributions, ecology, and evolution. As a test case, we used data from Texas Parks and Wildlife Department records, iNaturalist, and VertNet to better understand the distribution of the American black bear (*Ursus americanus*) in Texas. Our results indicate that black bears may not have a wide presence in many areas of Texas and likely are only breeding in a small number of counties. Importantly, our study highlights the usefulness of successful citizen science programs and the long-term historical importance of museum records to better understand not only geographic distributions, but also the ecology and evolution of various species, including the American black bear. These initiatives paired with improved communication and collaboration between natural history museums, citizen scientists, and state and federal agencies can greatly increase knowledge for a variety of species, facilitating future research in untold ways.

302^E: Niche-based distribution modeling of the grey wolf (*Canis lupus*) in North America: a subspecies approach

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The gray wolf, *Canis lupus*, formerly had a circumboreal distribution; however, persecution drove its populations almost to extinction. In North America, several studies have aimed to delineate distributions of gray wolf subspecies, yet most of the limits are controversial. This study aimed to compare the different

proposed subspecies distributions and to explore the climatic structure of *Canis lupus* to improve our understanding on the distribution of the diverse forms of wolves in North America from a climatic perspective. We compared the distributions of recognized gray wolf subspecies using niche-based distribution modeling and a cluster analysis to propose a configuration of subspecies based on climatic profiles. We found that no climatic arrangement matched the proposed subspecies distribution limits, noticing that in most of them, there was a high degree of overlap that does not allow a clear differentiation. From our cluster analysis, we found that the optimal number of climatic groups was four, designated as: Mexican, Central, Northern, and Coastal groups, and their distributions are different from previous subspecies delimitations, with transitional boundaries located at their geographical limits. Subspecies designations have conservation implications for reintroduction, translocations and conservation projects with sociopolitical implications. New approaches to identify distinct subunits should include all evidence available, including genetic, morphological and now ecological.

303^E: Comments about *Anoura fistulata* (Phyllostomidae: Glossophaginae) from Peru and remarks in Bolivian specimen

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Recent published records of *Anoura fistulata* extended its geographic distribution from Colombia to Bolivia. However, the recognition of *A. fistulata* from Bolivia has been questioned based on the absence of the glossal tube (GT) and because a morphometric analysis showed more similarity with *A. caudifer* than with *A. fistulata*. In this work, we evaluated the state of GT in preserved specimens of *A. fistulata* from Peru, incorporate craniodental features, and an update of the distribution range of *A. fistulata*. Specimens (n=15) from Peru were suitable to evaluate the GT. The GT was evident only in specimens preserved in fluid. In specimens with skull removed or just carcasses, we noticed that the suture between the sternohyoid muscle and the base of the tongue is located more anterior than the level of the heart. A greater mandibular symphysis, and an almost straight lateral sides of the rostrum were consistent features in all samples including the Bolivian specimen. The PCA of *A. fistulata* from Colombia to Bolivia showed a greater similarity among Bolivian, Peruvian and some Ecuadorian specimens. Including *A. caudifer* in the PCA, the Bolivian specimen grouped more with *A. fistulata* than *A. caudifer*. The absence of GT in Bolivian specimens was probably because of the type of preparation. Based on craniodental and morphometric analysis, we identify the Bolivian specimens as *A. fistulata*.

304: Challenging ecogeographical rules: changes in size and shape along tropical elevational gradients and through time

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Endotherms count on several mechanisms to live under cold conditions: an increase in the basal metabolic rate, insulation improvement, and a decrease in the surface area/volume ratio. Two main ecogeographical generalizations related to this last mechanism are Bergmann's and Allen's rules. Bergmann (1847) proposed a negative association between body size and temperature for endothermic species, while Allen (1877) predicted a positive correlation between appendage relative length and temperature. Despite the simplicity of these rules, there is still ongoing discussion after almost two centuries, with numerous studies and reviews. However, most of the studies which test these rules have been performed in areas with a marked seasonality. Despite seasonality being known to affect the evolution of body size, just a handful of studies have tested these rules in non-seasonal elevational gradients. A likely explanation for this is that species in the tropics tend to have narrow elevation ranges. Mountain treeshrews (*Tupaia montana*) provide a scarce and unique opportunity to test Bergmann's and Allen's rules along wide tropical elevational gradients. Furthermore, the availability of extensive series of both historic and modern specimens, has facilitated the study of body size and body shape variation through space and time. Preliminary findings suggest no support for Bergmann's and Allen's rules and point towards other selective pressures rather than temperature shaping the spatial morphological variation.

305^{E}: Managing the demands of viral immunity and reproduction in Madagascar fruit bats**

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In order to survive and reproduce, individuals must allocate energy strategically among competing physiological demands. Reproduction often is found to require a shift in resource allocation away from self-maintenance in favor of reproductive tissues and offspring. Bats are a particularly interesting model for examining potential reproductive/immune trade-offs because of their inherently high metabolic rate and known role as reservoirs for notable virulent zoonotic diseases. Little, however, is known about the mechanisms controlling both reproductive physiology and viral seroprevalence. Female fruit bats (*Rousettus madagascariensis*) exhibit seasonal shifts in positive viral seroprevalence overlapping with reproductive activity while males do not show this pattern. Our aim was to assess immunocompetence and circulating metabolic hormone concentrations in wild-caught male and female *R. madagascariensis* to pair with serostatus and viral shedding data. Bats were captured by mist net over 4 weeks within Maromizaha Reserve (Madagascar), blood sampled, and swelling response to phytohemagglutinin (PHA) measured over 24 hours. Preliminary findings suggest reproductive female bats maintain greater immune capacity than non-reproductive females and males. Interestingly, we found a potential interaction between offspring sex and immune response within lactating females. These results provide a foundation for asking molecular questions surrounding mechanisms that may mediate changes in female bat physiology during reproduction and emphasize the need to consider species life history when analyzing annual immunological patterns that shape our predictions surrounding zoonotic disease. This research was supported by an ASM GIAR awarded to Mattina M. Alonge in 2018.

306^E: Preliminary assessment: spatial ecology of the plains spotted skunk (*Spilogale putorius interrupta*) in southeastern Texas

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Habitat loss and alteration are major causes of decline at both the species and population level. The plains subspecies of the eastern spotted skunk (*Spilogale putorius interrupta*) has experienced population decline, at least partially due to habitat loss and alteration, both range-wide and throughout Texas. The West Gulf Coastal Plains ecoregion is adjacent to the Gulf of Mexico and stretches from western Louisiana to south Texas. This ecoregion was historically prairie habitat but has experienced extensive alteration via conversion to crop and rangelands, urbanization, fire suppression, and invasive species proliferation. In January 2019, we initiated research into the spatial ecology of the plains spotted skunk on the Katy Prairie, an undeveloped albeit altered Gulf Coast prairie in Harris and Waller Counties, Texas. Spotted skunks were captured, fitted with GPS tracking collars, and located weekly. Representative habitat characteristics (ground cover, visual cover, litter depth, canopy cover, stem density, and Macartney rose (*Rosa bracteata*) density) were recorded at randomized locations identified by the GPS collars. Home range size was calculated using minimum convex polygons for each skunk. We provide a preliminary assessment on home range size and habitat utilization of the plains spotted skunk. While preliminary, our analysis indicates this population's habitat utilization differs from previously reported populations in Arkansas.

307: Immense, dense, and intense: challenges to monitoring mammal populations across large areas with citizen scientists

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Citizen science has the potential to increase the spatial and temporal resolution of biodiversity monitoring data, but these schemes can be of questionable scientific value if they don't have built-in checks for quality

control and clear measures of sampling effort. Camera traps offer a potential solution to this trade-off for citizen science mammal surveys, as species ID can be verified through photographs, and effort can be explicitly recorded as the time the camera is in place. However, running camera traps with a standard protocol and uploading and identifying pictures requires more time investment than typical citizen science protocols, raising questions as to its scalability. Here we describe our work using citizen science camera trapping for a survey that is both large-scale (across the entire state of North Carolina) and intense (sampling all 100 counties of the state). This project, North Carolina's Candid Critters, has been successful as a tool for collecting data in an immense and intense protocol while also engaging the public with mammal conservation. We think that future work to decrease the intensity of their involvement through improved data management with AI species identification and improved feedback with automated analytics would help reduce the dropout rate of interested participants and help further scale up the potential for citizen science mammal surveys.

308^{E,HTA}: Microhabitat adaptation in generalist species: the case of *Praomys rostratus* in a cacao dominated landscape

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Throughout the planet, tropical forest systems are being converted for cash crop production. Deforestation in West Africa, primarily Côte d'Ivoire, is driven by cocoa production, in total producing 40% of the world's chocolate. Generalist species adapt well to human created microhabitats. Understanding how species adapt to microhabitats can give us insight into ecological limits and evolutionary projections of species. This project used geometric morphometrics (GMM) to study ontogenetic and intraspecific variation of *Praomys rostratus*, a West African generalist rodent. GMM was used to quantify the crania and mandible shape of *P. rostratus*. We implemented a multivariate framework to explore the morphometric variation of this generalist species in five different microhabitats: cocoa, fallow, rubber, primary forest, and secondary forest. We used TPSDig to quantify homologous landmarks on 118 specimens. We then implemented canonical variates analysis (CVA) and multivariate analysis of variance (MANOVA) to test significance in cranial shape among microhabitats. Our results did not show evidence of sexual dimorphism. However, we were able to quantify the three major components of ontogenetic variation: development, growth, and allometry, for each microhabitat. Understanding morphometric variation in *P. rostratus* in Côte d'Ivoire will allow us to better understand the effects of habitat loss on species variation in biodiversity hotspots. These results are applicable to biodiversity conservation as deforestation of habitat continues in tropical forests around the world.

309: Meso- and large mammals of non-protected areas in the Planas River Basin floodplains, Colombia

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Understanding the richness, abundance, geographic distribution and conservation status of species is vital to promote effective wildlife protection strategies, especially in unprotected areas. We describe the diversity of meso- and large mammals from the unprotected Planas River in Colombia's Orinoco River basin over three years. We systematically used camera traps at 72 stations and hiked along forest and savanna transects to determine meso- and large mammal diversity. Relative abundance was documented for 30 native and 2 feral mammals from a sampling effort of 1789 camera-days and walking 469.5 km. Thirty-two species of mammals were recorded representing 19 families and 9 orders. We recorded threatened species, including Giant Armadillo (*Priodontes maximus*), Tapir (*Tapirus terrestris*), White-lipped Peccary (*Tayassu pecari*) and Giant Anteater (*Myrmecophaga tridactyla*). The most frequent species through the relative abundance index (RAI) were *Pecari tajacu*, *Didelphis marsupialis*, *Cuniculus paca* and *Dasyopus pastasae*. The documented species face diverse pressures, including hydrocarbon extraction, extensive crop development, competition with invasive species and livestock, among other threats. Our results suggest that these non-protected areas are important for conserving mammals in the eastern plains of Colombia.

310^F: Drought and temperature influence spatial and temporal variation in growth of North American bison

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We tested the hypothesis that bison (*Bison bison*) body mass (BM; kg) declines with rising temperature over temporal and spatial scales along the Great Plains (GP). Spatially, we used photogrammetry to measure body height (H; m) of 773 bison (579 female; 194 male) to estimate BM from Gompertz equations in 19 herds from Saskatchewan (52.2°N) to Texas (30.7°N), including Wind Cave National Park (WICA; 43.6°N), South Dakota. Temporally, we modeled the relationship of annual measures of BM and H of 5781 bison (3698 female; 2075 male) at WICA from 1966 to 2015. We used Gompertz equations to estimate asymptotic BM (ABM) against age (y). We used mean decadal temperature, precipitation, and Palmer Drought Severity Index to model the effects of climate on ABM. Drought decreased ABM temporally at WICA (-46 ± 17 kg) and spatially along the GP (-17 ± 2 kg). Temperature decreased ABM temporally (-75 ± 23 kg) but did not affect ABM spatially. Precipitation weakly decreased ABM both temporally (-1.1 ± 0.6 kg) and spatially (-0.02 ± 0.01 kg). Our data suggest that interactions between water and temperature in drought drive growth of bison. Bison body size is likely to decline over the next five decades throughout the GP due to projected increases in summer temperatures and both the frequency and intensity of droughts.

311: Demography of snowshoe hare population cycles

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The spectacular ten-year cycles exhibited by snowshoe hare (*Lepus americanus* Erxleben) populations across the boreal forests of North America have fascinated generations of ecologists. Using mark-recapture data spanning 5 population cycles (1977-2017), we examined demographic mechanisms underlying snowshoe hare population cycles in southwestern Yukon, Canada. Snowshoe hare populations always decreased during winter and increased during summer; the balance between winter declines and summer increases characterized the four, multiyear cyclic phases: increase, peak, decline, and low. There was little or no recruitment during winter, but summer recruitment varied markedly across these phases with the highest and lowest recruitment observed during the increase and decline phase, respectively. Population crashes during the decline were triggered by a substantial decline in winter survival and by a lack of subsequent summer recruitment. In contrast, population growth during the increase were triggered primarily by a sharp increase in summer recruitment and winter survival. Though demographic processes underlying hare population dynamics were generally consistent across the 5 cycles, there were also some differences among them in the net annual growth rate, that appeared to drive the substantial variation in peak densities.

312^F: Climate-mediated rewiring of small mammal trophic networks in response to defaunation on a Kenyan savanna

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An important consequence of defaunation is the disruption of ecological networks, which can be rewired via changes in the composition of species and the interactions between them. Defaunation has direct, well-studied impacts on savanna vegetation structure and function. However, the indirect effects of species losses are more difficult to detect, and failure to measure them can lead us to underestimate the full impacts on ecosystems. Here, we use a replicated defaunation experiment across a 20km rainfall gradient to understand how small mammals (<1kg) respond to defaunation-induced increases in vegetation abundance and diversity on Kenyan savannas. We hypothesized that small mammal dietary diversity and overlap would increase, and interactions with climate would determine the extent of this competitive release. We collected fecal samples from 788 small mammals over the course of one year and used DNA metabarcoding to determine diet composition for each individual, generating diet profiles with high taxonomic resolution for

192 plant taxa. We paired these data with an 11-year mark-recapture census to quantify changes in network structure. Our results show that, although individual species increase dietary diversity and overlap in response to defaunation, these changes do not scale to the network level. Moreover, dietary network structure is more strongly impacted by climatic factors such as rainfall than by biotic factors such as vegetation.

313: Seed masting causes fluctuations in optimum litter size and lag load in red squirrels

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The episodic production of large seed crops by some perennial plants (masting) is known to increase seed escape by alternately starving and swamping seed predators. We tested whether these pulses of resources also act as an agent of selection on the life histories of North American red squirrels (*Tamiasciurus hudsonicus*), which could indirectly enhance seed escape by inducing an evolutionary load on red squirrel populations. Across 28 years and five white spruce (*Picea glauca*) masting events, observed litter sizes were similar to optimum litter sizes during non-mast years but were well below optimum litter sizes during mast years. Mast events, therefore, caused selection for larger litters and resulted in a lag load on red squirrels during mast years. Reduced juvenile recruitment associated with this lag load increased the number of spruce cones escaping squirrel predation. Squirrels plastically increased litter sizes in anticipation of mast events, which partially, although not completely, reduced the lag load resulting from this change in food availability. These results, therefore, suggest that in addition to ecological and behavioural effects on seed predators, mast seed production can further enhance seed escape by inducing maladaptation in seed predators through fluctuations in optimal trait values.

314: Retrospective population analyses for marine mammal conservation

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Population projection models have been used extensively to project future mammal abundance for conservation assessment. A less common application of population models is to reconstruct abundances from the past. Integrated population models (IPMs) can be used to improve estimates of past abundances, generally using abundance data from each year. Here we use the example of a model for Florida manatees (*Trichechus manatus latirostris*) to illustrate benefits and limitations of retrospective approaches using sparse abundance data. We developed an IPM that allowed us to estimate historical trends in abundance of the manatee population and effects of environmental stressors on it. The model uses 19 years of survival and reproductive estimates, abundance estimates from two years, and carcass recovery counts. Our analyses show that reasonably precise estimates of abundance could be derived from this model; coefficient of variation was always under 0.09. This result has implications for determining the frequency of costly abundance surveys. The population was estimated to be growing or stable in most years, but a red tide event in 2013 was estimated to drive the population down by about 300 animals. Retrospective analyses can be useful: (1) to infer historical trends in abundance, improving our understanding of population dynamics and therefore our ability to forecast; (2) to understand the impacts of stressors on populations; and (3) to assess the conservation status of wild populations.

