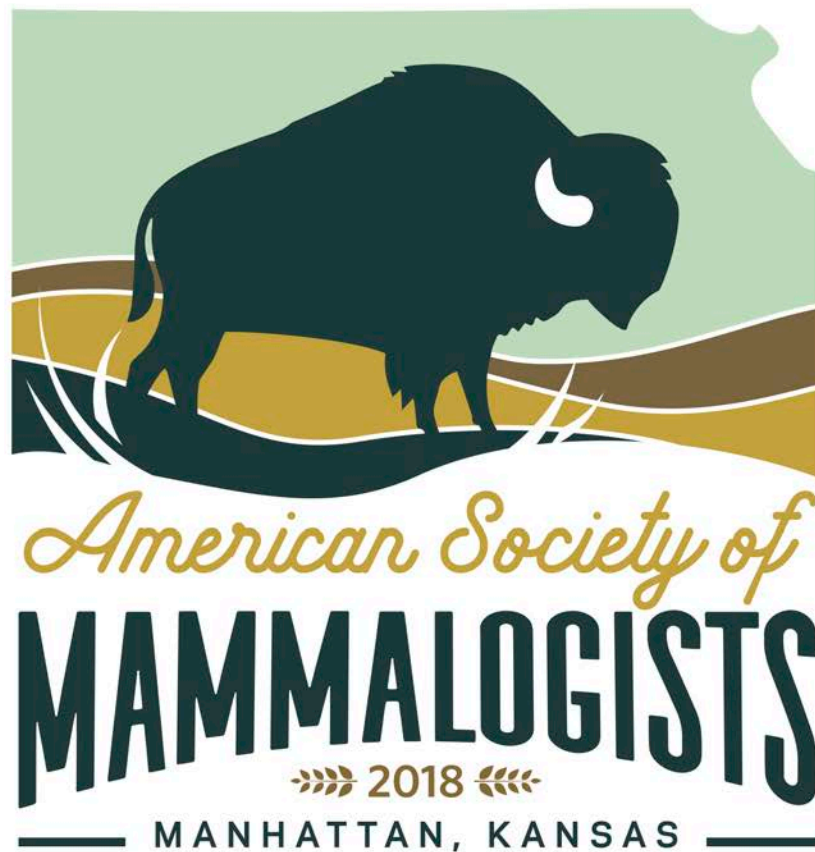


**98TH ANNUAL MEETING
OF THE
AMERICAN SOCIETY OF MAMMALOGISTS
25-29 JUNE 2018
KANSAS STATE UNIVERSITY
-MANHATTAN, KANSAS-**



ABSTRACT BOOK

The 2018 American Society of Mammalogists Annual Meeting logo was designed by Hayley Ahlers. It features the American bison (*Bison bison*), the national mammal of the United States of America, overlaid on the state of Kansas.

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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 who 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 6 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 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 98th annual meeting of the American Society of Mammalogists!

As we return to Manhattan for our annual meeting this summer, I think back to when we last met there in 1991. The Konza Prairie and the Flint Hills provided a gorgeous backdrop for our meeting and I look forward to returning. Our Program Committee and Local Hosts have made sure that we will see the Konza site again, so old and new members alike will have an opportunity to experience this wonderful environment. Judging from registration and abstract submissions, our members are certainly eager to visit, so whether you are a long-term member or have just joined, you are sure to find talks of interest about species you know well and about those with which you just becoming familiar. Perhaps even more important, you can establish and deepen friendships with colleagues who share your interests.

A look at our program shows content covering all aspects of mammalogy. You will find contributed papers arranged in topical technical sessions; one symposium that covers the breadth of the Cenozoic era and a second on major issues in bat conservation; workshops on holistic specimen collection, biological applications for UAVs, and on new software for modelling species niches and distributions, and then we have two additional workshops geared specifically for students and early career mammalogists—one on non-academic careers for mammalogists, and a second on interviewing strategies. Our first plenary session showcases work by recipients of our student awards and the second plenary gives recipients of our senior a platform to address the membership. We have two poster sessions designed to facilitate one-on-one interactions, and we end the scientific presentation components of our meeting with a capstone presentation on carnivores across the ages.

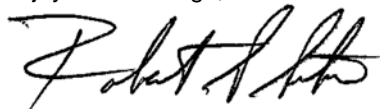
Keeping abreast of new advances in mammalogy brings us to the meeting, but I will remind attendees that ours is a working society and members have responsibilities. For example, you are responsible for important decision regarding our governance of our organization. Your vote matters so I urge you to attend our two Member's Meeting to participate in these important decision-making events. Members have an additional opportunity to participate in ASM work by joining one of our committees. These committees are active throughout the year, so if you have a particular interest in the focus of one of these, I encourage you to introduce yourself to the chair or other committee members.

Yes, the work of mammalogy is hard and appears never-ending, but all work and no play would never fly at an ASM meeting, so we have sprinkled in plenty of opportunities for socializing. These include the various socials, our picnic on the Konza Prairie, an auction, the Run for Research, a student mixer, mammal crawl, and a karaoke contest that surely will attract the attention of talent scouts from Hollywood.

I can say with absolute certainty that ours is an organization that welcomes new members and new ideas and encourages participation and interactions among all attendees. The only prerequisites are an interest in mammals and a willingness to walk up and engage individuals who share these same interests in conversation. For those of you who are new members or are attending your first meeting, please make the most of this opportunity to meet fellow mammalogists, share in the latest findings, and learn about upcoming opportunities. Indeed, for many of us, the camaraderie at these meetings makes it as much a reunion of an extended family as an opportunity to stay current on great science, so I welcome you to the reunion!

I thank you all for attending 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,



Robert Sikes
President, American Society of Mammalogists

ACKNOWLEDGEMENTS

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ABSTRACTS

1^{HTA}: Applying island biogeography to small mammals in the Ozark glades while accounting for imperfect detection

Emily M. Beasley* and Sean P. Maher

Department of Biology, Missouri State University, Springfield, MO 65807 USA

Island Biogeography Theory (IBT) explains large-scale ecological patterns among islands and habitat patches. IBT predicts the number of species per habitat patch differs as a function of area and isolation as a result of local colonization and extinction. Accurate richness estimates are essential for application of IBT, but differences species detectability can bias empirical data sets. Hierarchical community models correct for imperfect detection by leveraging information from across the community to estimate species-specific occupancy and detection. Using the Ozark glades as our model system, we constructed a hierarchical community model to 1) estimate site-level and regional species richness while correcting for detection error, and 2) determine environmental covariates driving occupancy. I predict that species richness will increase with patch area; however, due to spill-over colonization from the matrix, isolation will not have a significant effect. Patch shape will also affect occupancy, but these effects will vary due to differences in life history of the species in the community. We sampled 16 glades in southwest Missouri in summer 2016-2017 and quantified mammal community structure therein. The detected species pool included *Reithrodontomys fulvescens*, *Peromyscus attwateri*, *P. leucopus*, *P. maniculatus*, *Sigmodon hispidus*, *Neotoma floridana*, *Tamias striatus*, and *Sylvilagus floridanus*. The model yielded a regional estimate of 8.6 species. Species richness increased with patch area but not isolation, and effects of shape varied between species in the community.

2^{E,HTA}: Does the social environment matter to solitary animals? Fitness benefits of familiarity in red squirrels**

Erin R. Siracusa*, Stan Boutin, Murray M. Humphries, David W. Coltman, Ben Dantzer, Jeffrey E. Lane, and Andrew G. McAdam

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An important question in evolutionary biology is how conflict between interacting conspecifics can be resolved, allowing the evolution of various forms of stable social organization. In group-living species, social bonds among group members help to mitigate conflict and enhance fitness. Similarly, long-term social relationships in solitary, territorial species may help to minimize conflict between neighbors, though the fitness benefits of these social relationships are poorly understood. In this study, we used 22 years of data from a population of territorial North American red squirrels (*Tamiasciurus hudsonicus*) to assess how familiarity with neighbors affected the reproductive success and survival of individuals. We also modeled how kinship influenced fitness, to determine the importance of mutualistic interactions relative to kin-selection. We found that familiarity with neighbors had substantial benefits for survival, and increased both the number of pups sired and the number of pups recruited annually. These effects were particularly pronounced in the 'senescent' period (i.e. squirrels aged 4 and older) suggesting that familiarity may play an important role in buffering squirrels against effects of age-related declines. Relatedness among territorial neighbors was not an important driver of survival or reproductive success. This study is among the first to show that familiar relationships among territorial neighbors can have direct fitness benefits. Mutually beneficial interactions among unrelated individuals may therefore play an important role in the evolution of social systems. This research was supported by an ASM Grant-in-Aid of Research awarded to Erin Siracusa in 2014 and 2016.