315: Demographic drivers of a refugee species: large-scale experiments guide strategies for reintroductions of hirola**

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Effective reintroduction strategies require accurate estimates of vital rates and the factors that influence them. The hirola (*Beatragus hunteri*) is the rarest antelope on Earth, with a global population size of <500 individuals restricted to the Kenya–Somali border. We estimated vital rates of hirola populations exposed to varying levels of predation and rangeland quality from 2012 to 2015, and then built population matrices

to estimate the finite rate of population change (λ) and demographic sensitivities. Mean survival for all age classes and population growth was highest in the low-predation–high-rangeland-quality setting ($\lambda = 1.08 \pm 0.03$ [mean \pm SE]), and lowest in the high-predation–low-rangeland-quality setting ($\lambda = 0.70 \pm 0.22$). Retrospective demographic analyses revealed that increased fecundity (the number of female calves born to adult females annually) and female calf survival were responsible for higher population growth where large carnivores were absent. In contrast, variation in adult female survival was the primary contributor to differences in population growth attributable to rangeland quality. Our analyses suggest that hirola demography is driven by a combination of top-down (predation) and bottom-up (rangeland quality) forces, with populations in the contemporary geographic range impacted both by declining rangeland quality and predation. To enhance the chances of successful reintroductions, conservationists can consider rangeland restoration to boost both the survival and fecundity of adult females within the hirola's historical range. This research was supported by a Hornaday Conservation Award awarded to Abdullahi H. Ali in 2013

316^{E}: Little brown bat population dynamics in relation to white-nose syndrome**

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Hibernating bat populations throughout eastern North America have declined drastically since the emergence of the fungal disease white-nose syndrome (WNS). Little brown bats (*Myotis lucifugus*) are one of the hardest hit species, losing over 90% of the population in the Northeast. Whereas some colonies show recent signs of stabilization and growth, the impacts of WNS on demographic rates, such as reproduction, survival, and recruitment remain unclear. Using a mark-recapture design, we seek to determine the current and future status of the little brown bat population. In the summers of 2016 – 2018, nearly 2,000 bats were captured at seven maternity colonies in New Hampshire, Vermont, and Massachusetts. All bats were banded and a subset were also PIT-tagged. Reproductive condition was assessed for adults while epiphyseal gap length was measured for juveniles to estimate the timing of birth. Approximately 20% of captured bats were banded and over 80% of bats PIT-tagged in 2017 were detected in 2018. Our data show that adult females are reproducing over multiple years. In addition, bats banded as juveniles are surviving and returning to their natal colonies. Comparisons to pre-WNS data from New Hampshire suggest possible shifts in life-history strategies. The results of this study will ultimately be used to develop conservation strategies that promote the recovery of little brown bats in the region. This research was supported by a Grant-In-Aid awarded to Katherine Ineson in 2016.

317: Untangling competing restoration needs of mammals and other taxa in a space-limited estuary

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Tidal marsh habitat in the San Francisco Estuary has been reduced by over 90%, and is now largely surrounded by urban development, with little opportunity for expansion. Remaining wetlands are further threatened by impending sea-level rise, as many have no upland margin for migration. Habitat requirements of endangered mammals, birds, and fish in the estuary have largely been framed in competing terms, with limited consideration of how restoration for one taxa could benefit others. These dynamics were influenced by mandated acreage requirements from various recovery and management plans, and resulted in a mindset of focusing on acreage goals for specified species, not ecosystem function. However, recent research in the estuary coupled with the increasing realization that sea-level rise will be more severe than previously expected has forced managers to consider creative restoration solutions. I will present emerging research influencing innovative approaches to restoration, including sea-level rise models, studies of ecosystem functions, and species-specific data, with an emphasis on a long-term study of the endemic salt marsh harvest mouse. While it was historically managed as a specialist, recent research reveals that the salt marsh harvest mouse is very adaptable, and not strictly dependent on tidal marshes. These findings have opened the door to the possibility of win-win, creative habitat restoration and enhancement options, but can we overcome the momentum pushing us to maintain the norm?

318: Small mammal species richness is predicted by mountain peak elevation in Mindanao, Philippines

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Species richness of small mammals usually increases with increasing elevation in mountainous regions. We recently proposed, based on studies on Luzon Island, Philippines, a related pattern that we predict to be equally common: higher mountains in any given region will have more species than lower mountains, i.e., there is a correlation between species richness and peak elevation. For 8 isolated mountain ranges on Mindanao, we found a positive correlation ($r = 0.875$, $P < 0.01$) between species richness of native small mammals and peak elevation, supporting our prediction. Further, we found that the regression line from the Luzon sample ($n = 12$, $r = 0.906$, $P < 0.01$) predicted the exact number of species in three cases, was about one species less on Mindanao than predicted in two cases, and lower by about 3 or 4 species in two cases; in only one case was the observed number of species higher than predicted from the Luzon regression. Although Mindanao is similar to Luzon in area, climate, topographic diversity, and geological age, the two islands differ dramatically in the mammals that are present at the species and higher phylogenetic levels. We conclude that the correlation between species richness and peak elevation is remarkably consistent in two faunally highly distinct parts of the Philippines, and should be investigated as a potentially widespread and important pattern globally.

319: Geographic variation in diets of Eurasian pine martens and sables

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For many species, diets vary across their geographic ranges because of differences in climate and local conditions. Comparing dietary responses of closely related species to variation in climate and prey availability should highlight shared and divergent behavioral adaptations. We compared patterns of geographic variation in diets of Eurasian pine martens (*Martes martes*) and sables (*M. zibellina*). We hypothesized that pine martens and sables exhibit similar patterns of diet variation across latitudes and different climates due to shared physiological and behavioral adaptations. Winter diets of pine martens and sables are well described by 3 diet categories: small mammals, medium-sized mammals, and plants. Both sables' and pine martens' diets are dominated by small mammals, but sables eat fewer small mammals at mid-latitudes (50-60°N), while pine martens eat more small mammals at mid-latitudes. Sables eat plant materials most at mid-latitudes, where they eat the fewest small mammals. Pine martens eat more plant material at low latitudes (35-45°N), where they eat the fewest small mammals. Despite these differences, mean prey size correlates positively with winter severity for both species. Our results suggest that both species exhibit similar foraging strategies in response to winter conditions. Differences in geographic patterns of diet may be caused by differences in food availability across the ranges of these species or by local differences in availability during the specific years of study.

320: Morphological variation in *Peromyscus maniculatus* and Allen's rule

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Allen's rule states that, "among endothermic species, limbs and other extremities are shorter in and more compact in individuals living in colder climates ... " (Lomolino, et al., 2006 :27-28). *Peromyscus maniculatus* (Rodentia) occupy most of North America and should easily illustrate this rule. Tail length in the most northerly subspecies (*P. m. borealis*) positively, and significantly, correlate with the average low January temperature, but this is not necessarily so in other subspecies. Other extremities (feet, ears, skull) in *Peromyscus maniculatus* also do not necessarily correlate with climatic variables.

321^{HTA}: Drivers of Central American mammal biodiversity

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As part of the Mesoamerican biodiversity hotspot, Central America contains an abundance of species within its relatively small land area. Complex topography from ever-shifting geology, a series of species exchanges between North and South America, and Plio-Pleistocene glacial climate cycles have all played a part in creating a rich, unique biotic community. However, as the effects of anthropogenic impacts encroach, it is imperative to understand how biodiversity is structured in this region and what processes drive this structure. We calculated four biodiversity indices for Central American mammals, taking into account shared evolutionary history and range size. We then modeled each biodiversity index to 14 variables representing climate, topography, biogeographic history, and land cover using boosted regression trees. Our results show hotspots of index values in high elevation areas and the lowlands of Panama. Variable importance from our models identified low values of temperature seasonality and higher elevation as important for fostering biodiversity for all mammals. Although biodiversity hotspots remained mostly congruent across multiple mammalian orders, variable importance showed more fluctuation. We encourage researchers to explore biodiversity data from multiple perspectives, as our results shifted dramatically based on taxonomic inclusion. In Central America specifically, the identification of past refugia appears integral for future conservation efforts, as climate stability is an important predictor of high biodiversity areas.

322^{E,HTA}: Does the Forage Maturation Hypothesis predict seasonal movements of wild equids?

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The Forage Maturation Hypothesis (FMH) predicts that ungulates should optimize their energy intake by selecting high-quality forage of intermediate biomass. Although the FMH was developed to explain aggregation and seasonal movements of ungulates in general, it has been tested primarily on ruminants from temperate regions. Therefore, it remains unclear whether and how the FMH applies more broadly to non-ruminant ungulates. Because of differences in their digestive physiology, we expected that wild equids would prioritize (1) forage biomass over forage quality to meet their nutritional needs; and (2) free water to compensate for their physiological limitations. We used a step selection framework to test for the effect of forage biomass, forage quality, free water, and human activity on movements and resource selection of seven populations of wild equids distributed globally. Results for the seven populations of equids were compared with sympatric ruminant populations. Unlike ruminants, no population of equids selected areas with high-quality forage. Instead, forage biomass and distance to free water were the primary drivers of movements in equid populations. Although the FMH provides a useful framework for understanding the distribution of herbivores, our work indicates that predictions of the FMH should be updated to include alternative predictions specific to the digestive physiology of particular clades.

323^{E,HTA}: Niche dynamics of the felid guild following the Pleistocene megafaunal extinction

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During the Pleistocene, megafelids such as the saber-toothed cats *Smilodon* and *Homotherium* dominated North American ecosystems, potentially suppressing smaller-bodied felids such as the cougar (*Puma concolor*) and bobcat (*Lynx rufus*). The terminal Pleistocene megafaunal extinction (~ 13,000 years bp) resulted in the loss of these more massive hypercarnivores, potentially resulting in vacant habitat/niche space. Here, we evaluated whether cougars and bobcats began to occupy this unfilled niche-space following the megafelid extinctions. We employed an ecological niche modeling (ENM) approach that utilized fossil felid occurrences from the *Neotoma*Database and paleo-climatic reconstructions from the *PaleoClim*Database. We produced ENMs of felids in environmental space for multiple time periods pre- and post-megafaunal extinction, testing for cougar/bobcat niche expansion into previously occupied megafelid niches. Results suggest that cougar/bobcat niches expanded somewhat post-megafaunal extinction, but this was primarily attributed to warming climates. Contrary to our expectations, we found that neither cougars nor bobcats appeared to fill in vacant megafelid niche space post-extinction. Unexpectedly, our analyses revealed that the disappearance of acutely cold non-analog habitats from the Pleistocene likely contributed to the extinction of *Homotherium*, but not any other megafelid. Our findings suggest that

the niches of modern felids were not significantly constrained by interactions with larger megafelids during the Pleistocene. Furthermore, specific warmer/colder habitat availability appears to have most strongly influenced felid niche occupancy during the late Quaternary.

324:** The disparate evolutionary histories of Great Basin ground squirrels (*Urocitellus*)

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The Great Basin is a massive, internally drained region of western North America that represents a natural laboratory for understanding community assembly and diversification in mammals. Substantial research has focused on these processes among mountain ranges of the Great Basin ('sky islands'), but the evolutionary histories of lowland, arid-adapted Great Basin mammals have often been cryptic and harder to resolve. We used a combination of phylogenomics and paleodistribution modeling to resolve the diversification histories of *Urocitellus* ground squirrels endemic to the broader Great Basin. Using a taxonomically-comprehensive ddRADseq dataset (>7,700 loci), we resolved phylogeny of six species-level lineages of *Urocitellus* and delineated the distribution of genomic diversity across the Great Basin. To investigate species-specific responses to past environmental change, we modeled past habitat suitabilities at high temporal resolution (six time slices since the Last Glacial Maximum) and measured correlations between genetic distances and habitat suitabilities, while also accounting for modern landscape connectivity. We found positive correlations between genetic distinctiveness and paleohabitat suitability in some species, consistent with expectations if species tracked their climate niche through time. Conversely, this relationship was absent in narrowly-distributed species, suggesting long-term isolation in northern portions of the Great Basin during major late Quaternary environmental changes. Our results resolve species diversity and relationships in *Urocitellus* and reveal the idiosyncratic geographic and genomic histories of these Great Basin endemic mammals. This research was supported by an ASM Fellowship awarded to Bryan McLean in 2016.

325^E: Reconstructing an unexpected carnivore recolonization: American martens on the Apostle Islands of Lake Superior

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Sudden and extreme changes to landscapes, largely through human activity, have resulted in the fragmentation and isolation for a number of mammal species globally. Such changes are particularly consequential for forest carnivores, which are typified by specific habitat requirements. Thus, identifying suitable habitats, potential climatic and habitat refugia, and predicting species viability needs to be placed in historical and future context for effective conservation and management. American martens (*Martes americana*) were extirpated from most of the Great Lakes region in the 1920s due to unregulated trapping and extensive habitat loss from logging. Regional reintroduction efforts began in the 1950s and continued into the 2000s. However, martens remain a state endangered mammal in Wisconsin and have declined in Michigan. Unexpectedly, martens were observed on the Apostle Islands, WI in 2010 after a nearly 50-year absence. We used genetic and demographic analysis to determine the source and colonization history of martens on the Apostle Islands and identified fine-scale structure within the archipelago. The Apostle Islands are genetically distinct within the Great Lakes region and measures of genetic differentiation are lowest between the Apostle Islands and Michigan martens. In addition, we found fine-scale structuring across the Apostle Islands largely by island and identified inter-island migrants. The recolonization of the Apostle Islands provides a unique refuge for a sensitive species at their southern range boundary.

326: Identifying convergent evolution in New World rodents

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Adaptive radiation is thought to be a major driver behind the remarkable diversity of New World rodents. Independent adaptations to similar conditions can lead to phenotypic convergence among ecological analogues, producing forms that are more similar than expected given their phylogenetic relatedness. Here, we characterized morphology and ecology for 101 species of Neotropical rodents. We collected 16 measurements from skulls, mandibles, and study skins, while gathering data on diet, locomotion, and the evolutionary relationships between species. To quantify convergence, we applied a distance-based approach (C_1 index) that can tell us if two or more taxa evolved to be more similar than their ancestors were to one another. Rather than assigning ecomorphs qualitatively, we identified groups by applying unsupervised clustering to the morphological and ecological data, reduced in dimensionality with a nonlinear method (UMAP). We found that ecological analogues generally evolved to resemble each other more than expected under a null model of Brownian Motion evolution. Our approach supports existing hypotheses of how similar features evolved in response to similar adaptive regimes, in a diverse group with both relatively unspecialized and highly convergent forms. Financial support: FONDECYT 3170246.

327: Phylogenomics and intraspecific variation in the sifakas (Genus *Propithecus*)

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Madagascar contains unrivaled primate diversity (Infraorder Lemuriformes), most of which are threatened with extinction. One group of lemurs include the sifakas, a diurnal genus of nine nominal species, which are widely distributed in Madagascar. Previous research has split the original two species into nine based on pelage and morphology, however published molecular studies have sequenced limited samples at few mitochondrial genes to reconstruct the evolutionary relationships of these animals. Additionally, procuring adequate samples of each species for intraspecific investigations is logistically difficult and all previously published studies have limited sampling, with some studies lacking representation of one or more species. Here we sequence all nine species of sifakas (>200 individuals), from as many locations as possible across thousands of nuclear markers (UltraConserved Elements), for the most comprehensive phylogeny to evaluate the evolutionary history of sifakas. We found novel intraspecific variation within the diademed sifaka, and reconstructed the ecological niche of this species to identify patterns explaining the cryptic diversity. Preliminary results confirm introgression between the crowned and Decken's sifakas. These results demonstrate possible subspecies or ecotypes linked to different climate zones in the diademed sifaka, and ongoing hybridization in the crowned/Decken's sifakas, both results which may have impacts on the conservation of this genus.

328^F: Looking gift horses in the mouth: an examination of the Inhibitory Cascade in equid evolution

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The Inhibitory Cascade is a developmental model for the molar row of mammals that predicts that posterior molar size is controlled by the size of the molar directly anterior to it. Many modern mammal groups adhere to this pattern; notably, however, modern horses fall outside of expected proportions in molar sizes. Given that horses have an excellent fossil record, we have examined the evolution of relative molar sizes for fossil and modern horses using tooth measurement data compiled from the literature. This allows us to trace the position of horse species through time within the Inhibitory Cascade morphospace from the first appearance of horses ca. 56 million years ago in the Eocene epoch to extant equids. The dataset, consisting of linear molar measurements for 39 fossil horse species, has allowed us to recognize evolutionary trends throughout equid evolution. The earliest equids fall neatly within the morphospace predicted by the Inhibitory Cascade, but late Eocene to late Miocene horses are mostly outside the predicted morphospace and a distinct trend over time towards equant size of the three molars is evident. We hypothesize these patterns may relate to the origin of hypsodonty and the emergence of the grassland ecosystem in the late Oligocene to early Miocene.

329: Ecological and genetic interactions between species of woodrats: how environmental variation mediates species interactions

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Identifying the mechanisms that keep closely related species distinct is key to understanding how biodiversity is created and maintained. Contact zones, where similar species come into secondary contact, provide excellent opportunities to examine the range of ecological and genetic interactions that can change the evolutionary trajectories of the species involved. The selective pressures that contribute to these evolutionary shifts are, in part, determined by the environmental setting in which these zones of secondary contact occur. Here, we present data from our long-term investigations of a hybrid zone between *Neotoma fuscipes* and *N. macrotis* where their distributions meet in coastal California. We show how environmental and habitat variables contribute to the nature of species interactions in this contact zone and how these contribute to asymmetry in survival, and ultimately, movement of this hybrid zone. Specifically, we show that despite being the larger and more aggressive species, *N. fuscipes* shifts its habitat use more in the area of contact than does the smaller-bodied *N. macrotis*. Further, we show that *N. macrotis* has a significant survival advantage over *N. fuscipes* under certain climate conditions, which may be leading to the expansion of *N. macrotis* into the range of *N. fuscipes*. Our data suggest that climate conditions can influence competitive and fitness advantages that ultimately determine the ecological and evolutionary outcomes of species interactions at range limits.

330^E: Plasticity and evolutionary divergence in tail length between tropical and temperate house mice

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House mice (*Mus musculus domesticus*) have recently expanded their range across many extreme environments throughout the Americas. This rapid environmental adaptation has led to large morphological, behavioral, and physiological differences between populations. For example, mice from temperate regions are larger and build bigger nests than mice from tropical regions. Tail length also differs between tropical and temperate house mice, as mice from northern latitudes have shorter tails than mice from the equator, consistent with Allen's Rule. These differences persist in the lab, indicating that they have a genetic basis. However, it is unknown whether these tail length differences are due to the number of caudal vertebrae or the length of individual vertebrae. With the use of CT-scanning, we quantified skeletal differences in caudal vertebrae between Brazil mice (tropical) and New York mice (temperate). Furthermore, to understand the effects of temperature on tail length, we exposed Brazil mice and New York mice to a cold temperature during development. All mice, regardless of origin, grow shorter tails when reared in cold temperatures, with Brazil mice showing more plasticity in tail growth. Overall, this study sheds light on the evolutionary processes governing tail length differences in wild populations of house mice and highlight the role plasticity plays in adaptive evolution.

331: Molecular phylogenetics and species delimitation of the bat families Miniopteridae and Nycteridae

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The Old World bat families Miniopteridae and Nycteridae each comprise a single genus, *Miniopterus* and *Nycteris*, respectively. Both lack comprehensive phylogenetic analyses of their African members. Morphological conservatism and cryptic speciation have led to conflicting conclusions regarding their classification and synonymy, and continental African lineages of neither have been subjects of multilocus phylogenetic studies. We investigated genetic variation, phylogenetic relationships, and clade membership using gene tree, species tree, and species delimitation approaches. Analyses of both families focused on Afrotropical taxa, including Madagascar, Comoros Islands, and Sao Tome. We included mitochondrial

cytochrome-*b* (*cyt-b*) and nuclear intron (4-5 genes) data from 349 individuals for *Miniopterus* and 253 individuals for *Nycteris* representing a majority of currently recognized Afrotropical species from both families. Multiple deeply diverged Afrotropical lineages are recovered from both genera, and most of these lineages are supported as genetically isolated entities using species delimitation of nuclear loci. Mean genetic distances among species-ranked *Nycteris* clades (22% for *cyt-b* and 4% for concatenated introns) and strong statistical delimitation support suggest high levels of undescribed phylogenetic diversity. A similar pattern is apparent in *Miniopteridae*, with an additional pattern of long terminal taxon branches subtending short backbone internodes in phylogenetic analyses suggesting a rapid radiation model of diversification. Results presented here support Africa as a center of undescribed species diversity in both families. Biogeographic, conservation, and taxonomic implications are discussed.

332: Extinction susceptibility in Caribbean bats

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Caribbean islands are among the top biodiversity hotspots and have some of the highest levels of endemism in the world. This archipelago also sustained large losses of bats since the Last Glacial Maximum (~25–18ka), with ~18% of species extinct and up to 33% extirpated from one or more islands. Fossil chronologies coupled with time-scaled Ecological Niche Models (ENMs) rejected the classic climate change hypothesis and confirmed that bat losses did not result from the Pleistocene-Holocene transition (~11–9ka). Thus, bats survived for thousands of years into the Holocene only to become extirpated during a time with climatic conditions similar to today (~4–1.8ka). Here, I combined methods of community phylogenetics applied to all Caribbean bat species to show that these bat losses are phylogenetically and ecologically randomly dispersed. Then, I used a novel machine learning approach of artificial neural networks on this bat community to estimate which functional traits likely contribute to susceptibility of extirpation. Across all Caribbean bats, plant visiting and endemism were traits with the highest importance explaining extinction susceptibility. Understanding these losses using a community-wide approach provides insight into the factors linked to extirpation susceptibility that help us better understand the structuring of Caribbean bat communities and generate hypotheses of current potential threats.

333: Did paleoenvironmental change drive the loss of genetic diversity in colonial tuco-tucos?

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Identifying the factors that contribute to pronounced changes in genetic diversity is essential to understanding the evolutionary dynamics and conservation needs of natural populations of mammals. Colonial tuco-tucos (*Ctenomys sociabilis*) are subterranean rodents that are endemic to Neuquén Province, Argentina. Paleogenetic data indicate that although *C. sociabilis* underwent a significant loss of genetic diversity ~ 3,000-5,000 ybp, the partially sympatric Patagonian tuco-tuco (*C. haigi*) did not experience a similar reduction in variability. Using radiocarbon- dated stratigraphy, paleogenetic variability, and stable isotope signatures, we explored the effects of the following factors on genetic diversity in these species: volcanism, interspecific competition, and gradual changes in local Holocene environments. Comparisons of data from three cave deposits in the Limay Valley revealed that the timing and spatial distribution of genetic changes in our study species were not consistent with either the volcanic or competition hypotheses. Carbon isotope signatures from sub-fossil tooth samples revealed significant changes in Holocene food resources consumed by *C. haigi* but not *C. sociabilis*. We propose that general changes in environmental conditions in the Limay Valley in conjunction with the greater ecological specialization of *C. sociabilis* led to a significant reduction in availability of suitable habitat for this species but not for *C. haigi*, with associated demographic impacts contributing to the pronounced historical reduction in genetic variability in *C. sociabilis*.

334^{E,HTA}: Morphological consequences of captivity: a meta-analysis

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Captive morphological change has been a recurrent theme in scientific literature for at least a century. While the topic has been examined in isolated studies, the commonality across these studies has yet to be examined using a thorough, quantitative approach. By conducting a meta-analysis, this study examined the documented morphological impacts of captivity to address whether captive animals show predictably distinct morphology and whether the magnitude and direction of those changes was impacted by lifestyle covariates shared across species. Cranial measures, including those associated with zygomatic breadth, palate width, basal length, and overall skull length differed significantly between captive and wild individuals of several mammalian orders, although the magnitude of change was greater among carnivorous species. The direction of these trends varied, however, certain traits, such as palate width and skull length, tended to increase among captive carnivorans but frequently decreased among herbivorous species. These results may support the notion that carnivorans experience more extreme changes in captivity due to differences in dietary abrasion, where captive carnivoran diets are often softer than wild diets, whereas captive herbivore diets may overlap more closely with wild preferences. This may also suggest that captive morphology frequently changes on a predictable trajectory and that captive specimens should be avoided in morphological studies unless hypotheses are directly related to captivity.

335: Vertebral trabecular bone architecture in the hero shrew *Scutisorex*: evolution of an extraordinary morphology

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Extraordinary bony reinforcements have evolved in the lumbar spine of the hero shrew, genus *Scutisorex* (Soricidae), but the purpose of these reinforcements is unclear. There are currently two species in the genus, which have different degrees of external vertebral modification. Because their vertebrae are so unique, they are difficult to compare with other shrews in conventional homology-based morphological analyses. To circumvent this problem, we used X-ray micro-computed tomography to analyze the internal structure of the vertebrae in a phylogenetically and ecologically broad sample of shrews. Internal trabecular bone architecture (TBA) correlates to in-vivo bone loading, and is therefore informative about locomotion, and by inference, behavior and ecology. We used phylogenetic comparative methods and a variety of measurements collected on soricid TBA to investigate the following hypotheses: i) vertebral loading schemes vary across Soricidae according to locomotor type rather than size; and ii) a greater degree of external modification corresponds to a vertebral column that is superior in bearing high in-vivo loads. Results show *Scutisorex* vertebral centra have higher bone volume fraction and trabecular thickness, but similar anisotropy values, compared to those of other shrews, even species of similar body size. This suggests *Scutisorex* may experience vertebral loads that are higher in magnitude but similar in direction to those experienced by other shrews of various locomotor ecologies.

336^F: Convergent evolution of olfactory and thermoregulatory capacities in small amphibious mammals

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Olfaction is a key function for mammals that helps for feeding behaviours, sexual matting and predator avoidance. Despite studies related to olfaction in marine mammals, small amphibious mammals are poorly understood for that sense. We investigated olfactory capacities in amphibious mammals using a large-scale sampling representing most transition events toward amphibious lifestyle in Rodentia, Eulipotyphla, and Afrosoricida. We used a comprehensive 3D CT-scan dataset (N=189) to infer that amphibious mammals converged toward reduce olfactory turbinal bones and might rely on poor olfactory capacities as compared to their terrestrial counterparts. Using comparative phylogenetic methods, we tested and identified a convergent loss pattern of olfactory capacities related to amphibious lifestyle. Our results are consistent with genetic and histological evidences. We further demonstrate that amphibious species convergently display large respiratory turbinal bones that reflect efficient heat conservation capacities. Indeed, mammals also use the nasal cavity as a heat-exchanger with the environment. Because body heat is lost quicker in water than in air, the nasal cavity of amphibious mammals independently evolved to limit thermal loss.

337^{E,HTA}: Age matters: the hidden role of demography in mammal body size trends

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One of the many challenges in studying the biological effects of rapid climate change is measuring complex organismal responses over contemporary timescales. One predicted response—changes in body size—has been well documented in mammals, but increases and decreases have both been reported across taxa and, in some cases, within the same species. There are two primary hypotheses for these opposing trends. The first predicts size decreases consistent with Bergmann's rule, which posits that individuals in warmer climates tend to be smaller than those in colder regions. The second attributes size increases to greater year-round resource availability. However, a third alternative has been overlooked in most studies. We hypothesize that age may be an important underlying factor. Specifically, increased survivorship due to milder winters and/or longer growing seasons may lead to a larger proportion of older, bigger individuals in a population. To test this, we reanalyzed published studies on American marten and Canadian lynx in Alaska that reported significant body size changes in the latter half of the 20th century. Our findings suggest that age is a confounding variable in these studies, which relied on cranial dimensions known to change over an animal's lifetime as a result of muscle action. This work has the potential to improve our understanding of body size trends and climate change response in mammals over short timescales.

338: Functional anatomy and 3-D morphometric analysis of the occiput in the giraffe-necked gazelle (*Litocranius walleri*)

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The gerenuk (*Litocranius walleri*, (Brooke 1879) is a medium-sized antelope closely related to springbok and gazelles. Distinguishing traits of the gerenuk are its very long neck and legs and its unique feeding behavior of standing in an upright position. The strict browser is able to support the vertical posture merely by standing on its hind legs. This ability and the gerenuks elongated neck allow it to reach foliage of up to two meters.

The upright posture is not an ability the gerenuk is born with. Leuthold and Leuthold (1973) observed a captive young gerenuk, two weeks of age, attempting to perform this feeding posture. At one month, the youngling was able to successfully stand on its hind legs and at three months the position was mastered and frequently used when feeding. This behavior most likely leads to a change in muscle forces acting on the occiput, which could be responsible for the stark postnatal changes of the skull. The neonate skull resembles that of related gazelles, whilst the adult skull is comparatively flat and possesses an extremely elongated braincase. The relative length of the skull bones does not change during growth; however, the curvature of the skull and thus its overall shape does change. We quantify these developmental changes by analyzing 14 skulls of three different age classes with 3D-Landmark analysis.

339: Using geometric morphometrics to test resource partitioning in sympatric species in forest remnants

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Resource partitioning results to reduce the stress of competition between sympatric species. General morphological patterns in skull are well documented in rodents based on diet. *Akodon montensis*, *Akodon paranaensis*, and *Oligoryzomys nigripes* can all be found in high abundances in the eastern Atlantic Forest of Paraguay. We hypothesize this scenario results in competition of resources and niche partitioning, which is driven by diets, thus quantifiable in their morphology. Using geometric morphometrics we quantify differences in cranial and mandible morphology. We digitized crania and mandibles of *O. nigripes* (n = 119, 121), *A. montensis* (n = 159, 124) and *A. paranaensis* (n = 61, 58) using 16 and 13 homologous landmarks, respectively. Specimens were aligned using Generalized Procrustes fit for comparison. We used principal

component analyses (PCA) to identify the variables that best captured and described the variation between species. We used discriminant function analysis (DFA) to identify character variation, compare differences in shape, and to discriminate species groups. The rostrum showed the maximum variation between species based on PCA. DFA visualization identified the characters in the cranium and mandible where species differed the most. Most of the variation occurs in the rostrum portion of the cranium that is associated with eating. Our analysis leads us to conclude that insectivore in *Akodon* aids in minimizing competition stress between genera.

340: Testing competing molecular phylogenies of the Chiroptera with features of the inner ear cochlea

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Competing phylogenies offer contrasting scenarios of evolution of echolocation in bats. The traditional phylogeny of megachiropterans and microchiropterans suggests a single origination of echolocation in microchiropterans. Molecular phylogenies of chiropterans identify two alternative clades of Yinpterochiroptera and Yangochiroptera, each with echolocating taxa, and the possibility echolocation has a dual origin. To evaluate these competing hypotheses, we used Computed Tomography to examine the crucial hearing structures of Rosenthal's canal and the spiral ganglion for 21 echolocating and nonecholocating bats, plus outgroups. Histological sections confirmed the position of the spiral ganglion in the canal, or in the internal auditory meatus for 12 species. In all Yinpterochiroptera, the spiral ganglion is enclosed entirely in bony Rosenthal's canal. Within Yangochiroptera, however, the ganglion is enclosed in Rosenthal's canal in the basal turn only, but it is exposed in the internal auditory meatus in apical cochlear turns. This corresponds to a shift of the ganglion relative to the cartilaginous otic capsule during early ontogeny. The shift of cochlear ganglion and reduction of its bony canal in Yangochiroptera provide support for the dual origin hypothesis of echolocation suggested by molecular phylogenies. It sheds light on contrasting development of the inner ear and different ontogenetic transformations of the spiral ganglion to accommodate different cochlear innervation for echolocation among yinpterochiropterans and yangochiropterans.

341^E: Oreodonts adapt to expanding grasslands in Miocene North America and then go extinct

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Oreodonts are one of the most abundant, widespread, and diverse mammal groups in early Neogene North America. As grasslands expanded during the Miocene, open savannas replaced closed forests. This change increased selection for grazing morphologies reflecting a change of diet and movement through feeding patches. Other less abundant groups such as camels and peccaries survived these environmental changes, but oreodonts went extinct. The current paradigm attributes oreodont extinction to a lack of adaptive change. To assess the response of oreodonts to environmental change, a series of 73 skull attributes and 34 postcranial attributes were measured on 237 individuals. All skeletal elements were evaluated for deformation to ensure proportional accuracy. Ecometric analysis of the skull attributes resolves four taxonomic groups through time. The first three groups progress through origination, radiation, and specialization with a directional shift from browsing to grazing morphologies. The final survival group, shifts toward a more generalist morphology of medium size and mixed feeding morphology. Analysis of limb attributes does not indicate a clear trend through time toward grazing morphologies, but does resolve a similar pattern of origination, radiation, specialization, and survival. These results challenge the existing paradigm that oreodonts did not adapt to their changing environment with additional implications for current controversies in oreodont phylogenetics. Future research will test community versus environmental stresses for correlation with oreodont extinction across multiple biomes.

342: The importance of apex predators for forest ecosystem – an example of the wolf

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Large predators can both, directly and indirectly, influence ungulate populations and consequently can help shape the structure and functioning of terrestrial ecosystems. That is why we analysed the role of wolf presence on deer pressure on forest regeneration at two scales. At the country scale, 116 forest districts located in different parts of Poland were chosen for this analysis. These forest districts were divided into three categories: (1) wolves present at least from the year 2000, (2) wolves present from 2007, (3) without wolves. The impact of ungulate populations on forest ecosystem was calculated as an area of trees damaged by deer. On the fine scale, we created the study with experimental manipulation of wolf predation risk by exposition of their scats in artificially created plots with oak seedlings. Generally, in forest districts where wolves were present, the ungulate pressure on youngest forest stages was significantly lower than in districts without this predator. The lowest damage was observed on forest plantations where wolves were present. However, in forests recently inhabited by wolves, the intensity of tree damages in forest thickets was the highest. Further, the wolf presence changed deer behaviour and caused significantly lower pressure on oak regeneration. Our results indicate that the long-lasting presence of large predators like wolves in European forest ecosystems has a positive impact on forest regeneration.