3^{E,HTA}: Individual based modeling of an endangered carnivore can be simultaneously pragmatic and paradigmatic

Casey C. Day*, Patrick A. Zollner, Jonathan H. Gilbert, and Nicholas P. McCann

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It is generally accepted that evaluations of functional landscape connectivity should go beyond structural landscape configuration to account for factors such as animal behavior and dispersal costs. Individual-based models of animal movement that incorporate animal behavior and adaptive decision-making in real time can facilitate our understanding of such integration. We used the individual-based model (IBM) framework SEARCH to simulate the dispersal of translocated American martens (*Martes americana*). Our best model matched all dispersal patterns except for time spent dispersing. We found support for the hypothesis that a time-limited disperser should be willing to accept lower quality habitat over time as well as for an initial 2-week exploratory phase prior to home range establishment. Next, we applied this calibrated simulation to a new landscape where we evaluated how mortality, land use change, and asymmetrical landscape configuration affected population connectivity. Results indicated that mortality had the greatest impact on the ability of martens to traverse the landscape and establish a home range. Land use change and landscape configuration also affected functional landscape connectivity, primarily when mortality probability was set to zero and only for the subset of individuals that traveled furthest. Interestingly, dispersal metrics displayed different relationships with these factors than did functional landscape connectivity. Our IBM was “pragmatic” in addressing management needs for an endangered species and “paradigmatic” by explicitly testing theories of dispersal behavior.

4^{E,HTA}: Immunogenetics of mating behavior in *Peromyscus*: a genomic approach**

Jesyka Meléndez-Rosa*, Ke Bi, and Eileen A. Lacey

Department of Integrative Biology and Museum of Vertebrate Zoology, University of California, Berkeley, CA 94720 USA (JMR, EAL); Computational Genomics Resource Laboratory, University of California, Berkeley, CA 94720 USA (KB)

Mammalian mating systems are complex, encompassing both individual mate choice decisions and population-level patterns of spatial and social relationships. Major Histocompatibility Complex (MHC) genes are thought central to reproductive decisions due to their critical role in the adaptive immune response and the associated impacts on offspring success. At the individual level, animals are expected to prefer mates with MHC genotypes that are dissimilar from their own so as to increase MHC diversity and immunocompetence among offspring. At the population level, the number of partners per individual is expected to increase pathogen exposure and lead to greater diversity at MHC loci. This research uses genomic and transcriptomic technologies to study relationships between reproductive behavior and immunogenetic variation in free-living *Peromyscus* rodents with different mating systems. Specifically, we test whether mate choice in the monogamous *Peromyscus californicus* is associated with disassortative mating at MHC loci and if monogamy in this species is associated with reduced expression and/or variability at MHC loci compared to sympatric, polygynandrous congeners. Results from analyses indicate that mate choice in *P. californicus* is not correlated with MHC genetic characteristics and highlight important expression and nucleotide-level differences that underscore the apparent role of mating system in shaping immunogenetic expression profiles and adaptive variation. Collectively, these analyses generate new insights into relationships among mate choice, mating systems, and immunogenetic variation in wild mammal populations. This research was supported by a ASM GIAR awarded to Jesyka Melendez-Rosa in 2016.

5: Jaguar Corridor Initiative: a collaborative wide-ranging conservation strategy**

Roberto Salom-Perez*, Daniela Araya-Gamboa, Daniel Corrales-Gutierrez, Deiver Espinoza, Stephanny Arroyo-Arce, Lisanne Petracca, Hugh Robinson, Claudia Wultsch, Rafael Hoogesteijn, Esteban Payan-Garrido, Bryan Finegan, Lisette Waits, and Howard Quigley

Panthera, New York, NY 10018, United States of America (RSP, DAG, DCG, DE, SAA, LP, HR, CW, RH, EPG, HQ); Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, NY 10024, United States of America (CW); University of Idaho, Moscow, ID 83844, United States of America (RSP, LW); CATIE, Cartago, Costa Rica (RSP, BF)

Jaguars (*Panthera onca*), an iconic species in the Western Hemisphere, have been wiped out from half of their historic distribution. The Jaguar Corridor Initiative intends to address this situation and guarantee the connectivity of the species throughout its distribution. Scientific investigation, policy building and local collaboration are the basis of this ambitious enterprise. Least cost path corridors are verified in the field through interviews made to local people and occupancy modeling analyses. Monitoring of core populations and corridors between them are also executed using camera trapping and non-invasive genetic sampling mainly. Main threats to jaguars, such as the retaliatory killings due to cattle depredation, and the impact of developing projects, are also addressed through innovative implementations, research and collaboration with local agencies and financial entities. So far, environmental agencies from eight different countries have signed an agreement supporting this initiative. Critical corridors and core areas in Mesoamerica have been identified. Anti-predatory mitigation actions have been successfully implemented and a conflict response unit has been created in collaboration with the Costa Rican government. Additionally, the impacts and mitigation actions related to road development, hydroelectric and geothermal projects are being identified. Only through strong local collaboration, identification and mitigation of the impacts of development projects, and the application of management measures based on sound science will conservation of this, and other wide-ranging species, be possible.

6^{E}: Microbiome composition and social learning as pathways to dietary specialization in moose**

Brett R. Jesmer

Program in Ecology, Department of Zoology and Physiology, University of Wyoming, Laramie, WY 82071 USA

Theory and empirical evidence indicate that population-level diet breadth expands as resources become limited. The niche variation hypothesis predicts that population-level diet expansion stems from groups of individuals specializing on alternative, less 'optimal' foods. In Class Mammalia, tests of the niche variation hypothesis have been restricted to sea otters and demonstrate that increased manual dexterity facilitates diet expansion by allowing individuals to consume previously unexploited foods. For ruminant herbivores, the gut microbiome plays an important role in determining the types of foods that can be digested, and diet selection is thought to be socially learned. I tested the niche variation hypothesis in moose (*Alces alces*) using DNA metabarcoding and microsatellites to quantify population-level dietary niche width, individual diet specialization, microbiome composition, and relatedness (a proxy for social interactions in this species). Individuals in more resource-limited populations had more specialized diets and more specialized microbiomes, and diet similarity increased with relatedness. This work demonstrates that individual specialization in moose is maintained through inheritance of microbiomes and foraging behaviors, and shows an alternative means through which individual specialization may arise in mammals lacking manual dexterity. This research was supported by a Albert R. and Alma Shadle Fellowship awarded to Brett Jesmer in 2017

7^{}: A critical review of mammalian faunas endemic to the Cerrado and the Caatinga**

Eliécer E. Gutiérrez, Neander M. Heming, and Jader Marinho-Filho

PPG em Biodiversidade Animal, Universidade Federal de Santa Maria, Santa Maria RS 97105-900, Brazil (EEG); Departamento de Zoologia, Universidade de Brasília, 70910-900 Brasília, DF, Brazil (EEG, NMH, JMF)

In this study, we present results of a critical review of literature concerning the taxonomy, biogeography, and conservation status of species of mammals endemic to the Cerrado and the Caatinga, the two largest biomes of the South American Dry-Diagonal. Two major findings are worth highlighting. First, we report the existence of a group of species endemic to both the Cerrado and the Caatinga (i.e., present in both biomes). This group of species deserves special attention from the biogeographic point of view. Second, we show that a substantial portion of the mammals endemic to these biomes faces risks of extinction that are unrecognized in the Red List of Threatened Species published by the International Union for Conservation of Nature. "Data deficient" is a category that misrepresents the real risks of extinction of these species considering that (a) some of these species are known only from a handful of specimens collected in a single or a few localities long ago; (b) the Cerrado and the Caatinga have been sufficiently sampled to guarantee collection of additional specimens of these species if they were abundant; (c) natural habitats of the Cerrado and the Caatinga have been substantially altered or lost. Finally, we show

examples of current (methodological and empirical) efforts employing ecological niche modeling to assist actions that might increase the chances of survival of these species. Oliver Pearson Award, awarded to Eliecer E. Gutierrez in 2017

8^{E,HTA}: Pumas as ecosystem engineers for carrion-dependent invertebrates

Joshua M. Barry*, Mark Elbroch, Ronald J. Sarno, Matthew E. Aiello-Lammens, Howard B. Quigley, and Melissa M. Grigione

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Ecosystem engineering is the ecological process by which an organism creates, modifies, or maintains habitat. Specifically, ecosystem engineers create physical changes in abiotic and biotic material, and through this process, control the availability of resources for other species. Indeed, predators could be considered ecosystem engineers by creating habitat for carrion-dependent invertebrate scavengers that utilize carcasses during critical life-history periods. Carcasses function as micro-habitat for numerous beetle species, where they commune, seek mates, reproduce, feed, and seek refugia from predators. Here we sampled beetle communities at 24 prey carcasses killed by pumas and matching control sites in the southern Greater Yellowstone Ecosystem, USA, to measure how beetles utilize these carcass "habitats". We used linear mixed-effects models to test for significant differences in beetle abundance, species richness, and diversity. We collected 24,209 beetles, comprised of 215 species. We identified eight carrion-associated beetle families that had significantly higher abundance at carcasses than control sites. Mean beetle abundance and species richness were also significantly higher at carcasses. In addition, diversity increased over time at fresh carcasses but remained constant at control sites. Our research revealed one way in which predators create and modify physical habitats for carrion-dependent species, providing ecologists with a novel view on the importance of predators on the landscape. Further, our work highlighted a strong effect of an ecosystem engineer on biodiversity heterogeneity and species distributions. This research was supported by the Annie M. Alexander award, awarded to Joshua M. Barry in 2017.

9: The importance of multiple methodologies to survey tropical bat communities

Karen A. Campbell and Stephen G. Mech
Albright College, Reading, PA 19604 USA

We surveyed the bat community at a property owned by Albright College in southwest Costa Rica, near Corcovado, Puntarenas, in January 2018. Over 6 nights and 7 days, we captured 29 bats representing 9 genera using a combination of single-tier mist nets and vegetation surveys. Most of these bats (21/29) were in the family Phyllostomidae, and the others were Thyropteridae (6), Mormoopidae (1) and Vespertilionidae (1). While mist-netting, we performed acoustic surveys using a hand-held Echo Meter Touch ultrasonic receiver. Recordings revealed a very different bat community, as we detected no Phyllostomidae ultrasonically, but we did detect representatives from five families of aerial insectivores (Emballonuridae, Molossidae, Mormoopidae, Noctilionidae, and Vespertilionidae) based upon characteristics of their echolocation signals. Aerial insectivores are not readily captured using single-tier mist nets as they typically fly near the top of the canopy. Phyllostomidae are visually-oriented bats that also use echolocation, but their low intensity calls don't readily detect mist-nets placed in areas that are heavily cluttered acoustically, such as the vegetation on which they feed. The results of this study emphasize the importance of using multiple techniques to assess the bat community to take advantage of the strengths of different survey methods to form a more comprehensive picture of a complex community.

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

James M. Ryan
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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.

11: Urban Wildlife Information Network (UWIN): A multi-city approach to urban wildlife research

Seth B. Magle, Mason A. Fidino, Elizabeth Leher, Travis Gallo, Maria Jazmin Rios, Matthew Mulligan, Adam Ahlers, Julia L. Angstmann, Carmen M. Salisbury*, Travis J. Ryan, Laurel M. Hartley, Christopher Schell, Ashley Gramza, Amy Belaire, Barbara Dugelby, Kelly Simon, David Drake, Heather Sander, and Brandon MacDougall

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Urbanization is one of the most prominent forces altering landscapes worldwide. Consequently, many wildlife species inhabit urban landscapes and co-exist with human populations. Most research to date that examines urban wildlife is based on data from a single city. This limited scope prevents us from revealing global patterns regarding urban wildlife and the broad impacts of the human altered landscape. In this study, we present a multicity approach, the Urban Wildlife Information Network, designed to monitor urban wildlife with the objective of overcoming these limitations and revealing first principles regarding urban wildlife ecology and behavior. We positioned trail cameras along urban to less urban transects in seven cities in the United States. Each city followed a similar protocol for the timing and positioning of cameras across the landscape. Examination of the results from the summer 2017 camera deployment shows that many large-to-medium sized mammal species were common in each city but geographic region influenced the presence of the less common mammalian species. Further, the proportion of sites that the common species occupied was a function of both geographic location and human population density. This preliminary analysis points to the value of information gained from a multicity network with regard to understanding broad scale trends for urban wildlife and ultimately for informing policy decisions that affect human wildlife interactions in urban areas.

12^{E}: Small mammal communities in Nevada's swamp cedar woodlands, a globally unique and imperiled habitat**

Brooks A. Kohli*, David A. Charlet, and Rebecca J. Rowe

Department of Natural Resources & the Environment, University of New Hampshire, Durham, NH 03824 (BAK, RJR); Department of Biology, College of Southern Nevada, Henderson, NV 89002 (DAC)

We conducted the first comparative assessment of small mammal diversity and habitat characteristics for three unusually low-elevation stands of Rocky Mountain juniper (*Juniperus scopulorum*), known locally as swamp cedars, in White Pine County, Nevada. These small patches of woodland add considerable habitat diversity to the expansive low elevation shrublands in Spring Valley and White River Valley. Spring Valley stands supported unique small mammal communities, most notably through the occurrence of pinyon mice (*Peromyscus truei*) and absence of heteromyid rodents (*Dipodomys* and *Perognathus*). In

contrast, no pinyon mice were detected in the much sparser and smaller White River Valley stand. Instead, it harbored typical Great Basin shrubland mammals. Our results suggest the novel communities in Spring Valley swamp cedar habitats may be threatened by planned groundwater removal. This research was supported by a Grant-In-Aid awarded to Brooks Kohli in 2016.

13^{E,HTA}: Effects of ectoparasites on survivorship and reproduction of *Peromyscus leucopus*

Stephanie Dea* and Stephen Mech

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White-footed mice (*Peromyscus leucopus*) are frequently parasitized by botflies (*Cuterebra fontinella*) and other ectoparasites. According to previous studies, botflies may minimally affect *P. leucopus* or may increase survivorship. There is no evidence of fleas or ticks affecting mouse survivorship. There is evidence of increased botfly parasitism on white-footed mice near woodland edge. Because logged areas resemble forest edge habitat, mice in logged areas may have higher infestation of botflies. We examined the effect of ectoparasite load on survivorship and other population demographics of white-footed mice in a managed forest near Reading, PA. We tested three hypotheses: 1) mice with botflies will have a greater survivorship, 2) the frequency of infestation will be greater in a selectively logged site than the control site, which was unaffected by logging, and 3) infestation will affect mass of the mice. We used mark-recapture and log-linear analyses to test our hypotheses. We found that mice infected with botflies had significantly greater survivorship than uninfected mice. Contrary to our hypothesis, the proportion of infected individuals was greater on the control site; but this may be due to higher population density. Mass was highest in botfly-infected individuals at the control site, but equal among infected and uninfected individuals at the select cut site. There was no difference in infection rate for age, site, or sex.

14^E: The functional roles of cattle and bison grazing in North American grasslands: a meta-analysis

Caroline R. Wilford* and Jason L. Malaney

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Historically, bison (*Bison bison*) played a keystone ecological role in shaping grasslands of North America. After migrating from Beringia, their co-evolution with other organisms the landscape provided heterogeneity to influence native biodiversity and ecosystem function. However, replacement by domestic cattle (*Bos taurus*) raises concerns of relative ecological roles. As conservation priority increases for grasslands due to rapid change by anthropogenic causes (climate change and land conversion), questions arise of the parity of ecological roles regarding cattle and bison. In this meta-analysis, we screen and quantify over twenty peer-reviewed studies from across prairie (tallgrass, mixed grass, and shortgrass) and montane ecosystems to compare functional roles of bison and cattle in grassland ecosystems based on grazing preferences and social behaviors. We found that cattle often have an increased affinity towards riparian and woody areas, and spend more time grazing than bison. Bison wallows can influence local microhabitats around depressions and create landscape heterogeneity. More broadly, we detect insufficient information to thoroughly assess if grazing increases native biodiversity, but grazing pressure appears to increase abundance of deer mice and improve species richness of some native plants. The implications of this review suggest room for development of additional research regarding ecological significance of shortgrass prairies, cascading trophic effects across ecosystems, and standardizing study of responses across grazing regimes.

15^E: Island-inhabiting voles have larger skulls than their mainland relatives: indications of the Island Rule?