343^F: Resource selection in female desert bighorn sheep: tradeoffs associated with reproduction

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Selection of resources that effect the development of a fetus and increase probability of survival for neonates is essential for maintaining viable populations in large ungulates. It is crucial that biologists understand how species select resources across gestation to increase their ability to manage recruitment. This information is largely lacking in desert bighorn sheep (*Ovis canadensis nelsoni*) populations; therefore, to increase understanding of sheep resource selection during gestation and following parturition, we captured and collared 30 adult, female sheep on Lone Mountain (west of Tonopah, NV), of which 15 were translocated to the Garfield Hills (west of Mina, NV) range. In addition to receiving collars, all individuals were given vaginal implant transmitters to provide parturition timing information. Following captures, we monitored parturition events, adult resource selection, and neonate survival. We used a machine-learning algorithm, random forest, to identify habitat selection during gestation, following parturition events, and following the mortality of neonates. Our results indicated that adults shifted resource selection from areas with higher nutritional availability to more precipitous terrain immediately following parturition events. In addition, our results indicated that females shifted resource selection to areas with higher quality vegetation and reduced terrain ruggedness following the mortality of a neonate and as neonate age progressed. However, following the death of a neonate, females adjust resource selection to increase nutrient intake.

344^{E,HTA}: Understanding spatiotemporal patterns of bat assemblages in highly-altered agricultural riparian systems

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Ecological roles and ecosystem services of bats are known to be important. However, despite their widespread distribution throughout North America, spatiotemporal patterns of this taxa are poorly understood both on the continental and regional scale. We conducted a year-long systematic survey of bat communities along a typical Californian riparian corridor, Putah Creek, in the Central Valley in order to better understand bat ecology in highly-altered agricultural riparian ecosystems. Putah Creek is flanked by agricultural lands, and intercepted by a county dam, making it a good representation of Central Valley waterways. Full-spectrum acoustic recordings were collected and analyzed with SonoBat 4.2.2 for one week per month for a year at eight sites of differing habitat and fluvial characteristics along 30 miles of the creek. Our inventory revealed a bat assemblage consisting of 15 species, as incidental visitors, seasonal migrants, and year-round residents. Generalized linear models suggest that species occurrence and activity levels were influenced more strongly by spatial characteristics than seasonality, and that seasonality influenced all species' activity levels similarly. Findings of this project tells us that even a relatively short stretch of a riparian system can harbor significant ecological variations for bats, which provides insights for conservation and management as well as foundation for asking more fine-scaled ecological questions.

345^{E,HTA}: Determining palatability of common cover crops and variation in choice by voles (*Microtus*)

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Midwestern farmers have dramatically increased their use of cover crops over the last decade. Cover crops provide vegetative cover and forage that may support more diverse and abundant rodent communities than those found in conventional row-crop agro-ecosystems. However, increasing vole populations may lead to depredation of the soybean commodity crop. We tested the relative palatability of 15 commonly planted cover crops to meadow (*Microtus pennsylvanicus*) and prairie (*Microtus ochrogaster*) voles using cafeteria-style feeding trials. Red clover (*Trifolium pratense*), alfalfa (*Medicago sativa*), and hairy vetch (*Vicia villosa*) were commonly preferred among voles and canola (*Brassica napus*) was avoided. Individual meadow and prairie voles consistently chose highly and minimally palatable species but were more variable in choosing moderately palatable species. However, when we compared deviation in choice to average palatability, we found a negative linear association for meadow voles and no significant association for prairie voles. Palatability scores were negatively associated with the number of plants offered in a trial, and positively affected by the relative preference for the plant species. Vole identity also was significant in predicting palatability scores for both vole species. Identifying plants of low palatability that are avoided consistently by voles allows farmers to plant cover crops that do not encourage immigration of small mammals into fields, thus reducing negative consequences that might otherwise limit future adoption of a valuable soil conservation practice.

346^{HTA}: Investigating the utility of spatially-explicit capture-recapture for black bears in Wisconsin

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Black bear management and harvest is of great interest to the citizens of Wisconsin. Wisconsin Department of Natural Resources (DNR) relies on age-at-harvest state-space models to predict population responses to harvest rates, but these models require periodic calibration with a population point-estimate. To provide that, we investigated the utility of spatially-explicit capture-recapture (SECR) to estimate the black bear (*Ursus americanus*) population using hair samples collected at barbed-wire hair corrals. As our state-wide study area was expansive, we needed a design that both provided reasonably unbiased (relative bias < 10%) and precise (relative standard error < 20%) estimates and minimized existing staff effort. We performed a pilot study to identify efficiencies for a state-wide project and incorporated those pilot parameter values into simulations to test the performance of a state-wide study design. We tested the precision of deploying 2 x 2 clusters (4 hair corrals within a cluster) using the lower and upper sigma values (900m, 1200 m) and g_0 (0.3, 0.5, 0.7) parameters informed by our pilot data. Our results suggest that at densities > 15 bears/100 km², our study design would provide relatively precise and unbiased estimates. Clustering hair corrals into groups provides necessary information on bear movements, and systematically spacing these clusters allows us to utilize existing staff and efficiently cover a large geographic area. This research was supported by an ASM Early Career Travel Award awarded to Laura McMahon in 2019

347: Altered ecosystems and narrowed niches: habitat mediates survival of a threatened habitat specialist

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An understanding of the effects of biotic and abiotic factors on demographic rates is important for species conservation planning. Without such information, managers risk creating ineffective or even detrimental habitat for target species. The New England cottontail (*Sylvilagus transitionalis*) is an imperiled shubland specialist endemic to New England and eastern New York. Habitat management to benefit New England cottontails has been fraught with challenges including a poor understanding of factors constraining their realized niche. We assess survival of adult and juvenile New England and eastern cottontails (*S. floridanus*) in response to environmental, health, and landscape factors. Tick burden was the most important predictor of juvenile survival, with burdens greater than 10 resulting in a dramatic reduction in survival when individuals were in poor body condition. Survival of adult New England cottontails declined with increasing

movement, suggesting that the need for long-range dispersal and exploratory movements due to habitat loss and fragmentation could have negative impacts on populations. Survival also increased with increasing canopy closure, while the inverse was true for eastern cottontails. Survival of both species declined with increasing densities of an invasive shrub, Japanese barberry (*Berberis thunbergii*) at low levels of canopy closure. These findings are consistent with recent publications on resource use by New England and eastern cottontails; however, they run contrary to ongoing land management practices aimed at recovering New England cottontails.

348^E: Settlement of adult American red squirrels after translocation

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Translocation has been largely used as a conservation technique to increase population size, genetic diversity, or to reintroduce a species inside its indigenous range. Once released in the new territory, the tactics used by the individuals to search and identify the new area where to settle can help in identifying the key factors determining the success or failure of the translocation. The animal space use right after the release is a good indicator of the decision making and can be informative of habitat features required to have a successful settlement and survival. We translocated 22 American red squirrels (*Tamiasciurus fremonti*) within the White Mountains (AZ) and studied their space use and subsequent settlement in the new environment. Squirrels showed a stronger homing response during the fall than in winter. Moreover, in winter squirrels settled within 500 m from the release site, while in the fall 900 m. The decision making to select the final settlement site followed the Bayes' rule with squirrels visiting the same areas repeatedly to gather information before selecting the site where to settle. During this process, the intraspecific competition played a significant role in determining the final site. The result obtained from this study will influence future management actions to better protect the endangered population of the Mt Graham red squirrel.

349^E: Fawning site selection by female white-tailed deer in the presence of a large stalking carnivore

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During fawn-rearing, many adult ungulates limit space use to a proportion of their home range, and selection of these sites affect the quality of concealment cover available to fawns and forage availability for adult females. Predation risk can create tradeoffs that induce nutritional deficits in prey by reducing forage intake (e.g. increased vigilance or selecting safer but unproductive areas). Thus, fawn-rearing habitat selection can affect processes such as neonate growth, fawn survival, and recruitment. To determine how the presence of a stalk-ambush carnivore, the Florida panther (*Puma concolor coryi*), impacted fawning habitat selection, we captured and collared adult white-tailed deer (*Odocoileus virginianus*) with GPS tracking collars (n=28), and concurrently monitored remote trail cameras between 2014-2017 within Big Cypress Basin in south Florida. We estimated birth dates for fawns born by collared does via trail cameras, and for collared does we used a step-selection function to evaluate selection two weeks of late gestation and parturition and two weeks during lactation in regards to predator activity rates, cover types, seasonal hydrology, and productivity metrics (e.g., time since fire). Does selected for recently burned areas, and hammock, cypress, and marsh cover types. Others have demonstrated does avoid open areas during parturition as to increase the amount of concealment cover for fawns. Our results highlight the importance of predator hunting mode when considering life history strategies for ungulates.

350: Landscape genetics across multiple cities reveals influence of the built environment on commensal brown rats

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Brown rats (*Rattus norvegicus*) exploit urban landscapes, attaining widespread distributions while displaying population genetic structure over fine spatial scales. Yet, the ecological mechanisms driving distribution and gene flow patterns for rats are poorly understood. Moreover, it is unclear whether species respond to a common set of features between cities. We studied rat populations in four independent cityscapes to understand species distribution and migration using habitat suitability modeling and landscape genetic. Results suggest that a combination of landscape features predict gene flow better than distance alone in each city, reflecting their generalist exploiter ecology, while habitat suitability was primarily driven by factors related to population density, building condition, and local income. Models combining built physical features (roads, infrastructure, buildings) performed reliably well across each city. Linear features facilitated gene flow across cities exhibiting clinal genetic structure, while linear features such as waterways and high-traffic roadways posed migration barriers in rat populations exhibiting stark genetic breaks. Further, we found habitat suitability and genetic connectivity were uncoupled and habitat was not the best predictor of gene flow for urban rats in most cases. Together these results reflect the complex ways cityscapes influence commensal ecology and evolution, with implications for pest management strategies and mitigating zoonotic disease. This work highlights the limits of modeling gene flow with habitat quality alone and the utility of multi-landscape comparisons in landscape genetics.

351: Microhabitat selection and behavior of field mice along an urban gradient

Microhabitat selection and behavior of field mice along an urban gradient

Danielle Lee, Hannah-Beth Griffis

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A variety of small rodent species successfully occupies habitats in cities, suburbs, and rural areas. Not all mouse species respond to human-modified environments in equal or equivalent ways. Some species, *Peromyscus* spp. for example, respond negatively to human development and suffer population declines and distribution range contractions or marginalization. Other species, such as the common house mouse, do very well in proximity to humans and are noted nuisance animals in both urban and rural environments. Microhabitat selection focuses on the environmental features that may favor survival, such as predation protection, food distribution, and cover. The ongoing research of my lab group involves identifying mouse species that are most prevalent and ecologically successful across anthropogenic habitat gradients in the St. Louis Metropolitan area. We compare functional traits, general behavioral responses, and stable isotopic composition in locally occurring mouse taxa to examine how human disturbance influences rodent behavior. Understanding the ecology and behavioral responses of nuisance rodents sheds light on how plasticity shapes fitness traits across these species, as well as informs pest management practices and urban planning policies. As human populations continue to grow and spread, we will need solutions to manage these types of human-wildlife conflicts that also take into account conservation protocols for species of concern.

352: Studies at a large urban population of Mexican free-tailed bats (*Tadarida brasiliensis*) in downtown Houston

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Mexican free-tailed bats (*Tadarida brasiliensis*) range from the southern half of the United States into central South America. With the expansion of urban development and human habitations, colonies of free-tailed bats occupy buildings, parking garages and bridges, which has resulted in significant range expansion. Houston is home to a sizable population of free-tailed bats at the Waugh Bridge since its construction in 1994. We have been casually monitoring the colony since the mid 1990's, and initiated formal studies over the last decade. This work has included taxonomic studies to designate subspecies (*T. b. mexicanus*). Observations have also documented the actions of predatory birds in an urban setting, primarily the hunting behavior of Swainson's hawk (*Buteo swainsoni*), as well as both black-crowned (*Nycticorax nycticorax*) and yellow-crowned night herons (*Nyctanassa violacea*), as novel predators of free-tailed bats. The effects on the colony due to a major flooding event associated with hurricane Harvey (August 2017) was also documented. We discuss results of these studies in this presentation. The significance of this work is that while thousands of observations have been made at the colony by wildlife enthusiasts, little has been done

in regards to research on this large urban population of free-tailed bats, which is so easily viewed and accessed within the city, less than 2 km from downtown Houston.

353: Effects of urbanization on the ecophysiology of raccoons

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Urban landscapes have well-known effects on wildlife populations with most species suffering population declines in and around cities. Nonetheless, a subset of species thrive in urban environments, driven in part by the consumption of human food wastes. Despite the ubiquity of this observation, little is known about the physiological and fitness consequences of replacing a "natural" diet with this evolutionarily novel food resource. Anthropogenic food wastes should be high in carbohydrates, sugars and fats, and we therefore predicted that urban raccoons will have elevated body mass, blood glucose and serum leptin (a hormone produced by fat tissue that regulates appetite) relative to their counterparts living in non-urban habitats. We acquired blood samples from raccoon populations in southern Ontario, Canada that varied in their presumed access to food waste. We found that raccoons from sites with the highest presumed access to food waste were significantly heavier and had significantly higher levels of glycated serum protein (GSP, a marker of elevated blood glucose). In addition, GSP concentration was positively related to body mass. No significant differences in serum leptin were detected, nor was serum leptin related to body mass. Our work on raccoon ecophysiology suggests significant effects on physiology but further work will examine stable isotopes to ascertain diet differentiation among urban and non-urban raccoons, as well as determining the fitness consequences of urban diets.

354: Integrating research and behaviour change strategies to conserve urban mammals in La Paz, Bolivia

Mariana Da Silva Loayza

Wildlife Conservation Society, La Paz, La Paz, Bolivia, Plurinational State of

Around 70% of Bolivians live in urban areas, leading to poorly planned and accelerated conversion of natural areas that impact associated mammal communities. We have been studying some aspects of the ecology of mammals in urban and periurban areas of La Paz, the main city in Bolivia, and some human dimensions of their conservation, as a base to apply behaviour change strategies to conserve them. In 2011, thorough indirect sign search in transects, camera trapping and interviews in the municipal protected areas of the city, we confirmed the presence of eight large and mid-size mammals; most were new records for this area, including Geoffroy's cat (*Leopardus geoffroyi*), whose distribution and altitude range increased to the northwest and to 3745 m asl, respectively, with this data. In 2013, we started the initiative Nuestros Vecinos Silvestres (Our Wild Neighbors) which integrates ecological research on urban wildlife and behaviour change strategies to conserve it. We currently are focusing on the distribution, activity patterns and interactions of mammals with people and domestic animals, using camera trapping, social sciences methods and citizen science. Our behaviour change strategy is directed to the city residents and authorities so they adopt practices and urbanization planning that considers the urban fauna and the remnant natural areas they depend on.

355: Making movement personal: inferring personality traits from GPS tracking data of urban coyotes

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Examining how animals navigate urban landscapes can uncover the ecological factors driving behavioral shifts in cities. Animal movement data inherently represent a repeated-measures design across contexts and time, which coincidentally is a necessity for estimating animal personality. Yet, studies investigating the potential utility of telemetry data for inferring personality-dependent movement are relatively nonexistent. We tested whether GPS data could be used to estimate repeatability (i.e., personality) in urban coyotes (*Canis latrans*). We quantified daily travel distance, displacement, road selection, and habitat

selection of 40 GPS-collared adult coyotes in Denver, CO and Edmonton, Alberta from 2012 to 2017. Our metrics corresponded with three behavioral traits (activity, exploration, and boldness) that we assessed for repeatability. Estimates (R) for all traits ranged from 0.19 to 0.50. Moreover, daily travel and displacement varied with development, suggesting coyotes modify their behavioral strategies according to urban landscape features. Covariance among travel distance and displacement suggested an activity–exploration syndrome. Our data highlight the utility of movement data in approximating personality of taxa in urbanized environments. Moreover, this design may be particularly useful for estimating personality differences in large or clandestine species that are difficult to observe repeatedly in wild settings.

356^E: Mortality costs of reproduction to females in a system of allied sexual coercion

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Indo-Pacific bottlenose dolphins (*Tursiops aduncus*) have a complex, polygynandrous mating system in which both males and females mate multiply within a breeding season. Male bottlenose dolphins form stable, long-term alliances and use coercive mating strategies, including aggression towards rival alliances and estrous females, to increase mating access. Maternal investment in dolphins is high; the gestation period is twelve months, and lactation lasts three to eight years. The Shark Bay Dolphin Project has been collecting longitudinal data on >1600 individuals in Shark Bay, Australia, for 35+ years, enabling us to examine costs of reproduction to females in this coercive mating system. Contrary to many species with high levels of male-male competition, the median age of death for both sexes in the study population is similar (~32.5 for both males and females), and males survive to the oldest age classes (>47 years old). Notably, females show an increase in mortality hazard at 13 years of age, coincident with the age of first reproduction. We found that 23% of adult females never successfully raise a calf to weaning, and reproductively successful females have significantly higher survival than reproductively unsuccessful females ($\chi^2(1) = 15.1, p < 0.001$). These data suggest that the costs of reproduction to females in this system are substantial enough to alter reproductive trajectories for some females, and may alter sex-specific life history patterns.