Mariah C. Schlis-Elias* and Jason L. Malaney

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Island Rule remains an important, albeit often contested, topic in biogeography. In general, large-bodied mammals tend to decrease in size while smaller mammals frequently get larger when occupying island systems. Voles of the genus *Microtus* are one system hypothesized to experience island effects, so this project aims to expand upon past research by comparing morphological variation of island and mainland voles using 26 craniodental morphometric measurements. Preliminary multivariate results show that skull

variation overlaps amongst island and mainland populations, but these groups display differences indicative of active divergence. The five measurements with the highest importance to the Principal Component Analysis were evaluated via ANOVA and Tukey tests, which showed that the island populations tend to have larger skulls. These data and analyses will be broadened to include more islands on the east coast, in addition to a set of islands in Southeast Alaska. Morphological analysis will be expanded to analyze size and shape variation in concert with environmental and geographic variables to test if differences are attributable to the Island Rule.

16^E: A study of endoparasites within the eastern spotted skunk (*Spilogale putorius*)

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To date little has been reported on the extent of endoparasites within the eastern spotted skunk (*Spilogale putorius*) whereas conspecifics have extensive research completed in regards to endoparasite prevalence. The eastern spotted skunk has been declining in the United States and is now listed as threatened or endangered in some states. Although reasons for the decline are uncertain, endoparasite infection may have played a role. We salvaged specimens from roadkill or purchased them through legal trapper take for necropsy. Examination for parasites will include as many organs as possible, mesenteries, and the body and nasal cavities. Three of our current thirteen total skunks have been necropsied, to date, and all three specimens had nematodes found within the stomach and intestine; however, one specimen also contained cestodes and acanthocephalans within the intestine. None of these parasites have been identified to a lower taxonomic level yet. The data collected from this research could result in uncovering previously unidentified parasites in *S. putorius*, as well as parasites not known to inhabit other hosts in the genus *Spilogale*.

17: In the shadow of the moon: small mammal activity during the 2017 solar eclipse

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A total solar eclipse is a profound but rare natural phenomenon. There is abundant anecdotal evidence that animals respond to changes in light intensity and air temperature during an eclipse. Responses often are those normally seen with approaching dusk; diminishing activity of species that are diurnal and increasing activity for those that are nocturnal. Among mammals, most reports are for large, often domesticated species, or for zoo animals. Although there are reports of bat activity during totality, we found no information on small non-volant mammals. Our aim was to gather quantitative information on small mammal activity during the total eclipse of 21 August 2017 while simultaneously recording changes in light and temperature. Our study site was in south-central Idaho, near the center point of the path of totality where the eclipse reached totality at midday. Trapping prior to the eclipse recorded only diurnal chipmunks active at midday. During the eclipse, changes in air temperature and light intensity were comparable to those occurring with approaching dusk and following dawn. During the three-hour event, we captured one diurnal species and two species with seasonally facultative activity that are generally nocturnal/crepuscular during August. Despite their numerical predominance, strictly nocturnal species were not recorded during the event, perhaps due to the brevity of totality or the stronger influence of endogenous activity rhythms in such species.

18: Leveraging citizen scientists in the interpretation of bat bioacoustical data

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The Wisconsin Bat Program (WBP) was established in 2007 in response to threats facing our nation's bats, particularly the spread of white-nose syndrome. The WBP involves citizen scientists that collect bat bioacoustic data via walking, driving, or boat routes throughout the state. We investigated the potential for

citizen scientists in interpreting bat sonograms. We used bat calls collected at a permanent bat recording stations located in southeastern and central Wisconsin. Ninety-seven undergraduate students were divided into 20 teams of 5 students each, with each team assigned to one of two experimental groups. The treatment group earned a digital badge in bioacoustical analysis and the control group was not told about badges. Seventy-nine students scored 463,638 sonograms. There was no significant difference in the quantity of sonograms scored between groups (Control = 5,826 sonograms/student, Treatment = 6,053 sonograms/student, $p=0.442$). There was also no difference in the quality of work between groups when compared with computer analysis of the bat community using Kaleidoscope Pro software (Control Morisita Community Similarity Index = 0.985, Treatment Morisita Community Similarity Index= 0.989). This study illustrates that citizen scientists can be trained to reliably score sonograms collected during bat bioacoustical surveys. We also provide evidence that earning a micro-credential in the form of a digital badge could encourage some members of the public to engage in citizen science.

19: Body size and reproductive characteristics of deer mice in anthropogenic and native habitats in Kansas

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Often, a standard value for body size has been used for a given species in studies or specific models, but we were interested in how plastic body size could be in association with environments that differed in plant composition. Likewise, the same statement is true for reproductive characteristics. We used a common species in native prairies, the deer mouse (*Peromyscus maniculatus*), to begin to examine factors that influenced body size (indexed by both body length and mass) and reproductive characteristics in north-central Kansas. We collected 616 deer mice during two summers to examine the effect of precipitation (which differed between the two summers) and of habitat type, native (grazed mixed grass prairie) and anthropogenic (crop fields, old fields and planted grass). We also examined the effect of sex, as a biotic factor, on body size relative to environmental drivers. We asked if the distribution of body size was similar among habitats, followed by whether means of body sizes differed among habitats. Sex was not a significant factor on body size. We then asked if habitat and year had significant effects on body size and reproduction and if synchrony in timing of reproduction occurred in females. Our data suggest that body size is plastic and one size does not fit all. Furthermore, reproductive characteristics are affected by both biotic and abiotic factors.

20: Small mammal communities in experimentally manipulated sites within the Flint Hills tallgrass prairie

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In 1981, we initiated the Konza Prairie Small Mammal Research Project focused on tallgrass prairie that was manipulated by fire and grazers, varied in topography, and experienced highly variable weather within and among years. We used standardized procedures to sample small mammals in 14 local sites during autumn and spring (autumn 1981-spring 2013). During the 32 years, we captured >1 individual of each species present (13 rodents; 2 shrews) in this region of Kansas. Total species recorded over the study period varied noticeably among local sites (autumn: 9-13; spring: 6-9). Average richness per sampling period in each local site was much lower than the total (autumn: 2.3-4.7; spring: 1.2-2.5). Average local richness was lowest in ungrazed, annually burned prairie as compared to sites that were less frequently burned, bison grazed, varied in topography, or some combination of these. Within local sites and seasons, communities typically were temporally nested through the 32 years. *Peromyscus maniculatus* was the most frequently recorded species in prairie sites; *P. leucopus* was the most frequently occurring species in woody-encroached long-term unburned sites. In contrast, other species (autumn: 5; spring: 10) were recorded only infrequently (<5% of the total 448 site-years). Many ecological lessons can be learned from understanding long-term patterns of abundance, composition, and richness of local small mammal communities and their possible drivers.

21: Large-herbivore exclusion and soil enrichment, not prescribed fire, enhance small-mammal abundance on East African savannas

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Density of small mammals (SM) increased with exclusion of large mammalian herbivores (LMH; wildlife and cattle, by electric fencing) and soil enrichment (long-term “glades” resulting from nocturnal cattle pens) on both red-sand soils and black cotton soils in the savanna/scrub habitats of Laikipia, Kenya. SM were 20-fold more abundant on fenced glades than matrix habitat on both soils and 9-fold more abundant on fenced bushland (non-glades) on red sands. Unfenced glades supported intermediate densities in black cotton, but lower densities in red sands because of LMH cropping. In black cotton, SM diversity also was enhanced by LMH exclusion. Total SM biomass was greater on red sands (though mean body mass was greater on black cotton for 2 common species), within exclosures, and on glades. SM community composition differed between the 2 soil types, with red sands being intrinsically more diverse. In a landscape-scale burn experiment on black cotton, SM were more abundant on unburned than burned patches; the latter had shorter grass due to LMH cropping 20-50 months post-burn. LMH grazing and fire (and the feedback loop between them) have a suppressive effect on grass height and SM abundance in the black cotton, as do LMH grazing and enrichment on the red sands. On balance, these effects suggest reduced cover is a primary driver of LMH suppression of certain small savanna mammals.

22: 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 2017 at Hawk Mountain Sanctuary (PA). Habitat consisted of hardwood deciduous forest dominated by oaks (red, white, and chestnut) and hickory. Sampling began with three 6x6 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 2011-2013). Small mammals experienced large population fluctuations at Hawk Mountain, with moderately high densities at all sites in 2006-2007 that then decreased, before showing tremendous population growth in 2010 that peaked in 2011. Only with such large rodent populations was a significant number of weasels captured. Following such high capture rates, each grid was converted to 7x7 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 (2013-2017). 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.