357^{E}: Social assortment and the role of personality in *Octodon degus***

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Exploring the relationship between animal personality, defined as consistent individual differences in behavior, and associations between individuals in social species has become a topic of recent interest in behavioral ecology. While inflexible behavior can be detrimental when an animal must respond to environmental changes, having consistent behavior within social groups leads to stronger bonds between individuals. Animals may form social groups with individuals with similar (e.g., more bold animals with other bold animals) or dissimilar (e.g., more bold animals with less bold animals) personality types. Both association structures exist in a variety of taxa, and there are fitness consequences associated with each structure. In a wild population of degus, *Octodon degus*, we quantified the individual repeatability of five behavioral traits (emergence from hide, latency to emerge, distance moved, time spent along an edge, and velocity) in open field trials and determined if social groups assorted similarly or dissimilarly based on these traits. Personality has been previously shown in degus for two behavioral traits, boldness and exploratory behavior, and dissimilar social assortment has been shown for exploratory behavior. We found behaviors in an open field to be repeatable, and analysis of social assortment is ongoing. This study serves as a follow-up to prior research and we provide suggestions for the future of personality research in wild populations. This research was supported by a Grants-in-Aid of Research awarded to Nicholas Johnson in 2017.

358: Seasonal variation in space use and territoriality in an invasive large mammal (*Sus scrofa*)

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An individual's spatial behavior is shaped by social and environmental factors, and can be characterized by estimating home range and core areas. Understanding heterogeneity of spatial overlap among conspecifics can be used to understand intraspecific behavioral factors shaping spatial use and improve management actions. We examined wild pig (*Sus scrofa*) spatial behavior between sexes and seasons, and used this information to evaluate patterns of spatial use and territoriality. Home ranges and core areas were estimated for 54 wild pigs at Buck Island Ranch, FL from 30 minute GPS locations. Overlap indices were used to estimate the strength and number of potential interactions within three dry and two wet seasons. Males had larger home ranges ($M = 10.36 \pm 0.16$, $F = 3.21 \pm 0.16 \text{ km}^2$) and interacted with a greater number of individuals than females within seasons. Home range size ($p=0.75$) and strength of interactions ($p=0.21$) did not vary between wet and dry seasons. The strength and number of interactions decreased for overlap between core areas compared to between home ranges, and this territorial pattern was greater for females than males. The increased home range and greater number of potential interactions by males is likely to facilitate the spread of parasites and disease in wild pigs. Based on spatial patterns of behavior, management actions in both wet and dry seasons should perform equally in this system.

359^F: Mesopredator omnivory generates both direct and indirect effects on seed fate

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Mammalian mesopredators often use fruit as a supplementary resource and disperse digested seeds. Since rodents will reduce foraging in response to predator cues, mesopredator scat could improve seed survival; however, rodent responses may vary with scat composition. Rodents and arthropods have different seed preferences, so scat effects likely are contingent upon seed traits and granivore identity. We measured seed predation of two animal-dispersed seeds (*Prunus serotina* and *Rubus allegheniensis*) in the presence and absence of coyote scat, varying in composition (meat-rich, fruit-rich, mix), in trays that manipulated rodent access to test if mesopredator omnivory's effects on seed fate depend on granivore identity and seed size. Scat reduced total seed removal from full access trays by 12% but increased removal from arthropod-only trays by 43%. *Prunus serotina* seeds were only removed from full access trays, indicating that only rodents consumed these larger seeds. Scat decreased *P. serotina* removal by 21%, and the effect size of meat-rich scat was >50% greater than other compositions. Scat decreased rodent removal of *R. allegheniensis* by 66% but increased arthropod removal by 43%. Scat significantly reduced the dominance of *R. allegheniensis* over *P. serotina* in seed survival, so mesopredators could alter competitive asymmetries amongst plant species. By dispersing seeds and modifying granivore behavior, mesopredators have direct and indirect effects on seed fate that could drive large-scale patterns of plant recruitment.

360^F: Spatiotemporal responses of wildlife to tourism in a low-visitation national park

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Researchers often use highly visited protected areas as study systems to set baselines regarding wildlife behavior. However, the level of human disturbance that causes a detectable change in wildlife behavior remains unknown. In response to humans, wildlife can exhibit "fear effects", where they avoid humans, as well as the "human shield effect", where wildlife use humans as a buffer against predation. Here we investigated the spatiotemporal responses of brown bears (*Ursus arctos*), black bears (*Ursus americanus*), moose (*Alces alces*), and wolves (*Canis lupis*) to tourism in Glacier Bay National Park, Alaska (GLBA). We used camera traps to document wildlife activity and a paired-plot, crossover experimental design to manipulate human visitation during summers 2017 and 2018 ($n = 5$ pairs of sites). Single-season occupancy models and activity overlap analyses indicated that brown bears were unaffected by human use in GLBA, black bears exhibited fear effects temporally but the human shield effect spatially, moose utilized human presence as a shield temporally, and wolves exhibited fear effects temporally. Visual inspection of the detection data showed nonlinear relationships in which detections did not exceed four per week for any species unless human activity was absent. These results indicate the threshold level of human activity for sites to function as baseline controls in studies of anthropogenic impacts may be lower than those found in most protected areas.

361: Evolution of precociality in caviomorph rodents: a synthesis and review

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Caviomorph rodents are known for producing precocial offspring, but levels of precociality vary widely among species. Moreover, species also vary widely in levels of sociality, ranging from solitary to highly social, with some social species living in large groups with evidence of complex recognition abilities, and some having communal nursing, and biparental care. The relationship among precociality, sociality, and environmental constraints poses intriguing questions. Here, we review the existing literature and suggest that precociality is intricately related to environmental variables and social organization. Specifically, the highest levels of precociality occur in social species living in challenging habitats, for example, harsh and fluctuating environments, environments with fluctuating resources, and/or environments with high predation rates (although there are notable exceptions to the latter). In contrast, species producing less precocial young are more likely to be solitary and appear to counteract predation by being fossorial or nocturnal. The correlation between precociality, sociality, and adaptations to harsh environments is consistent with the hypothesis that precocial young have larger brains which allow for greater behavioral plasticity, social complexity, and ability to successfully adapt to unpredictable or hostile environments. However, definitive data on this point do not currently exist. An additional caveat is that so few caviomorph species have been studied that it is difficult to conclusively identify clear patterns in this taxon. Future research on these questions is required.

362: Diets of omnivorous prey are driven by habitat selection but not moonlight in an agroecosystem

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Post-dispersal weed seed consumption is an important ecosystem service provided by vertebrate and invertebrate granivores in agriculture. Omnivorous deer mice (*Peromyscus maniculatus*) commonly forage for grains and invertebrates in crop systems, but their contributions to biocontrol could be altered by perceived predation risk. Patterns of risk avoidance by small mammals include refuge-seeking in vegetated habitat, but the effects of risk on fine-scale processes, such as within-patch movement and diet, are less explored. Using seed removal assays, fluorescent powder tracking, and stable isotope analyses, we assessed effects of a predation risk cue on mouse movement patterns and diet in risky and refuge habitats. Within cover crop patches, mouse foraging was unaffected by moonlight, but decreased on exposed ground during the full moon. Sinuosity of movement was greater in cover but was not affected by moonlight. Weed seed removal was greater in cover, and most was attributable to invertebrates. Mice and invertebrates both exhibit higher foraging activity in cover, indicating co-occurrence of intraguild predators and prey. However, stable isotope analyses revealed that mice occupied a lower trophic position in refuge than in exposed habitats, which was not affected by moonlight. Despite increased availability of invertebrate prey in cover patches, mice may not switch from plant-based food when avoiding predators. Therefore, intraguild predator-prey interactions may not interfere with weed biocontrol when mice seek refuge from predators.

363^{E,HTA}: Ecosystem impacts of an Amazonian megadam: mammalian and dung beetle distributions across an artificial archipelago

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Hydropower projects in the Amazon have resulted in habitat loss and fragmentation by flooding lowlands and isolating remaining habitat as islands. Such landscape transformation results in local extinctions of fauna on remaining islands and wide-ranging ecosystem change—however, long-term assessments of dam impacts on trophic interactions between multiple ecosystem levels are rare. We evaluated impacts of the Balbina dam in the Brazilian Amazon on the distribution and composition of dung beetle assemblages and mammals across 30 islands and 3 mainland sites, using relative abundance data gathered with pitfall and

camera traps. Using generalized linear mixing models, we found strong positive relationships between abundance and richness of mammals and dung beetles, but these relationships were highly collinear with forest patch area and isolation metrics, consistent with the Theory of Island Biogeography. We performed partial least square analyses to examine the correlative strength of mammal distribution for predicting dung beetle richness and abundance compared to landscape metrics. Variables related to area, isolation and vegetation explained 92% of dung beetle abundance; mammal abundance predicted an additional 1.5%. Area predicted 57% of dung beetle richness; mammalian richness explained 34%. These correlations suggest remaining dung beetle diversity within these islands is partially controlled by diversity limitations of mammalian dispersal; we expect further causal analyses to illuminate top-down influences of vertebrates on bottom-up ecosystem processes by regulating communities of nutrient-cycling arthropods.

364^{E,HTA}: Correlates of declining bat activity and night-flying arthropod communities

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The community interactions between insectivores and their prey are complicated. In North America, bats are currently threatened on a continent-wide scale by the emergence and spread of White-nose syndrome (WNS), a devastating disease resulting from infection with the fungus *Pseudogymnoascus destructans*. WNS was detected in Wisconsin in March 2014, and has since caused precipitous declines among Wisconsin bats. During the summer period from 2015-2018, we performed bat acoustic monitoring and insect black-light trapping surveys at paired locations both near and far from little brown (*Myotis lucifugus*) and big brown bat (*Eptesicus fuscus*) roosts. We identified insects by microscope and compared abundance, diversity, and richness with levels of bat activity as well as pre- and post-volancy roost counts. Overall, we found that higher bat activity was correlated with higher insect abundance and diversity. Insect abundance, particularly among aquatic taxa, also declined consistently over the four-year period. These results suggest that WNS-related population declines in bats may have top-down effects on insect communities.

365^E: Synergistic effects of land-use and climate change on rodent communities: a half-century of anthropogenic change

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Given the growing biodiversity crisis related to accelerated extinction rates, understanding effects of environmental change on species represents a significant challenge for conservation. For example, both land-use and climate change have had well-documented, profound impacts on species distributions and biodiversity patterns. Although it is becoming increasingly clear that climate change will continue alongside human modification of the landscape, few studies have jointly examined both land-use and climate change, and their interaction, as drivers of faunal change in terrestrial systems despite their potentially synergistic effects. We used historical museum specimen records coupled with contemporary field surveys to identify trends in rodent community composition across the convergence of two ecoregions in north-central Texas. Specifically, we examined changes in both species composition and associated functional traits, including habitat association, body size, locomotion (i.e., bipedal versus quadrupedal), and diet (e.g., omnivore, granivore, folivore). We detected spatial variability in climate change effects on rodent community composition based on different responses to underlying differences in land use, particularly in the eastern versus western portions of the region. This work demonstrates the value of museum records for characterizing faunal changes in response to shifts in climate and land-use practices. Moreover, results from our work should improve understanding of drivers of faunal change within this region, with implications for managing rare species in the face of future environmental change.

366^E: Amino acid $\delta^{15}\text{N}$ tracks ecosystem and dietary changes within a mammalian community across the Holocene

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One of the likely consequences of the late Pleistocene megafauna extinction was a reorganization of mammalian communities, including trophic niche shifts of medium- and small-bodied mammals. Cutting edge techniques in $\delta^{15}\text{N}$ analysis of individual amino acids (AAs) provides a way to simultaneously track animal trophic level and changes in baseline (vegetation) $\delta^{15}\text{N}$ values through time and space. 'Source' AAs are routed directly from diet to consumer and so their $\delta^{15}\text{N}$ values change little with trophic level, whereas 'trophic' AAs show a strong relationship between trophic level and $\delta^{15}\text{N}$. Here we apply this approach to fossils of four mammal species (*Sigmodon hispidus*, *Canis latrans*, *Bison* sp., *Odocoileus* sp.) from Hall's Cave in west-central Texas, a site that spans from before the late Pleistocene extinction through the Holocene from ~20,000-1,000ka. For all taxa we found a significant decline in $\delta^{15}\text{N}$ of source AAs from the mid to late-Holocene, indicating a shift at the base of the food web. In contrast, the offset between source and trophic AAs varied depending on species and time period. Whereas our herbivores exhibited fairly consistent trophic-source $\delta^{15}\text{N}$ offsets, *C. latrans* exhibited a large amount of variation, indicating they may have been trophic generalists through the entire Holocene. Our study demonstrates that AA $\delta^{15}\text{N}$ analysis of ancient consumers can provide a useful way of quantifying both ecosystem shifts and trophic dynamics.

367^E: Sex differences in roost selection of Northern long-eared bat in the Kisatchie National Forest
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Roosts play an important role in ecology and evolution of bats, serving as sites for many activities, such as hibernation, rearing of young, and mating. Roost type selection can vary depending on season or reproductive status, therefore bats may seek specific attributes of roosts to fulfill their specific needs and requirements. Because little is known about the roosting ecology of the Northern long-eared myotis (*Myotis septentrionalis*) in the southern portion of its geographic distribution, our objectives were to conduct a telemetry study throughout the Kisatchie National Forest of Louisiana to identify roost site characteristics important for *M. septentrionalis*. We hypothesize that female Northern long-eared bats will select different roost characteristics than male Northern long-eared bats for better thermoregulation and rearing young. We radio-tracked 17 males to 62 day roosts and 12 females to 39 day roosts. At each occupied roost, we quantified important roost and stand characteristics within an 18×18 m plot centered around the roost tree. We used a multivariate analysis of variance (MANOVA) and discriminate function analysis to determine if *M. septentrionalis* selected different tree or stand characteristics between sexes. Results from the MANOVA ($F_{18,79}=2.62$, $P<0.05$) and discriminate analysis suggest that female *M. septentrionalis* select roosts that are larger, while male *M. septentrionalis* select areas of high tree density. Results from our analyses will improve our understanding of the conservation status of *M. septentrionalis*.

368^{E,HTA}: Microbial diversity and its implications for disease in an endemic fox population

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The microbiome is increasingly recognized as a critical player in health and immunity. Symbiotic microbes have been shown to aid immune development, outcompete pathogenic invaders, regulate immune and metabolic processes, and maintain homeostasis in hosts. When these microbes are disrupted, dysbiosis can contribute to disease state and severity. Thus, characterizing healthy and disrupted microbial communities in wildlife populations can inform our understanding of disease pathogenesis and aid conservation management. Santa Catalina Island foxes (*Urocyon littoralis catalinae*) are an ideal case study for these analyses due to their extremely high prevalence of ear canal tumors. The exact cause is yet unknown, but infection with ear mites (*Otodectes cynotis*) has been linked to sustained ear infections, abnormal cell growth, and tumor development. To better understand these links, we sequenced the ear canal microbiome using 16S rRNA amplicon sequencing. We then compared microbial community composition, diversity, and evenness between healthy and mite infected individuals. We found that healthy foxes exhibited rich communities of diverse microbes, with numerous taxa in high abundance. In contrast,

mite infection was associated with reduced diversity and evenness, with one taxon dominating the community. These results support the hypothesis that ear mites disrupt microbial communities, and may contribute to chronic inflammation. They provide further insights into the pathogenesis of this complex system, and contribute to the broader effort of characterizing microbiome diversity in wildlife.

369^E: Seasonal variation in diet, microbiome, and metabolome of two species of woodrat (genus *Neotoma*)

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Mammalian herbivores must balance nutritional requirements while limiting exposure to toxic plant secondary compounds (PSCs). Therefore, mammalian herbivores must adapt to changes in dietary resources. Seasonal variation in food plant availability may result in corresponding changes in the diets of wild herbivores, as well as the microbiome and chemical metabolome. These factors have implications for future viability of populations of mammalian herbivores as climate and environmental change persists. We study two species of woodrat (genus *Neotoma*) that hybridize across a sharp ecotone in southern California where Mojave Desert scrub transitions to southern Sierra Nevada woodland. We present findings from a study in which we sampled woodrat fecal pellets across a seasonal gradient to characterize seasonal patterns in woodrat diet, microbiome, and metabolome. We found that woodrats maintained distinct diets on either side of the ecotone and that diet shifted seasonally in accordance with availability of annual forbs. Corresponding changes in microbiome and metabolome also occurred that correlated with seasonal changes in diet. Our findings indicate that mammalian herbivores modify their diet in response to available dietary resources and that these shifts co-occur with changes in the gut microbiome community and chemical metabolome. As climate and environmental change continue, our findings provide important insight into how herbivores acclimate to changes in food availability, which may help guide wildlife and habitat management efforts under changing environmental conditions.

370: Comparative genomics of desert adaptation in *Peromyscus* rodents

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How do mammals survive the intense heat and aridity common to deserts? While we have some idea about the behavior and physiological aspects of survival, we have relatively little understanding of how these selective forces may shape the genomes of mammals that have evolved in desert environments. To begin to characterize these effects in two focal taxa, we have recently generated chromosome-level assemblies and population genomic data from the cactus mouse (*Peromyscus eremicus*) and canyon mouse (*P. crinitus*), which are native to the desert regions of the Southwest United States. To enable the study of convergent evolution between these two species and many other aspects of adaptation genomics in *Peromyscus* we have also assembled whole genomes for 5 other *Peromyscus* species, with another 15 genomes in progress. While preliminary findings suggest that particular regions of the genomes are intensely shaped by desert adaptation, the broader outcomes of this work—the generation of multiple *Peromyscus* genomes—will power the next generation of research questions. Indeed, this work represents the next step in enabling *Peromyscus* (The *Drosophila* of North American mammalogy) researchers to ask critically important genome-scale questions about the relationships between ecology and evolutionary processes.

371: Ecology outweighs evolutionary history in shaping the bat microbiome

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Recent studies of mammalian microbiomes have identified strong phylogenetic effects on bacterial community composition. Bats (Mammalia: Chiroptera) are among the most speciose mammals on the planet and the only volant mammal. We examined 1,236 16s rRNA libraries of the gut, oral, and skin

microbiota from 497 Afrotropical bats (representing 9 families, 20 genera, and 31 species) to assess the extent to which host ecology and phylogeny predict microbial community similarity in bats. In contrast to recent studies of host-microbe phyllosymbiosis in other mammals, we found no correlation between chiropteran phylogeny and bacterial community composition across the three anatomical sites sampled. We found host species identity and geographic locality to be strong predictors of microbial diversity for all anatomical sites, and observed a positive correlation between elevation and bacterial richness of each anatomical site. Lastly, we identified significantly different bacterial associations within the gut microbiota of insectivorous and frugivorous bats. We conclude that the gut, oral, and skin microbiomes of bats are shaped predominantly by ecological factors and do not exhibit the same degree of phyllosymbiosis observed in many other mammals.

372: Comparative analysis of bat longevity using epigenetic clocks

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Recorded lifespans of bats exceed other placental mammals of similar body size. Moreover, considerable variation in lifespan is present among bats. Here we reconstruct bat longevity on a recent molecular phylogeny and identify at least four lineages of bats that exhibit extreme longevity, i.e. can live at least four times as long as similar-sized nonflying placental mammals. Phylogenetic generalized least squares analysis reveals that body mass, duration of hibernation - as estimated by latitudinal distance from the equator for the species range, use of a cave roost, and sexual conflict - as estimated by sexual dimorphism, predict longevity. We then describe a method for estimating age from DNA using patterns of methylation at conserved genomic regions that change over time. Using methylation scores from over 500 individuals of known age from 17 bat species we use elastic regression to derive a predictive relationship for estimating age. We then use this "clock" to identify species that have either accelerated or decelerated aging rates and genomic regions that have age-dependent methylation patterns.

373: Genomic impact of founder history on populations of the critically endangered dama gazelle (*Nanger dama*)

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Dama gazelles are the world's largest and rarest gazelle species, with only about 200 animals remaining in the wild. They are native to the Sahara Desert and Sahel, with only remnant populations remaining in Chad, Mali, and Niger. However, more than 2,300 dama gazelles are managed *ex situ* in zoos and private collections around the world, with the largest number of animals found on private ranches, mostly in Texas. Three geographic subspecies have been recognized based on color patterning differences among populations: addra (*Nanger dama ruficollis*), the nominate dama (*N. dama dama*), and mhorh (*N. dama mhorh*). *Ex situ* populations of mhorh gazelles were founded by only a small number of individuals, before this subspecies had become extinct in the wild, whereas those for addra gazelles were founded by a larger group of individuals. We examined the genome-wide effects of these different founding histories by generating whole genome sequences of addra and mhorh gazelles, which included a chromosome-scale reference genome assembly from one addra gazelle. Mhorh gazelles had almost 50% less heterozygosity, a genome occupied by up to 45% of runs of homozygosity, and about three times the number of putatively loss-of-function mutations compared to addra gazelles. These genomic data provide an important resource that can be applied to the long-term conservation of this critically endangered antelope.

374^{E}: Host taxonomic and dietary signal in microbial communities varies across the gastrointestinal tract in Sulawesi rodents**

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In natural populations of mammals, both diet and taxonomy have been found to structure gut microbial communities in samples drawn from the colon and feces. This may bias our understanding of gut microbial communities because of gradients in pH, nutrient availability, and concentration of anti-microbial peptides from the small intestine to the colon. We examined differences in the strength of dietary and host taxonomic signal with 16S rRNA gene amplicons drawn from the small intestine, cecum, and colon of six co-occurring species of rodents from Sulawesi, Indonesia. These species were chosen because they span a range of dietary differences and phylogenetic distances, but occupy the same environment. Stable isotope analysis clearly grouped species into insectivores, omnivores, and herbivores. All three GI regions had microbial communities distinguishable by host taxonomy and diet, but samples drawn from the cecum were more strongly correlated with both factors (determined via NMDS and ANOSIM testing). Differentiation of insectivores from omnivores and herbivores was partially driven by the presence of distinct Ruminococcaceae taxa (known fiber degraders) in these two groups. With most research on wild mammal gut microbial communities focused on fecal and colon sampling, there is an urgent need to recognize that the degree to which host taxonomy and diet relate to microbial community structure varies by GI region. This research was supported by a Grant in Aid awarded to Mark Swanson in 2016.

375: Tracking animal biographies through ancient DNA in Classic Mesoamerica

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Almost a millennium before Spanish chroniclers documented “Moctezuma’s Zoo”, the earliest evidence of wild animals in captivity in Mesoamerica has been observed during the rise of the ceremonial landscape at Teotihuacan, Mexico (A.D. 1-500). Teotihuacan ideology strategically embedded ferocious animals as symbols for the state by consecrating Mesoamerica’s most powerful apex predators, including pumas (*Puma concolor*), jaguars (*Panthera onca*), and wolves (*Canis lupus*) within the pyramids as ritual sacrifices. Zooarchaeological investigation of nearly two hundred animals cached inside the Moon Pyramid and Sun Pyramid revealed pathologies (injuries, infectious disease) and cooked stomach contents, some demonstrating a maize-based managed food chain. We build on this zooarchaeological and isotopic analysis (carbon and nitrogen) and integrate ancient DNA approaches to construct individual animal biographies. Shotgun DNA sequencing of four felids from two different contexts within the city of Teotihuacan—the Moon Pyramid and Plaza of the Columns—yielded intact felid DNA and confirmed zooarchaeological species identification. This early evidence of wild animal captivity in Classic Mesoamerica presents a unique opportunity to employ an interdisciplinary approach to track each animal’s biography through its archaeological, isotopic, genetic, and biological footprints. We use this novel approach to empirically reconstruct the first stage of the ritualization process, procurement of sacred animal, to understand the process that empowered these carnivores as material emblems of state authority in state-level rituals.

376: Extirpations of mammals at their southern range limits in California

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Isolated populations are prone to extinction, especially at southern range limits in the face of climate warming. Joseph Grinnell and colleagues documented the fauna of California intensively, including the San Jacinto Mountains in 1908 and the Mojave desert in what is now Mojave National Preserve and Joshua Tree National Park primarily from the 1930s to the 1950s. From 2008 to 2019, we revisited 50 sites in these areas to document changes in the fauna over the past 100 years. For mammals, our survey methods included motion-detection cameras, bat detectors, Sherman traps, and Tomahawk traps deployed at four plots for 4-12 nights per site, in the same season and within the same areas and habitats as were trapped previously. For rare species suspected of extirpation, we used additional targeted methods and trapping. Of the total 73 mammal species known from the study areas, seven have southern range limits in them.

Among those, we noted three examples of apparent extirpations at southern range limits, in the lodgepole chipmunk (*Tamias speciosus*), Humboldt's flying squirrel (*Glaucomys oregonensis*), and chisel-toothed kangaroo rat (*Dipodomys microps*). Though these range retractions are consistent with expectations from climate change, they may have preceded the surging temperatures and recurrent droughts of the 21st century. Interactions of surrounding urbanization, changing fire regimes, and exotic organisms continue to threaten isolated populations even in wilderness areas.

377:** Global conservation priorities for carnivores: patterns, regions and challenges

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Carnivores are among the most charismatic and yet threatened mammal groups across the globe. Despite many efforts for understanding and reducing threats to these important species, and previous efforts to prioritize globally for their conservation, still systematic geographical approaches are lacking that account for conservation-optimal targets and the challenges for securing such areas. Here we provide an assessment of global patterns of carnivore distribution and conservation, including species richness, threatened and endemic species distribution, the role of protected areas and priority areas for preserving different conservation goals (10-30% distribution); also, we assessed the status of such priority areas identified and assessed the challenges for securing those areas. Of the 240 carnivore species assessed, we found large variation and dominant large range size for all species, with the largest concentration of total richness, threatened and endemic species towards the tropics, and the largest concentration in Asia. Protected areas represent a significant conservation tool for carnivores, but many areas and species are still under-protected. Priority areas for preserving 10, 20 and 30% targets are located mainly in America, Central and Southern Africa, and Asia. Given the current threats for most carnivores globally, conservation action should move from global to national and regional scales, and should improve efficiency and coverage of protected areas to ensure the persistence of this important group in the long run. This research was supported by an Oliver P. Pearson Award awarded to José F. González-Maya in 2018.

378: Testing the Island Rule in sigmodontine rodents *Abrothrix olivacea* and *Oligoryzomys longicaudatus* in Chilean Patagonia

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Islands represent natural scenarios to test the evolution of body size of vertebrate taxa. In mammals, a tendency to insular gigantism and dwarfism is predicted for small and big body size individuals inhabiting the mainland, respectively. This is the "Island Rule" and could be explained in terms of the insular ecological release, immigration selection and resource limitation. *Abrothrix olivacea* and *Oligoryzomys longicaudatus* are small sigmodontine rodents distributed along Chile, south to the southern Patagonia. In the Patagonian range, these species reach nearby islands, setting a promissory scenario to test the island rule. We performed geometric morphometric analyses, digitizing 21 landmarks on the crania of *A. olivacea* (n=62) and *O. longicaudatus* (n=40). Differences due scale, rotation and translation were eliminated performing a Procrustes Fit. Shape variation was assessed through multivariate analyses. Additionally, we calculated the cranial centroid size to evaluate size differences. We observed significant differences between insular and mainland individuals for *A. olivacea*, being the cranium size of this species significantly bigger on islands. This pattern was not that evident for *O. longicaudatus*. Additionally, *A. olivacea* specimens from "Isla Wellington" exhibited a significant bigger body size in contrast to mainland forms. We discussed our results in terms of historical migrations routes of rodents in Patagonia, and through the ecology and evolution of body size of these two sigmodontine rodents.

379:** Environment predicts body size shifts in a young radiation of Australian mammals

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Closely related species that occur across steep environmental gradients often differ in body size, suggesting that many species adapt rapidly to changing environments via body size evolution. Australia encompasses a striking array of biomes, ranging from vast deserts to tropical rain forests. The Australian endemic *Pseudomys* Division (32 species in Muridae: Murinae) has repeatedly colonized arid, monsoon, and temperate mesic biomes over the last five million years. We use a published phylogeny of the *Pseudomys* Division, species occurrence data, species body mass data, and Bayesian phylogenetic multilevel modeling to test whether body size tracks biome occupancy in this radiation. We then model the effect of eight environmental variables on body mass. Across the clade, body size evolution is consistent with Brownian motion. However, at the subclade level, we find strong tendency to increase body size in temperate habitats and decrease in arid regions. Precipitation is strongly correlated with body mass, though several other environmental variables are also correlated. Our results highlight two important findings: first, body size in the *Pseudomys* Division has shifted rapidly with climate through the mid to late Pleistocene, likely due to a suite of environmental variables rather than a single factor; and second, because phylogenies are hierarchical, the level at which we test hypotheses can alter our interpretation of evolutionary processes. This research was supported by a Patton Award awarded to Jonathan Nations in 2017.

380: Systematic revision of *Thomasomys cinereus* (Rodentia: Cricetidae) with the description of a new species

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Thomasomys cinereus is the type species of *Thomasomys*, a rich genus of 44 species distributed along the Andes. Although it was suggested to be a species complex it has not yet been reviewed taxonomically. To accomplish that revision, 348 specimens from 34 localities were examined, and 19 meristic variables were measured. A MANOVA found no significant sexual dimorphism in the largest population ($n = 54$, $p > 0.05$). For geographic analysis, 10 operational groups were delimited using geographic discontinuities and a preliminary analysis of qualitative traits. A covariance matrix of log-transformed data was subjected to principal component analysis. In addition, a phylogenetic analysis based on cytochrome b was performed using *Chilomys instans* as outgroup. A plot of PC1 and PC2 shows two partially overlapping groups; a northern group from Piura, Lambayeque, and Cajamarca and the second group mostly from La Libertad and Cutervo (near the type locality). The molecular phylogeny and differences in some discrete characters concur with the existence of these two groups (genetic distance of 5.5%). This evidence suggests the first group may represent a new species. Apparently, the Huancabamba Depression was not an important barrier or speciation driver for these rodents in contrast to the role of Río Marañón which clearly limits the distribution of *T. cinereus* to the east.

381: Possibilities and pitfalls in documenting range shifts in mammals from the Quaternary to the present

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Large databases of mammal records have the potential to address how mammals will respond to climate change. One approach to address this question is to examine how mammals responded to climatic fluctuations through the Pleistocene and Holocene. These data are found in the FAUNMAP II database, a catalogue of Quaternary mammal fossils from North America. This database was built from published identifications of fossils, some of which go back more than 100 years. Therefore, there is the potential for taxonomic issues associated with the species names in the database. Through the use of geographic information systems, a number of taxonomic problems were discovered, including the possibility that published identifications of species of fossils were not based solely on morphology, but were made using geography to restrict the number of species considered during identification. Our analysis examined over 40 species and found that there was bias in the identification of a wide range of mammals including species of rodents, shrews, deer, and skunks. Given the issues in the identification of these fossils, we explored how climate change affected range shifts at higher taxonomic levels. We found that environmental conditions are not the sole factor influencing the extant distribution of shrew genera. Other ecological

interactions may have a significant effect on mammal distribution and should be considered when assessing the vulnerability of mammalian faunas to climate change.

382: Latitudinal diversity and diversification in mammals

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The global increase in species richness from the poles to the tropics is among the most robust macroecological pattern known today. This latitudinal diversity gradient is well established in many groups of organisms, yet it remains unknown what balance of speciation, extinction, and dispersal processes have combined to produce it. Recent work on the Mammalia species-level tree of life revealed that lineages with the fastest rates of speciation are paradoxically not endemic to the species-dense tropics, implying that lineage turnover has been higher outside than inside the tropics. Herein, we follow up on these surprising results by (i) implementing a mechanistic model of trait-dependent speciation and extinction (GeoHiSSE); and (ii) accounting for uncertainty in the 5911-species phylogeny of mammals. We test for the influence of latitudinal biogeography using a 3-state model (tropical, temperate, or widespread) and newly developed 5-state model with north and south temperate separated. Of the 12 major lineages of mammals tested, we find that two lineages of marsupials show marked increases in speciation associated with tropical environments, as does Muridae (e.g., *Mastomys-Mus*), while chipmunks and squirrels show the opposite pattern of temperate-associated speciation. South American tuco-tucos display the fastest rates of recent diversification in Mammalia, yet are temperate burrowers subjected to repeated allopatric isolation and turnover. Contrary to one process underpinning the latitudinal diversity gradient, our findings imply a complex evolutionary tapestry.

383^E: Agree to disagree; varying estimates and model development with Maxent and different circulation models

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Ecological niche models frequently are used to create expectations for where species may occur, may have occurred, or will occur in geographic space. Studies investigating aspects of model complexity and background data when using Maxent implementations have highlighted the need to evaluate model structure and assumptions. We used climate variables from EcoClimate.org that are trained and estimated for 8 circulation models to ascertain the overall effect of dataset choice on model construction and expectations. We generated separate models under these variable sets and compared geographic estimates of modern, past (last glacial maximum and mid-Holocene), and future (four climate change scenarios) for fifteen species including *Ammospermophilus*, *Blarina*, *Glaucomys*, *Neotoma*, *Ochrotomys*, *Peromyscus*, *Poliocitellus*, and *Reithrodontomys*. Model structure varied by circulation model within species and generally yielded consistent estimates for modern projections, but with varying degrees of similarity in temporal projections. For instance, estimates at last glacial maximum for *R. montanus* were drastically dissimilar, but modern and forecast estimates were consistently similar across circulation models. Alternatively, hindcast and modern estimates for *O. nuttalli* had consistent similarity (albeit poor) values, and forecasts were more dissimilar. Overall, we emphasize the reliance on one circulation model could lead to misleading predictions and expectations. Using multiple datasets representing different circulation models could result in better estimates of potential refugia and will, at worst, better represent uncertainty.