23: Squirreling around for science: incorporating sciurid behavioral research into undergraduate curriculum

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Recently, Course-based Undergraduate Research Experiences (CUREs) have been proposed as a way to engage undergraduates in authentic research and to teach core concepts using inquiry-based activities. Compared to traditional labs, CUREs may better enhance intellectual independence and critical thinking because scientific outcomes are unknown. Here, we present preliminary scientific and pedagogical outcomes of a CURE to investigate tradeoffs between foraging and vigilance behaviors in sciurid rodents. We developed and piloted a simple, focal-animal observation protocol that works across habitats and species. Students submitted data via Google and then analyzed the nationally aggregated dataset to test their own hypotheses. In the past year, we implemented this activity for a range of species (ground/tree squirrels) and across an array of courses (upper/lower division, for biology majors/non-majors) and habitats. Preliminary assessments suggest that students gained confidence in their research abilities and became more interested in science career paths after participation. Additionally, several students sought out independent research opportunities to extend their results (e.g., giving up density and/or camera traps), highlighting the value of this project as a mammalogy student recruitment tool. Together, these results suggest that participation in course-based research projects enhances not only students' research skills but also their confidence in conducting research, which has important implications for their future as scientists and for increased retention/persistence of students from under-represented groups.

24: Southeastern Myotis and Rafinesque's big-eared bats switch their roosting habits seasonally in Arkansas bottomlands

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Tree roosts in bottomland forests are essential resources for Rafinesque's Big-eared (*Corynorhinus rafinesquii*; CORA) and Southeastern (*Myotis austroriparius*; MYAU) bats. Both bat species are considered rare across their range and little is known about their roost requirements as seasons change from fall to winter. The objective was to characterize roost trees in both seasons in the Cache River National Wildlife Refuge, Arkansas, one of few remaining tracts of unaltered bottomland hardwoods. In October-December of 2016 and 2017, we radio-tracked 38 bats (21 CORAs and 17 MYAUs) and found 78 roost trees. Tree species and cavity type (e.g., basal cavity) were recorded for each roost tree. Both species changed roosting habits as environmental conditions changed. Various tree cavity types were used for roosting by CORAs until they discontinued using basal cavities entirely late in the season. MYAUs showed no strong preference for cavity types early in the season but progressed to favor upper cavity openings later in the season. This suggests that both CORAs and MYAUs anticipated seasonal flooding that could trap them inside the cavity. Additionally, CORA used Water Tupelo (*Nyssa aquatic*; NYAQ) exclusively, but MYAU shifted from using mainly NYAQ initially to using a variety of tree species as environmental conditions changed. Changing behaviors may coincide with changing priorities from foraging to avoiding seasonally rising flood waters and maintaining homeostatic balance as seasons change.

25^{E}: Phylogenomics of South American tree squirrels: Tracing their evolutionary history through mitogenomes from museum specimens**

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Tree squirrels (Rodentia, Sciurini) are conspicuous inhabitants of all South American (SA) forest biomes, but in contrast to other widespread rodent groups, they have been largely neglected in taxonomic and phylogenetic studies. Basic information on the number of genera and species is still ambiguous for the group — 15 to 35 species have been recognized in three to eight genera, depending on the author — and their phylogenetic relationships remain poorly understood. This project outlines a pioneering effort to provide a comprehensive phylogeny of SA tree squirrels. Herein we present the first insights into their evolutionary history based on a phylogenetic analysis obtained from high-throughput sequencing of

mitogenomes from 26 museum specimens representing all genera and 2/3 of the currently valid species of SA tree squirrels. Our results recovered all SA tree squirrel species plus species from Panama composing a fully supported clade that is sister to *Syntheosciurus brochus* from Costa Rica. The Neotropical taxa are sister to the Southeast Asian *Rheithrosciurus macrotis*, and the Japanese *Sciurus lis* is sister to all. Our preliminary results on mitogenomic phylogeny fail to support the monophyly of the genera *Guerlinguetus*, *Microsciurus* and *Notosciurus* and suggests that the recently proposed taxonomic arrangement for SA squirrels based exclusively on morphology needs revision through an integrative approach. This research was supported by a Latin American Student Field Research Award awarded to Edson F. de Abreu-Júnior in 2016.

26^E: Character displacement of three sympatric rodent species in eastern Paraguay Atlantic Forest remnants

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The Interior Atlantic Forest of eastern Paraguay houses three abundant sympatric species, the terrestrial *Akodon montensis*, *A. paranaensis* and semi-arboreal *Oligoryzomys nigripes*, with high potential for competition and niche partitioning. Character displacement is defined as the discrimination of characters in sympatric closely related taxa and the convergence of characters when in allopatric conditions. Ecologists have expanded the theory to community-wide character displacement where taxonomic position is not taken into consideration, but rather, all species in a community are competing for resources. Using geometric morphometrics we test for character displacement in cranium and mandible morphology. We digitized museum samples and compared skull and mandibles of *O. nigripes* (n = 108, 121), *A. montensis* (n =141, 124) and *A. paranaensis* (n=56, 58) using 16 and 13 homologous landmarks respectively. We implemented Procrustes analysis, which transforms, scales, and rotates homologous landmarks. We implemented principal component analysis (PCA) to identify the variables that best describe variation between species. We used discriminant function analysis (DFA) followed by pairwise permutation tests, to compare differences in shape and to discriminate species groups. PCA identified maximum variation in the rostrum between species. We found significant differences evidence of character displacement between species in skull and mandible. Variation was highest in the rostrum and apparatuses associated with eating. This leads us to hypothesize that diet is a major driver for resource partitioning species.

27: Two new recent country records of mormoopid bats in The Bahamas (Chiroptera: Mormoopidae)

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The Caribbean is home to a large diversity of bats, spanning nine families and at least 60 genera. Within the Bahamas, there are 10 species of bats that have established populations, three more that are documented as single specimens and presumably were vagrants, and three (*Pteronotus parnellii*, *P. quadridens*, and *Mormoops blainvillei*) that are only known as fossils. In January 2017, we captured via hand nets a sooty mustached bat (*Pteronotus quadridens*) and an Antillean ghost-faced bat (*Mormoops blainvillei*) in a cave at the southern end of Long Island, in the Bahamas. These are the first modern records for both species in the Bahamas. Both species have present day distributions in Cuba, the Dominican Republic, Haiti, Jamaica, and Puerto Rico. No other individuals of either species were captured or seen in the cave. The most likely explanation is that they are vagrants, possibly blown into the Bahamas from Cuba by Hurricane Matthew in the fall of 2016.

28: Preliminary data on small mammal assemblages in a cacao dominated landscape in Cote d'Ivoire

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Cacao is the main ingredient for chocolate, estimated at \$80 billion global market. Demand for cacao is expected to increase by ~30% by 2020. The West Africa cacao industry accounts for ~70% of the world supply, led by Côte d'Ivoire (40%). In the last few decades, extensive expansion of no-shade cacao production has become the primary driver for forest degradation and deforestation of West Africa, primarily Côte d'Ivoire, where there are major gaps in basic mammalian knowledge. While some studies have reported greater biodiversity in cacao systems versus other anthropogenic land uses, these benefits are still not necessarily comparable to biodiversity in forest systems. We conducted sampling in five major habitat including primary and secondary forest, fallow, rubber, and cacao farms, totaling 7350 trapnights. We quantified various dimensions of diversity including species richness, evenness, and diversity. Finally, we calculated similarity between habitat types. Our preliminary data has recovered 366 specimens, including 10 rodent and 6 shrew species. Species richness and diversity was the highest in secondary forest. Meanwhile, the lowest richness and diversity was in rubber and cacao farms, which showed the highest evenness. Cacao farms had the highest similarity to rubber and fallow. Meanwhile, primary and secondary forest had the most similar assemblages. Our preliminary analyses suggest that cacao production has considerably changed the original Guinean Forest small mammal assemblages.