384^{E}: Occupancy dynamics of a climate sensitive mammal along a southern range boundary**

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Climate change has been linked to latitudinal range shifts in multiple species of mammals. Whereas broad distributional shifts have been readily observable across temporal and spatial scales, fine-scale dynamics of these shifts - only observable along range boundaries and during extirpation - have rarely been documented. Moreover, the role of habitat in buffering the effects of climate change and promoting

persistence is poorly understood. To document the role of habitat and winter conditions on occupancy and extirpation, we took advantage of an experimental translocation of snowshoe hares (*Lepus americanus*), a winter-adapted species sensitive to climate change, at a site along the species' southern range boundary. In 2017, 100 hares were released at Sandhill Wildlife Area, Wisconsin (44.3075°N, 90.1303°W) where hares recently became extirpated. To test the role of habitat and climate on persistence of hares along this trailing edge of their range, we used multi-season occupancy models to analyze camera trap data across a four-year period. Hares selected for areas with higher proportions of young aspen and alder, which had important demographic repercussions. Likewise, colonization was best predicted by patch size of aspen-alder, while interspersed habitat types on the landscape was the best predictor of extinction. Understanding the local drivers of climate-induced extinction is central in conservation efforts to promote the persistence of climate sensitive species. This research was supported by an ASM Grant-in-aid awarded to Evan Wilson in 2017.

385^E: Patterns in landscape characteristics surrounding ocelot-vehicle collision sites

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The development of roads has widespread negative impacts on wildlife populations including habitat fragmentation and wildlife-vehicle collisions. Roads can act as artificial boundaries and influence the spatial ecology and population sizes of species of conservation concern. The ocelot (*Leopardus pardalis*) is a federally endangered wild felid found in the Lower Rio Grande Valley (LRGV) of South Texas. Ocelots are habitat specialists requiring $\geq 75\%$ woody canopy cover. This area is one of the fastest growing population centers in the country resulting in rapid urban sprawl and increasing infrastructure development, consequently decreasing available ocelot habitat. Previous research has indicated that vehicle collisions are the highest direct source of mortality for this ocelot population. This study aimed to understand whether land cover spatial structure is related to ocelot road mortalities. Using classified satellite imagery, we examined the amount and distribution of six land cover types surrounding 30 ocelot-vehicle collisions from 1984-2017 at multiple distances from the road. We found road mortality sites consisted of higher percentages of woody cover as well as larger and more aggregated patches of woody cover compared to random road locations. This information will provide conservation planners a better understanding of the landscape features at ocelot road mortality sites and thus can be used to guide the placement of future ocelot crossing structures.

386^E: Defaunation in South American Gran Chaco: richness and distribution of mammals across different land uses

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The Gran Chaco region was historically covered by primary forests and woodlands, alternating with patches of grasslands, but has undergone a profound transformation since the 1990s, experiencing a rapid loss of native forests due to the expansion of agriculture. Currently, this region is a matrix with different land uses. This has had an indirect impact in the native fauna (along with direct impacts like hunting), resulting in extreme reduction of population densities or extinction of species. The aim of our presentation is to characterize the defaunation process of medium and large mammals across different land uses in the southern portion of the Gran Chaco Americano, corresponding to the Northwest of Córdoba province, Argentina. We have installed 10 camera traps (active for 30 days) in five representative sites, in all five land use categories: Primary Forest, Secondary Forest, Selective Clearing, Bushland and Crops (25 study sites: 250 sampling stations), in order to analyze the native mammal assemblage greater than 1 kg. In three years of field work we were able to detect the presence of 95% of the native mammals recorded in this region. We will present the findings of updated species distribution, richness and conservation status of Chacoan mammals, plus an occupancy analysis of 10 species. Mammals are facing a critical situation, efforts to preserve remnants of native forest in Chaco region need to be increased.

387: Framing the post-2020 global biodiversity agenda: improving mammalian conservation through restorative actions

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The Aichi Biodiversity Targets (2011-2020) have guided the Parties to the UN Convention on Biological Diversity (CBD) in actions to improve outcomes for human wellbeing and biodiversity. These targets address a number of factors affecting mammalian conservation including marine and terrestrial protected areas, prevention of habitat loss, and restoration of degraded terrestrial ecosystems. Success in achieving the Aichi Targets has been mixed, however, and this is particularly true for targets that directly invoke ecosystem restoration (5, 14, and 15). To further progress, the CBD and others have created tools to develop capacity for assessment and implementation of restorative activities. Consideration of how the Aichi Targets might be revised for 2021-2030 as an overarching framework has already begun. The need is clear for broader discussion of the benefits of a range of restorative activities to regain ecosystem structure and function, ensure landscape connectivity, and enhance the effectiveness of protected areas. The ambitions of the Aichi Targets must be scaled-up. Current Targets 14 and 15, for example, largely consider conservation and restoration as a means to provide ecosystem services and carbon sequestration, respectively. We suggest integration of the current framework for Forest and Landscape Restoration as one approach for expanding the scope of terrestrial restoration efforts. Mammalian conservation, while not considered directly in framing the post-2020 biodiversity agenda, will be greatly affected by the new targets.

388: Estimating bat fatalities at a Texas wind energy facility: implications transcending the U.S.-Mexico border

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Wind energy development has long been known to cause bat fatalities. Despite emphasis on understanding and reducing these impacts, there is a paucity of publicly available data in the Southwest region of the U.S. and Northern Mexico. We conducted a full year (March 2017-March 2018) of post-construction fatality monitoring at a wind energy facility in south Texas near the U.S.-Mexico border. In order to estimate bat fatalities, we established 100 x 100 m radius search plots at eight randomly selected turbines and searched the roads and pads at an additional 92 turbines. We conducted weekly searches from spring through fall and bimonthly during winter. We used a newly developed analysis known as GenEst (Generalized Estimator) to estimate fatalities corrected for searcher efficiency, carcass removal, and density weighted proportion of area searched. We found 238 bats, the majority of which were *Tadarida brasiliensis* at 76%. The corrected fatality estimates were 16 bats/MW/year (95% CI: 12–28 bat/MW/year). Species composition at our site is similar to that of northern Mexico, an area of expanding wind energy development with no published studies. These results might provide insights on impacts to bats in this region. Post-construction fatality monitoring data are rarely published, so making these data publicly available is of the utmost importance towards understanding impacts, and ultimately improving impact reduction strategies.

389^{E}: No impact of hunting concession management on occupancy of critically endangered lions in West Africa**

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Spatially varied resources and threats make conservation of African lions (*Panthera leo*) difficult in multi-management protected areas. Hunting concessions (HCs) often have higher revenues and smaller areas compared to national parks (NPs), allowing for high quality habitat and stronger regulation of illegal activity. Given this combination of benefits and risks, heterogeneity in habitat quality and management may result in differential space use for lions that influences the success of conservation efforts. We conducted the first camera survey of lions in the W-Arly-Pendjari (WAP) protected area, a 26,620-km² complex of national parks and hunting concessions. We combined occupancy modeling, which accounts for imperfect detection, and structural equation modeling to disentangle the relative effect sizes (β) of the variables influencing lion space use. Lion occupancy (ψ) did not show a response to management type ($\psi_{NP}=0.56$; $\psi_{HC}=0.58$), exhibiting no spatial avoidance of hunting concessions. Drinking water availability and diverse habitat were higher in hunting concessions and may indicate better habitat quality than in national parks that is negating mortality risks from trophy hunting. Lion occupancy was strongly influenced by prey availability in both management types ($\beta_{NP}=0.346$; $\beta_{HC}=0.264$). Prey responses to drinking water availability, edge effects, and fire pressure provide insight into management interventions to indirectly influence lion occupancy. We highlight the need for quantification of lion mortality between management types to understand true risks for lions across the landscape.

390: Inbreeding levels and bottlenecks of Stellar sea lions (*Eumetopias jubatus*) in the Gulf of Alaska

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Stellar sea lions (*Eumetopias jubatus*) experienced significant (>80%) range-wide population declines beginning in the 1970s eventually leading to their listing as threatened in 1990 under the ESA. Based on mitochondrial information, the species was separated into eastern and western distinct population segments along an east-west division at 144° W. By the 1990s, the Eastern DPS was steadily increasing while the Western DPS continued to decline and was uplisted to endangered in 1997. The Eastern DPS rebounded and was delisted in 2013. Continued population declines occurred in the Western DPS throughout the 1990s, though population trajectories continue to vary across the geographic range. The cause for the decline and slow recovery in the western DPS is not entirely understood, but likely multiple factors are restricting population recovery. We analyzed 11 microsatellite loci from 82 scat samples from three haulouts in the Gulf of Alaska. We tested for elevated inbreeding levels (F_{is}) and evidence of a genetic bottleneck under different mutation models in program Bottleneck as a result of a historic population crash. We found significant inbreeding at 66% of our sites as well as evidence of a bottleneck. This study demonstrated the feasibility of scats as a source of Steller sea lion DNA, and highlighted a high inbreeding level in sea lions that have not previously been studied genetically.

391: Landscape connectivity for large carnivores in northwest México and southern United States**

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Large carnivores are key species that regulate ecosystem processes through a cascade effect, promoting biodiversity stability and richness in the communities they live. However, habitat encroachment due to human activities has impacted ecosystems causing habitat loss and reducing connectivity, thus compromising species persistence. The main goal of this project was to identify areas that favor landscape connectivity for three large carnivores: cougar (*Puma concolor*), black bear (*Ursus americanus*) and Mexican gray wolf (*Canis lupus baileyi*) in northwestern Mexico and southern United States. We performed a habitat suitability analysis combining niche modeling and land cover information to identify the remaining habitat and identify the largest habitat high-quality patches to be connected. Finally, we developed a connectivity analysis to identify smaller suitable habitat patches within connecting paths to evaluate their contribution as stepping-stones. The results show that there are six large high-quality habitat patches where the three species converge, two in the United States and four in Mexico. Likewise, we found a biological corridor that crosses from the Sierra Madre Occidental in Mexico to the Gila and the Apache National Parks

in the United States and smaller key areas that facilitate connectivity among the largest patches. Monitoring of species in corridors is an important next step to determine their role in promoting connectivity in fragmented landscape. This research was supported by a Latin American Student Field Research award awarded to Zaira Y. González Saucedo in 2018.

392: Molecular phylogenetics and species limits of the African horseshoe bats (Chiroptera: Rhinolophidae)

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Recognized species of the Old World bat genus *Rhinolophus* have grown from 77 to 106 over the past 15 years, but knowledge of their interrelationships has not grown commensurately. Species limits and phylogenetic relationships of *Rhinolophus* remain problematic due to poor sampling and to repeated instances of mitochondrial-nuclear discordance. Recent surveys in East Africa and neighboring regions offer a new basis for understanding the group's evolutionary history. We investigated phylogenetic relationships and intraspecific genetic variation in the Afrotropical-Palearctic clade of *Rhinolophus* using mitochondrial cyt-b and four independent and informative nuclear introns for 423 individuals representing 24 of the 33 currently recognized Afrotropical species. The widespread occurrence of mitonuclear discordance in *Rhinolophus* was addressed by inferring concatenated and species-tree phylogenies using only nuclear data. Well resolved mitochondrial, concatenated nuclear, and species trees revealed phylogenetic relationships and population structure of the Afrotropical species and species groups. Multiple well-supported and deeply divergent lineages were resolved in each of the six African *Rhinolophus* species groups analyzed, suggesting as many as 12 undescribed cryptic species, including several instances of sympatry among close relatives. Coalescent lineage delimitation offered support for new undescribed lineages in four of the six African groups. Conversely, as many as five currently recognized species appear to be invalid based on the genetic analyses. Integrative taxonomy based on morphology and vocalizations is underway to resolve the nomenclatural issues.

393: An exploratory expedition to Peru: searching for one and revealing several new species of mammals

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As part of an effort to construct a comprehensive molecular phylogeny of Neotropical tree squirrels, we conducted an exploratory expedition to Rio Abiseo National Park (RANP), a World Heritage Site located in the department of San Martín along the Peruvian eastern slope of the Andes. The main objective was to document and sample small mammals, focusing on an allegedly new species of squirrel, *Syntheosciurus* sp., known from a few specimens collected almost three decades ago in RANP. *Syntheosciurus* is a poorly known genus with a single species formally recognized, *S. brochus*, from montane forests of Costa Rica and Panama. We conducted 15 days of sampling in montane forest sites at 2700-2900 masl, and collected 15 species of small mammals including several that are still unnamed or represent new records to science. We also documented *Syntheosciurus* sp. for the first time with photographs in its natural habitat. Additionally, we uncovered museum specimens of *Syntheosciurus* sp. in the Museo de Historia Natural de Lima and obtained ancient DNA from skin samples to infer its phylogenetic relationships with mitogenomic data. Surprisingly, our phylogenetic analysis recovered this species nested within the Amazonian lowland species of *Microsciurus* and not closely related to *Syntheosciurus brochus*, which is incongruent with the last taxonomic arrangement of Neotropical squirrels. Our results suggest that this is possibly an unnamed taxon that requires taxonomic reevaluation.

394^{E,HTA}: Detailing tail-less bats, species limits and phylogenetic relationships in *Anoura* Gray 1838

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Based on classical and geometric morphometrics approaches, the current taxonomic arrangement for the Neotropical nectarivorous bat genus *Anoura* Gray 1838 includes 10 species; however, previous taxonomic revisions did not include all closely related species in the genus. Phylogenetic studies including *Anoura* have focused on its position within the Glossophaginae and on broader understanding of the evolution of Noctilionoidea. To understand morphology-based species limits and the phylogenetic relationships within *Anoura*, we apply a morphological approach using Gaussian Mixture Model clustering and phylogenomics. Our morphometric analyses include 12 craniodental and 11 external morphological measurements commonly used to describe or diagnose *Anoura* species along with elliptical Fourier descriptors of the shape of the last upper premolar (P4) in the *A. geoffroyi* species complex, used to understand morphological gaps between *A. geoffroyi* and *A. latidens*. Finally, we use phylogenomic analyses of ultraconserved elements to infer species trees for the genus under multispecies coalescent models. We found that morphometric measurements do not support a separation within large or small *Anoura* species; however, P4 shape distinguishes *A. geoffroyi* from *A. latidens*. Phylogenetic analyses obtained four main well-supported clades supporting the monophyly of *Lonchoglossa*, the monotypic status of *A. caudifer*, the invalidation of *A. aequatoris* and *A. peruana* as independent species and polyphyletic patterns indicating putative hybridization/introgression events.

395^E: The current understanding of eulipotyphlan taxonomy and biogeography

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Eulipotyphla contains four families (Solenodontidae, Talpidae, Erinaceidae, and Soricidae) that taxonomists have previously allocated to 5 different orders. These species include a variety of primarily insectivorous small mammals found in most regions except for parts of South America and Australasia. There are currently 58 recognized genera in Eulipotyphla (531 species), making it the third most speciose mammalian order after rodents and bats. Although shrew-like morphologies are often considered primitive for mammals, eulipotyphlans express a number of unique adaptations, such as spines, complex and specialized dentitions, and venom in some species. Soricidae is the most speciose and generalist family and is represented by a large and complex radiation, spreading across much of the world. The other three eulipotyphlan families contain fewer species, especially Solenodontidae with two living species of Caribbean solenodons. Talpidae and Erinaceidae are primarily restricted to Holarctic and Afro-Eurasian regions, respectively. New species are named every year within Eulipotyphla and there are still many knowledge gaps to be addressed within the group. Here I assess the current systematic and biogeographic information for these taxa with the purpose of identifying future research questions in this globally important mammalian order.

396^{}: Further assessment of the Genus *Neodon* and the description of a new species from Nepal**

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Recent molecular systematic studies of arvicoline voles from Central Asia suggest the inclusion of *Phaiomys leucurus*, *Microtus clarkei*, and *Lasiopodomys fuscus* into *Neodon* and moving *Neodon juldaschi* into *Microtus (Blanfordimys)*. In addition, three new species of *Neodon* (*N. linzhiensis*, *N. medogensis*, and *N. nyalamensis*) have recently been described from Tibet. Analyses of concatenated mitochondrial (*Cytb*, *COI*) and nuclear (*Ghr*, *Rbp3*) genes recovered *Neodon* as a well-supported monophyletic clade including all the recently described and relocated species. *Neodon* specimens sampled from western Nepal (currently classified as *N. sikimensis*) were recovered sister to *N. sikimensis*, however analyses conducted exclusively with mitochondrial loci failed to support this relationship. Kimura-2-parameter distance between *Neodon* from western Nepal compared to *N. sikimensis* (K2P=13.1) was equivalent to genetic distances observed

between recognized species of this genus. Specimens of *N. sikimensis* from eastern Nepal and India and *Neodon* from western Nepal housed at the Field Museum of Natural History were examined for 12 craniodental characters, four external field measurements, occlusal patterns of the first lower (m1) and third upper (M3) molars. *Neodon* from western Nepal were generally smaller, had simpler molar occlusal patterns, and significantly differed from *N. sikimensis* in 10 out of 16 characters measured. Together the results of the molecular and morphological analyses indicate that *Neodon* from western Nepal is distinct under phylogenetic, genetic and morphospecies concepts. This research was supported by a Grant-in-Aid of Research awarded to Nelish Pradhan in 2013.

397: Global arvicoline rodent phylogenetics: insights into diversification and biogeography

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Molecular data can provide insight into the phylogenetic relationships of speciose clades for which morphology alone cannot elucidate species boundaries. Arvicoline rodents (voles, lemmings, and muskrats) are an exemplar of this. Past studies using molecular data focused on smaller groups (i.e., *Microtus*) or specific geographic ranges but none have attempted a comprehensive global arvicoline phylogeny using modern Bayesian phylogenetic methodologies. Here we present the results of such an undertaking. This analysis includes seven genes (nuclear and mitochondrial) and 136 (97%) of the globally recognized arvicoline species. Using the tremendous fossil record for this group we produce a time-calibrated phylogeny that allows us to test hypotheses of paleobiogeography. These sorts of questions are important, because paleontologists historically relied upon purported arvicoline rodent immigration events from Eurasia to North America to define North American Land Mammal Ages. Our results indicate that such models are not as simple as was interpreted in the past. Unsurprisingly, the molecular diversification of some of the North American groups predates their fossil record. Dental morphological features that have been deemed useful for species recognition, may not follow hypothesized morphological phylogenetic patterns; instead, our data suggest a tremendous amount of homoplasy within Arvicolinae. These results pose important challenges for paleontologists who rely upon dental remains to establish biochronological correlations and paleobiogeographic models of dispersal.

398: Mitochondrial DNA and UCEs illuminate the diversity of southern African gerbils

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According to the most recent checklist for mammals, the rodent genus *Gerbilliscus* (Thomas, 1897) contains 12 species that are restricted to sub-Saharan Africa. Previous molecular phylogenies have estimated that there is support for four divergent clades that correspond to geography: 1) eastern, 2) western, 3) and southern African clades, and 4) a fourth clade consists of the southern African endemic genus *Gerbillurus*, which falls out sister to the western + southern *Gerbilliscus* clades, rendering the genus *Gerbilliscus* paraphyletic. Within the southern clade, six species currently are recognized; however, previous molecular phylogenies have included only a few individuals representing *G. afra*, *G. brantsii*, and *G. leucogaster*. Here, we sequenced the mitochondrial cytochrome-b gene for >200 individuals and thousands of nuclear loci (Ultraconserved Elements) for subset of individuals in order to estimate a species tree for the southern African clade. We recovered at least 12 species within the southern African clade, doubling the currently recognized diversity. Additionally, by incorporating museum specimens (including type material), we were able to revise the nomenclature for this group by elevating historical names.

399: Phylogenomic estimation of species boundaries in the spotted skunks (Carnivora, Mephitidae, *Spilogale*)

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Taxonomic boundaries in spotted skunks (*Spilogale*) have varied dramatically over the past century, with as many as 10 and as few as 1 species assigned to the genus. Recent conservation concerns, including the potential listing of the plains spotted skunk, *S. putorius interrupta* as endangered under the ESA, have reignited interests in species boundaries for this genus of small carnivore. We extracted DNA from both modern and historic samples of 47 individual spotted skunks representing nearly all subspecies of the 4 currently recognized species. Mitochondrial genomes of 28 individuals (11 historic + 17 modern samples) and ultraconserved elements (UCEs) for 27 individuals (9 historic + 18 modern) were used to estimate phylogenies. Phylogenomic results indicate the presence of five distinct genetic lineages for both mitochondrial and nuclear genomes. These results support the evolutionary distinctiveness of the four currently recognized species of *Spilogale*, including *S. angustifrons*, *S. gracilis*, *S. putorius*, and *S. pygmaea*, although there appears to be two unique lineages represented within *S. putorius*, corresponding to *S. p. interrupta* and *S. p. putorius/S. p. ambarvalis*. These results are consistent with recent microsatellite work which supported the recognition of the plains spotted skunk, *S. p. interrupta* as a distinct species.

400^E: Latitudinal diversity gradients of parasites of cricetid rodents: importance of climate and host-associated factors

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The latitudinal diversity gradient (LDG), or the trend of higher species richness at lower latitudes, has been well documented in multiple groups of free-living organisms. Investigations of the LDG in parasitic organisms are comparatively scarce. I investigated latitudinal patterns of parasite diversity by conducting two novel investigations of the LDG of helminths (parasitic nematodes, trematodes, and cestodes) of cricetid rodents (Rodentia: Cricetidae). I collected host-parasite records from published surveys and from 300 rodents I sampled across six field sites along a latitudinal gradient in North America. I tested for the presence and direction of a latitudinal pattern of helminth richness at two geographic scales and examined four climatic factors (mean annual temperature, annual precipitation, annual temperature range, and annual precipitation range) and two host-associated variables (host body mass and host diet) as potential correlates of parasite richness. The analyses were performed with and without phylogenetic comparative methods, as necessary. Latitudinal diversity patterns differ among the three helminth taxa but are generally similar across geographic scales. Relationships between helminth richness and the climatic and host-associated variables are also variable between the helminth groups, suggesting taxon-specific responses to the drivers of diversity patterns. This study supports a complex association between parasite richness and latitude, indicating the importance of including both environmental and host-associated factors when trying to understand diversity gradients in parasitic organisms.

401^E: An itch to know: the relationship between a rodent community and ectoparasite abundance

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The salt marsh harvest mouse (*Reithrodontomys raviventris*) is an endangered wetland specialist, endemic to the salt and brackish marshes of the San Francisco Bay Estuary. However, habitat modifications associated with urbanization, including the diking of tidal wetlands into seasonal ponds, likely influence interspecific dynamics between the salt marsh harvest mouse and both native and non-native rodent conspecifics. Effects could include changes in competition for resources and apparent competition via spillover of disease. Ectoparasites can serve as an important indicator of the potential for vector-borne disease spillover. To understand if changes in rodent community composition affect salt marsh harvest mouse ectoparasite loads, and therefore the potential for vector-borne disease exposure, we collected and identified 130 fleas and 40 ticks from 650 rodents trapped year-round at eight sites in Suisun Marsh, from April 2018 to April 2019. Host rodents included the northern subspecies of the salt marsh harvest mouse (*R. raviventris halicoetes*), western harvest mouse (*R. megalotis*), house mouse (*Mus musculus*), and black rat (*Rattus rattus*). We are investigating relationships among ectoparasites (species and loads), rodent

species (diversity and density), and seasonality. Salt marsh harvest mouse recovery often is singularly focused on habitat restoration; this study will allow recovery efforts to more fully account for potential disease threats.

402^E: Population abundance of *Cryptosporidium* spp. and *Peromyscus leucopus* along a 70-km urban-rural gradient

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Within a natural system, selective pressures on a host-parasite complex are driven by surrounding environments, particularly those experiencing excessive anthropogenic influences. This study examines how variation in land use patterns affects the population of white-footed mice (*Peromyscus leucopus*) and their ability to serve as a reservoir-host to a zoonotic pathogen (*Cryptosporidium*). To estimate host abundance, we live-trapped 28 oak woodland preserves among Urban, Suburban, Agriculture, and Natural Macrosite regions along a 70-km gradient in Chicago, Illinois, USA. Quantitative PCR TaqMan assay was used to estimate parasite abundance from host fecal samples. We demonstrate that land type use has a significant effect on the population of the reservoir-host and its enteric parasite. The host-parasite abundance within three of four land cover regions fit a non-linear sigmoidal response; there was no relationship among host-parasite abundance in the Natural Macrosite. The high mouse abundance found in Urban preserves and the high parasite abundance within Suburban preserves suggest anthropogenic stressors on this host-parasite system. The high abundance of *Cryptosporidium* within the Suburban landscapes might indicate a hotspot for disease outbreaks, as the probability of disease spillover increases in regions with greater degree of shared space among wild and domesticated animals and humans. The low abundance of parasite load within the Natural Macrosite could be attributed to increased species richness afforded by large contiguous preserves together with minimal anthropogenic influences.

403^E: Infection prevalence and severity of skunk cranial worm (*Skrjabinogylus chitwoodorum*) in spotted skunks (*Spilogale* spp.)

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Eastern spotted skunks (*Spilogale putorius*) and western spotted skunks (*S. gracilis*) serve as definitive hosts for skunk cranial worm (*Skrjabinogylus chitwoodorum*), a metastrongylid nematode that spends its adult stage inhabiting the host cranium. Skunk cranial worm can cause severe damage to the skull in spotted skunks, and this damage is identifiable in preserved specimens. We used 578 spotted skunk skull specimens from six mammal collections to identify patterns in prevalence and severity of skunk cranial worm in spotted skunks across the U.S. and since the late 1800s. We tested for effects of specimen genetic clade, collection year, precipitation, and sex on infection and severity rates. We hypothesized that the midwestern genetic clade (*S. putorius interrupta*), which experienced a range-wide population decline in the mid-1900s, would experience the highest infection and severity rates. We expected precipitation, but not sex to influence infection and severity. Our top models indicated that specimen genetic clade, precipitation in the year prior to specimen collection, and the year prior to specimen collection best predicted prevalence and severity of skunk cranial worm. We suggest the positive association with precipitation is a result of local availability of gastropods, the obligate intermediate host for skunk cranial worm.

404^{E}: Temporal variation in arthropod-vectored pathogen prevalence in bats**

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Emerging infectious diseases in wildlife are a conservation concern that have been largely overlooked except in cases of mass animal mortality or those relevant to human health. As the risk of pathogen emergence in wildlife is increasing through greater human alteration of habitat, we must be better prepared to address wild mammalian epidemics by increasing our knowledge of disease ecology of non-emergent pathogens. By studying the transmission dynamics of arthropod-vectored bat pathogens prior to emergence of a disease, we can identify factors of the host-arthropod parasite system that contribute to disease

prevalence. To examine variation in prevalence of bat pathogens, we sampled blood and ectoparasites from a bat community in Orange Walk, Belize once a year for three years. We estimated prevalence of the pathogen *Polychromophilus* and *Bartonella* in 5 species of bats that are representative of a diversity of feeding niches and roost preferences. We also examined prevalence of these pathogens in bat flies associated with sampled bats. Bat flies, obligate blood-feeding parasites of bats, are the primary vector of *Polychromophilus* and may vector *Bartonella*. Preliminary results indicate that *Bartonella* prevalence is extremely high in this bat community across all sampling years, while *Polychromophilus* prevalence is low, corresponding with low prevalence in bat flies. Little research is available on disease ecology of bat pathogens, and this study provides valuable insight into the ways arthropod-vector pathogens vary through time. This research was supported by a Grants-in-Aid awarded to Kelly Speer in 2018.

405^E: The fox tapeworm in North America

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The fox tapeworm, *Echinococcus multilocularis* (EM; Leuckart 1863), is a parasite whose life cycle depends of the trophic interactions of canids and rodents. This species is the causative agent of human alveolar echinococcosis, which usually is fatal if untreated. Despite the public health importance of this parasite and the fact that it appears to be expanding its range in North America, there is insufficient knowledge of the distribution and ecology of the species on the continent. Here we report new records of EM outside its known distribution in the Nearctic and present a distribution model for EM using a new way of including mammalian host assemblage information. Our approach consists of including as predictor variables, spatial layers describing the proportion of potential intermediate and definitive hosts comprising rodent and carnivore species assemblages, respectively. We obtained a robust model of EM distribution, with an estimated distribution of suitable area for the parasite in North America comprising approximately 12% of the continent and including areas outside of the known range of the species such as the Appalachian Mountains. This model is a quantitative distribution hypothesis that could be used to guide future surveys. Also, because of the indicated increase in performance of the model when host-community-assemblage data were included, it appears that this approach may enable an increase in predictive capability of models concerning parasites with complex life-history patterns.

406: Twenty-first century conservation

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Mammal diversity is under drastic pressure from various direct impacts from human activity as well as many indirect impacts from land use change to climate change. A major international effort is needed to address the pressures. What might be priorities for conservation to address these combined drivers?

407: Our planet, our health

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Today we live longer and more prosperous lives than ever before, as a species we have made huge advances to create conditions for better health for billions of people, however this progress is taking a heavy toll on the planet's natural systems. I will explore the links and interdependencies between our health and the health of our planet with particular reference to understanding how rapid global environmental change impacts the emergence and spread of high impact infectious diseases like Ebola or SARS. I will discuss how recent advances in the resolution and coverage of remote-sensing satellite data and cutting-edge machine-learning algorithms open up the possibilities of developing global early warning systems to prevent and manage future epidemics.

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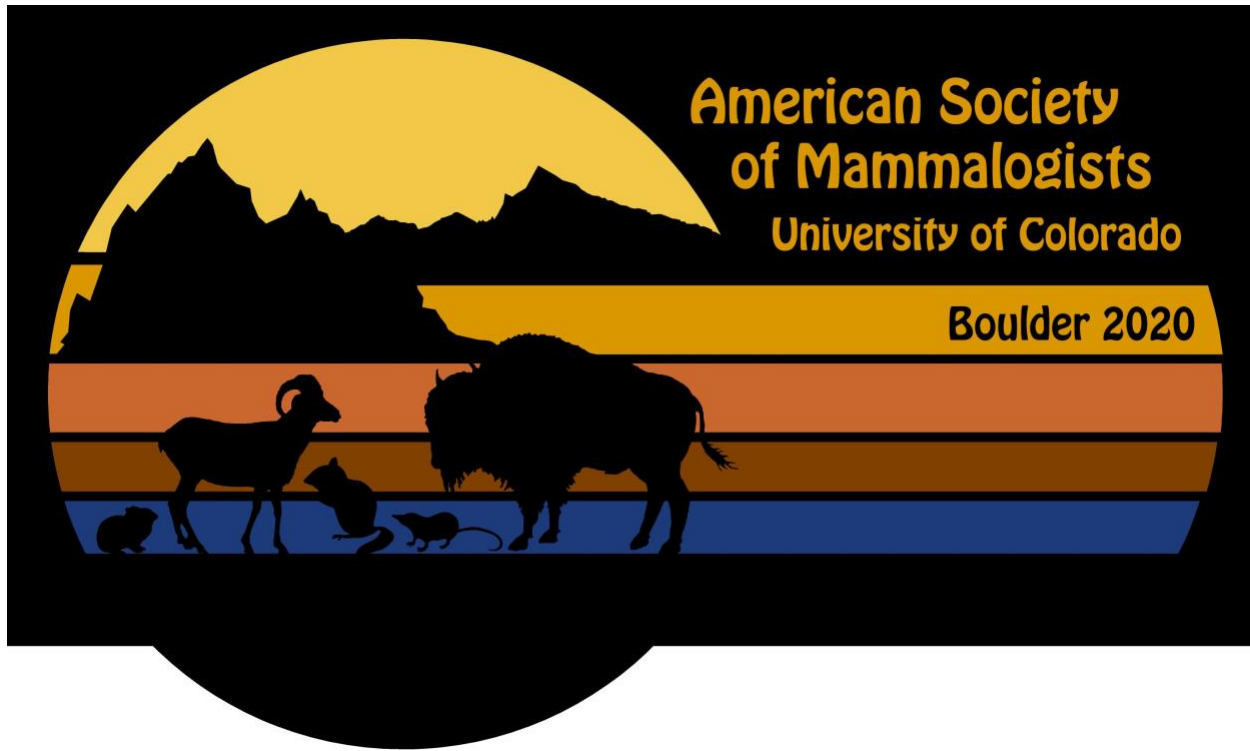
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**100TH ANNUAL MEETING OF THE
AMERICAN SOCIETY OF MAMMALOGISTS**



Please join us 5 to 9 June 2020 in Boulder, Colorado for the 100th Annual Meeting of the American Society of Mammalogists. The conference will be held on the campus of the University of Colorado, located at the foothills of the Rocky Mountains. Learn about the latest advances in the study of mammals and interact with researchers and educators specializing in these fascinating animals. Come celebrate this important milestone in modern mammalogy and enjoy the picturesque views of the Flatirons from the CU campus!

The scientific program will include contributed oral and poster presentations as well as symposia, plenary speakers, and workshops. In addition, the program will include contributions from the Society for the Study of Mammalian Evolution and the North American Pika Consortium. A full social agenda also is planned including fieldtrips to local attractions, the opening social at the UC-Boulder campus, the annual Run-for-Research, the picnic on the Norlin Quad Lawn, and closing social and awards ceremony at Folsom Field. On-campus housing and hotel blocks will be made available for meeting attendees. Detailed conference and registration information will be made available on the conference website (www.mammalmeetings.org).

For more information about the 2020 meeting, contact the program director, Cody Thompson (mammal.meetings@gmail.com); local host, Christy McCain (christy.mccain@colorado.edu); or meeting planner, Kerrell Dunsmore (kerrell@thenextgreatevent.com).

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