29^E: American black bear (*Ursus americanus*) density, diet, and distribution near Moab, Utah

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After building accounts of encounters with American black bears near the Rio Mesa Field Station near Moab, Utah I am investigating factors that influence the sustainability of these large mammals. The potential for more black bear migrants increases with rising populations and food availability changes from weather patterns. Camera trap photos gathered during our preliminary study from May-November 2017 confirmed frequent use of canyons in the field station. I've established monitoring stations where camera traps will be facing a scented fur snare. The snare will collect fur from the animal, which will later be retrieved and brought back to the University of Utah for stable isotope analysis. Ratios of carbon and nitrogen isotopes allow insight into the general diet of the individual, with implications on how much plants, animals, or human food is a part of their diet. Furthermore, hydrogen and oxygen isotopes between significantly different elevations such as that between Moab and neighboring populations give noticeable signatures. Well-preserved hairs can infer how much, if any, of an individual's lifespan was spent between the 2 localities, with particular interest on the location of parturition of cubs. Information on the nutritional behavior and movement of local bears can be valuable tools for approaches to decrease human contact in this highly visited region.

30: Cascading effects of island area and isolation on seed dispersal effectiveness of rodents

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Habitat loss and fragmentation often lead to local extinction of large-bodied mammals, which can trigger cascading events that could change interactions of granivorous rodents and seeds they disperse, with implications for seed dispersal effectiveness (SDE). Yet, changes in rodent-mediated SDE along mammalian defaunation gradients, and empirical support for underlying mechanisms, are unclear. We conducted seed dispersal experiments for a rodent-acorn conditional mutualism on 21 study islands in Thousand Island Lake, China, a land-bridge system, to assess direct and indirect effects of area and isolation on SDE of rodents. We used path analysis to test hypothesized links between area, isolation, defaunation of large-bodied mammals, competition among rodents for acorns (CRA) and SDE. Island area positively affected SDE indirectly via effects on defaunation and CRA, whereas isolation had negative direct and weaker positive indirect effects on SDE. Loss of large-bodied mammals negatively affected SDE indirectly by its impact on competition among rodents for acorns. SDE exhibited a unimodal relationship with intensity of competition among rodents for acorns, peaking at intermediate levels.

Indirect effects of island attributes mediated by defaunation of large-bodied mammals on small or isolated islands appear to drive altered resource competition among rodents and lead to decreased seed dispersal effectiveness. We conclude that altered trophic interactions caused by habitat loss and isolation have substantial impact on the acorn dispersal process in TIL.

31^E: Using captive lemurs to quantify the relationship between food toughness and feeding behaviors

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There is a complex relationship between a primate's masticatory morphology and the physical properties of the food it eats. To better understand the feeding process, we employed two methods of data collection using adult *Lemur catta* (dietary generalist/frugivore; n = 2) and *Propithecus coquereli* (folivore; n = 2) at the Maryland Zoo in Baltimore – (1) making use of engineering technology to quantify a key physical property of the foods in the daily diets – toughness (resistance to crack propagation) and (2) filming (for a total of 24 meals over 12 days) the oral behaviors these individuals used when eating these food items (including food choice). Using our Lucas FLS-1 tester, we calculated “Toughness Indices”, which quantified the total average food toughness encountered per day given the foods provisioned in that day. As predicted, the total daily diet presented to the captive *P. coquereli* at the start of feeding was significantly tougher than that of *L. catta*; however, behavioral observations demonstrated that – surprisingly – *L. catta* spend most of their feeding time (male – 69.4% and female – 50.8%) consuming the toughest food available (monkey chow). By contrast, *P. coquereli* spent more time on the most fragile foods (nuts and sumac leaves) than on tougher items (including romaine and kale). Our findings demonstrate the importance of pairing data on food material properties with data on feeding behavior.

32: Future research into the plains spotted skunk (*Spilogale putorius interrupta*) in a tallgrass prairie ecosystem

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The plains spotted skunk (*Spilogale putorius interrupta*) experienced range wide population decline throughout the second half of the 20th century and early part of the 21st. Habitat loss and alteration has been hypothesized as the primary causative reasons; however, additional factors such as disease, impacts from pesticide usage, and increased predation rates could play a role. Recent results from a statewide survey in Texas indicate a relatively robust population of spotted skunks is present at a remnant prairie near Houston. This site, Katy Prairie, was historically a mosaic of native tall grass prairie interspersed with temporal wetlands; however, due to expansion from the Houston metro area, less than 40% of the original ecosystem remains undeveloped. We will initiate a 3-year project in the summer of 2018 at conserved properties on the Katy Prairie. Skunks will be collared with both GPS and VHF radio collars and we will track skunks to learn home range and habitat usage, how differing land management strategies affect usage, maternal den and daytime resting place locations of female skunks, cause specific mortality factors, and abundance and density throughout the Katy Prairie. Research is planned to be concluded in time for results to be utilized by US Fish and Wildlife personnel for the fiscal year 2022 listing decision.

33^E: Assessing mesocarnivore competition for small carcasses: potential impacts on endangered American burying beetles (*Nicrophorus americanus*)

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The American burying beetle (*Nicrophorus americanus*) utilizes small carcasses, approximately 100g, for reproduction. Density increases of mesocarnivores might negatively affect American burying beetle reproduction through competition for the carrion resources. Mesocarnivores are medium-sized carnivores which range in size from striped skunks (*Mephitis mephitis*) to coyotes (*Canis latrans*). To gauge

persistence and scavenging of small carcasses we placed approximately 100g Norway rat (*Rattus norvegicus*) carcasses in two habitats, forests and fields. We checked the status of these carcasses every three days and noted whether the carcass had been removed by a scavenger. In addition, we noted any disturbance to the site, stage of rat decay and condition, and any insects utilizing the carcass. We placed trail cameras approximately 5 meters from the rat carcass so that we could identify scavengers and characterize their behaviors. While our study is ongoing, initial results have shown persistence of carcasses to average 4 days and a few different scavengers have been identified. Currently the most reoccurring scavenger, across both habitats, is that of the Virginia opossum (*Didelphis virginiana*). Increased understanding of small carcass persistence and potential availability as a food and reproductive resource could aid in identifying causes of decline of the American burying beetle and provide insight on the need for managing small carcass resources in American burying beetle management.

34^E: Land-use history and canopy thinning alter small-mammal foraging activity and spatial patterns of seed predation

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Past human activities can have persisting effects on ecosystems and habitats, yet it is unknown if past activities alter present-day mammal foraging. Spatial distribution of refuges is known to alter small-mammal movement; therefore, interacting effects of land-use history and present-day management on refuges may alter spatial patterns of small-mammal foraging. To test how land-use history and present-day management alter small-mammal foraging, we conducted an experiment using large-scale canopy harvesting in post-agricultural and non-agricultural longleaf-pine woodlands at 7 sites in the Savannah River Site (SC, USA). We deployed 1,000 nail-tagged *Quercus nigra* seeds in 28 experimental plots for 4 weeks, then recovered the tags to measure spatial patterns of seed predation. At each seed depot, we measured refuge distribution and positioned camera traps to monitor small-mammal activity. Seed-predation rates in harvested plots depended upon land-use history and were higher in non-agricultural plots than in post-agricultural plots. Predation in harvested plots increased with *Sigmodon hispidus* activity, and the average distance that seeds were moved and consumed increased with refuge separation and *Peromyscus* activity. Spatial concentration of seeds moved and consumed in unharvested plots was highest in post-agricultural plots. This study shows that land-use history, canopy harvesting, and refuge distribution can generate predictable spatial patterns for small-mammal foraging, which can have consequences both for small-mammal management efforts and for plants whose seeds are secondarily dispersed by small mammals.

35: Population genetics of the frugivorous bat *Sturnira parvidens* (Chiroptera: Phyllostomidae)

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Bats of the genus *Sturnira* are an excellent study model to analyze patterns and processes of diversification and endemism in Mesoamerica. *Sturnira parvidens* is a lowland species that occurs from Mexico to the Talamanca Mountains in Costa Rica. Phylogenetic analyses show that it represents a monophyletic group clearly differentiated at the species level, and phylogeographic evidence defines two lineages within it: one haplogroup along the Gulf of Mexico-Central America Slope and another on the Mexican Pacific Slope, with a limit between both units in the Balsas River Basin. Here, we analyze recent genetic information to generate a complete reconstruction of its evolutionary history. We used data from 12 microsatellite loci of 155 individuals from different localities throughout the species' geographical distribution, obtained from scientific collections. Preliminary findings of the tests of allocation of individuals to populations of origin suggest the presence of two groups from the genotypes obtained. The pattern of differentiation between group members is being studied in detail. Uniting the results from molecular markers with different forms of inheritance and mutation rates can help identify evolutionary processes that could not be detected or visualized with any of these markers independently. This approach can help

us interpret with greater confidence the historical and contemporary events that have affected the diversity and genetic structure of the populations.

36: Shrub encroachment, landscape restoration, and intraguild predation in the Chihuahuan Desert

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Shrub encroachment into grasslands in drylands is an issue worldwide leading to dramatic changes to landscapes. Substantial loss of grasslands in the Chihuahuan Desert of New Mexico has created concerns for biodiversity and ecosystem services. In response, land management agencies have implemented large-scale restoration programs in which herbicides are used to combat shrub encroachment. We asked how interactions among canid predators (coyote, *Canis latrans*; kit fox, *Vulpes macrotis*) and their lagomorph prey (black-tailed jackrabbit, *Lepus californicus*; desert cottontail, *Sylvilagus audubonii*) are affected by these extensive restoration efforts. We sampled mammals with camera traps on 28 sites including 14 pairs (treatment and reference) that represented a gradient in time since treatment (10 to 30 years). None of the species had simple responses to restoration treatments, but coyotes were more abundant in areas with older treatments. Kit fox abundance was related negatively to coyote abundance indicating intraguild predation (IGP) constrained foxes spatially. Abundances of the canid predators were unrelated to abundances of lagomorph prey, providing no support for the resource-ratio hypothesis for IGP. When released from heavy coyote pressure, kit foxes were more abundant on sites with low shrub cover. Kit foxes and coyotes also exhibited temporal niche partitioning in daily activity that may promote coexistence. Altered habitat structure from restoration efforts in our managed landscape have produced nuanced interactions among species including IGP for canids.

37: Hidden species diversity in the genus *Octodon* (Caviomorpha, Octodontidae)

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The genus *Octodon* contains *degus*, *lunatus*, *bridgesii*, *pacificus*; the phylogenetic hypotheses suggest that the species diversity is underestimated. With the aim of evaluating the taxonomic diversity of *Octodon*, we ran a Maximum Likelihood analysis of cytochrome-b of 41 specimens and principal component and multivariate analysis of variance on 13 craniodental measurements of 112 specimens. *Octodon degus* is recovered sister to the others species of the genus. *Octodon bridgesii* is recovered as paraphyletic with three main clades. Haplotypes from Andean piedmont localities, in the area of the type locality of *bridgesii*, form a clade sister to *lunatus*. The clade formed by haplotypes of *lunatus* and *bridgesii* s.s. is sister to a clade form by haplotypes of *bridgesii* from the Pacific coast. Finally, haplotypes from the southern range of *bridgesii* form a clade that is geographically structured into two subclades, one in Araucania (Chile) and other in Neuquén (Argentina). Finally, haplotypes of *pacificus* fall within the subclade of Argentinean *bridgesii*. Observed genetic divergences among the mentioned clades of *bridgesii* is comparable to that found among specific comparisons (*bridgesii* s.s. vs. southern *bridgesii* 6.3%). The discussed clades of *bridgesii* s.l. are also morphologically distinct in the buccinator-masticatory and oval foramen, posteroloph of M3, paraoccipital process; and morphometrically segregated in the multivariate space. As such, we consider them as candidate species, whose status should be tested with further analyses.

38: Short-term effect of helicopter-based capture on movements of a social ungulate

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Capture and handling wildlife is often required to obtain demographic, behavioural, or physiological data. However, capturing wildlife sometimes lacks public support. Thus, investigating the potential impacts of capturing wildlife is important in terms of informing public debate, as well as establishing data censoring protocols. Here, we investigated the short-term effect of helicopter-based capture and handling on the movements of free-ranging bison (*Bison bison*). We examined daily movement rates, home range size, and displacement of GPS-collared individuals after being captured. Our results indicate that there is minimal, short-term impact of capture on bison movements. In our sample, significant differences from baseline behaviour was observed only within the first 24 hrs after release; however, we observed variation among individuals. Some animals took up to 10 days after capture to return to baseline movements while others had no measurable response. Despite individual variation, 80% of individuals had returned to normal movements within five days after capture. Furthermore, there was a significant difference in the response to being captured by the sexes, with females increasing their movements, and males having decreased movement, after capture. Our results suggest that the effects of capture on movement is unlikely to have severe negative fitness effects on bison, and researchers should censure the first 10 days after capture. We encourage similar studies to inform data censoring protocols and public discourse about wildlife captures.

39: Craniodental morphological variation in southwestern chickarees (Genus *Tamiasciurus*)

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In the American Southwest, multiple disjunct populations of coniferous forests on mountaintops harbor a predictable mammalian fauna. Unfortunately, we still know relatively little about geographic variation in ecological and evolutionary features and biogeographic history for many species. For example, recent phylogenetic analyses question existing taxonomy of red squirrels (chickarees, Genus *Tamiasciurus*) and shows exceptionally high phylogeographic structure among regional, disjunct populations of the American Southwest. Consequently, in this study we revisit morphologically-based geographic variation of southwestern chickarees to evaluate taxonomy and test competing hypotheses of ecogeographic variation. We used geometric morphometrics across 20 craniodental characters across >300 specimens. Using spatial data and multivariate analyses, we detect strong correspondence between morphological variation and montane regions as predicted by phylogeographic patterns and a mismatch with taxonomy. Consequently, taxonomic revision may be warranted. Next steps are to quantify ecophenotypic variation and niche modeling to determine how ecological and evolutionary factors have led to diversification in this system, which may result in insights for other co-distributed species.

40^E: Morphometric review of the southern *Coendou ichillus* (Caviomorpha, Erethizontidae) from Peru

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The *Coendou vestitus* groups contains six species *ichilus*, *roosmalenorum*, *vestitus*, *pruinusos* and *melanurus*. The species *Coendou ichilus* was only known from specimens that came from southern Ecuador and northern Peru, but photographic records and a specimen collected of *ichilus* from the south of the Amazon River have expanded the distribution of this species. In order to evaluate if this new specimen of *ichilus* is within the variation morphology reported for the *vestitus* group, we performed multivariate analysis of principal components and discriminant analysis of 9 craniodental measurements of 20 specimens, that included all the species of the group. Principal components analysis showed that most of the species of the *vestitus* group occupy discrete separated morphospaces, and discriminant analysis categorized all the species in distinct separated morphospaces. Furthermore, the *ichilus* specimen from the south of Peru is not found within the morphospace of any of the species of the *vestitus*

group. This demonstrates the need for a necessary revision for the *ichilus* of the southern Amazon including molecular evidence since it could be a new species of *Coendou*.

41: Predictors of metabolic rates in aquatic mammals

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All biological activities depend on metabolic energy, thus understanding why metabolic rates vary across species is of fundamental importance in understanding how animals work. For mammals, it is generally understood that metabolic rates are elevated in aquatic species despite considerable taxonomic and ecological diversity. There are two prevailing, non-mutually exclusive hypotheses to explain this phenomenon: as an adaptation for aquatic endothermy and/or as a consequence of the high costs of carnivory. In this study, we used a phylogenetic comparative approach to examine the effects of environment (aquatic, terrestrial) and diet (carnivory, omnivory, herbivory) on the scaling patterns of basal and field metabolic rates in eutherian mammals (BMR = 537, FMR = 90 species). Best fit models indicate: (1) each diet*environment group is evolving towards a different optimum BMR; (2) all diet*environment groups are evolving towards the same optimum FMR; and (3) BMRs but not FMRs are elevated in aquatic species. These results support the hypothesis that maintenance of a high core body temperature, rather than carnivory, is correlated with elevated BMRs in aquatic mammals. In contrast, the FMRs of aquatic mammals are comparable to those of other mammals both on average and in their variability. Therefore, environment may be an important predictor of the idling costs of a resting mammal, but not the overall living costs of an active one.

42^F: Behavioral response of *Myotis lucifugus* and *Eptesicus fuscus* to restraint-related stress

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Understanding the impacts of handling and experimental procedures on animals is important for defining “normal” behavior under stress. While behavioral responses to stressors have been studied in a wide variety of taxa, little is known about handling stress in bats. Here, we examine behavioral responses to stress in two species, the big brown bat, *Eptesicus fuscus* and the little brown bat, *Myotis lucifugus*. Specifically, we were interested in comparing the response of animals to restraint to assess: 1) differences between the sexes within each species, and 2) overall differences between species. Animals were restrained as part of a wing morphometrics study in which they were secured to a board with wings open and photographed. Behavioral data was collected on 40 *M. lucifugus* and 17 *E. fuscus*. An ethogram was used to score the following behaviors during the restraint period: thrashing, stationary, open mouth, sit-up, shoulder shimmy, vocalization, and bending wing tips. Thrashing was the only significantly different variable between the two species, with *E. fuscus* exhibiting substantially more thrashing than *M. lucifugus*. Literature has provided major insight into understanding consistent behavioral differences between individuals which can also be applied at the species level, potentially explaining interspecific differences in behavior. Our results suggest that *E. fuscus* may exhibit a more aggressive behavioral type than *M. lucifugus*, although further studies are required to confirm this pattern.

43^F: Home range size of leopards in an increasingly disrupted world

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Home range size is one of the most fundamental measures of animal space use, providing insight into the habitat quality, density, and social organization of a species. As cryptic, generalist predators, leopards (*Panthera pardus*) are an ideal model for studying human impacts on wildlife space use. Leopards are clearly sensitive to human disturbance, as they currently occupy less than 40% of their historic geographic distribution, but they still coexist with people in areas of high and low human density across much of Africa and Asia. Using data from ten collaborative projects we have analyzed data movement data on over 70 individual leopards. We calculated autocorrelated kernel density home range sizes and found great variation of average size across countries; Namibia (1225 km²), Oman (126 km²), Iran (103 km²), Botswana (61 km²), South Africa (47km²), Kenya (36 km²), and India (17 km²). On a landscape scale, as human density and intensive land use increase, we expect to see an inverse relationship between leopard home ranges size and human density, possibly due to avoidance behavior towards humans or habitat fragmentation. Additionally, landscapes with higher precipitation, more vegetative NDVI values, and warmer temperatures and will likely decrease home range size. By examining the intersection off all of these variables on home range size, we can more effectively explore the impact of anthropomorphic disturbance on species sharing our landscapes.

44: Co-mapping coat-color with GIS data for *Peromyscus*: visualization as a tool for hypothesis testing

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Sub-specific differences in coat color across subspecies of both *Peromyscus gossypinus* and *P. maniculatus* are often attributed to environmental factors. We obtained data on coat color and collection locality from over 3,500 *Peromyscus* specimens (432 *P. gossypinus*, 3130 *P. maniculatus*) at the United States National Museum. We also obtained vegetative cover and albedo data from the National Land Coverage Database. We co-mapped specimen location and coat-color with either vegetative coverage (*P. gossypinus*) or albedo (*P. maniculatus*). For *P. gossypinus* we also coded for gender. These visualizations (and correlated statistics) confirmed the hypothesis that environmental factors contribute to coat-color differences. More importantly, our images illustrate the value of data visualization as an essential tool in analyzing the effect of varying environments on mammalian phenotypes.

45^F: A systematic assessment of endemic Galapagos rodents: *Nesoryzomys fernandinae* and *Nesoryzomys swarthi*

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The genus *Nesoryzomys* is currently restricted to Galapagos, Ecuador, specifically four of the major islands: Isla Baltra, Isla Santa Cruz, Isla Santiago, and Isla Fernandina. Throughout these four islands are five described species, with two now considered to be extinct (*N. darwini* and *N. indefessus*). These five described species of *Nesoryzomys* are split into two size groups, the larger of the species (*N. indefessus*,

N. swarthi, and *N. narboroughi*), and the smaller species (*N. darwini* and *N. fernandinae*). Previous systematic research has been almost exclusively on *N. narboroughi*, because *N. fernandinae* and *N. swarthi* were both thought to have been extinct. Discovery of populations on the islands of Fernandina (*N. fernandinae*) in 1995 and Santiago (*N. swarthi*) in 1997 allowed collection of specimens beyond the type series for these species. Only limited morphological descriptions are available for these two species. We describe gastric morphology, cranial measurements, and glans penis morphology for *N. fernandinae* and *N. swarthi* and compare these features to those reported for *N. narboroughi*. Using fluid-preserved specimens in the Angelo State Natural History Collections, we made observations and measurements of both the gastric and glans penis morphology. Images of stomach and glans penis anatomy were analyzed using ImageJ software and skull measurements were taken using digital calipers. Analysis of stomach anatomy showed similarities between *N. fernandinae* and *N. narboroughi*, but differed in *swarthi*.

46^F: Using ArcGIS to predict the co-occurrence of Virginia opossum (*Didelphis virginiana*) and raccoon (*Procyon lotor*)

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Species interactions play a key role in shaping community structure. Co-occurrence is one type of species interactions that has been the topic of recent ecological research. Previous studies share conflicting views on the association of Virginia opossums and raccoons. However, with their broad niche overlap, many opportunities for habitat sharing exist. Many studies have attempted to predict occurrence of animal species, but few have tried to predict the co-occurrence of taxa. This study utilized 6 years of live-trap data from Ames Plantation and Edward J. Meeman Biological Station in western Tennessee to predict the co-occurrence of Virginia opossum and raccoon via satellite imagery and the MaxEnt program. MaxEnt models produced from this study were successful in predicting species occurrence and co-occurrence. Areas with high percentage of deciduous forest near water displayed high probabilities of species co-occurrence. Because the niche breadth of Virginia opossums were smaller than that of raccoon, Virginia opossums could be the limiting factor in areas of co-occurrence. Future work could include gathering data that is more evenly dispersed to improve model predictions, prediction of co-occurrence over larger areas, or utilizing a different set of species.

47: Wildlife use of livestock water troughs in several states east of the Mississippi River

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Many factors influence availability and quality of natural water sources that wildlife might use on the landscape. However, when natural water sources are unavailable or undesirable, wildlife may opportunistically exploit artificial water sources provided for livestock. In 2016, we collected survey data from NRCS employees regarding the incidence of livestock producer reports of wildlife mortalities in livestock water troughs located east of the Mississippi River; 36.8% reported they or their producers observed dead animals in livestock troughs. In addition to the survey, Summer 2016, Summer 2017, and April 2018, we collected field data at livestock water troughs located in several states east of the Mississippi River. We examined the frequency of wildlife visits to troughs, the type of wildlife using these troughs, and the trough characteristics. During 48-hour sampling periods, we recorded wildlife use at each trough with trail cameras, and recorded bat activity and species richness in the vicinity of the trough with bat detectors. Several species of wildlife, the majority of which were either mammalian or avian, were observed at more than two-thirds of the livestock water troughs in our study. The level of wildlife use of water troughs observed in this study suggests that livestock troughs might be an important alternative source of water for some wildlife species, even on landscapes where natural water sources are not limited.

48^E: Evaluating the species distribution for the giant kangaroo rat (*Dipodomys ingens*)

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Understanding the range of a species is fundamental to enacting effective management strategies. This is especially relevant when it comes to the protection and recovery of endangered species. The giant kangaroo rat (*Dipodomys ingens*), an endangered keystone species endemic to California's Central Valley, is an example of a species with a range in need of clarification. The historic range map, drawn in 1992, covers the two largest giant kangaroo rat populations as well as some smaller populations that are not well-studied. No one has formally assessed the status of potential populations at the center of the Giant Kangaroo Rat range or whether boundary changes have occurred since this map was made 25 years ago. This study used several methods to assess the current distribution of the giant kangaroo rat, including areas that have so far received very little attention. These methods include surveys using satellite imagery, manned and unmanned flights, non-invasive transect surveys, and traditional live-trapping. This work features the findings of each of these survey techniques and the resulting distribution map.

49: The evolution of teaching and mentoring in the ASM: a brief and unauthorized history

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Jim Findley, one of our previous presidents, long-time society leader, and outstanding mentor frequently remarked, "If you want it done right hire a mammalogist." The American Society of Mammalogists is the strongest taxon-based society in the world—our journal is superbly run; we have an enthusiastic, dedicated membership; our leadership is dynamic and forward thinking; we take strong, activist, well-researched stands on political issues that we deem important; and not coincidentally, we have a significant endowment to help keep us strong. As we approach our 100th anniversary, it is useful to look back and reassess how we got here. I believe that one of the primary keys to our success is the mentoring that our students receive during their careers. Herein, I review some of the backstory on selected mentors, hoping to draw some insights into what made them good mentors. Although many mammalogists are good at "book-learning," leaders can usually credit their teaching and mentoring skills to outstanding mentors. Common characteristics of the best mentors in our society's history include working collaboratively with their students, creating opportunities for their students, and teaching by active example. Good mentors need to think critically but thinking critically is also thinking creatively.

50: Biological annihilation of mammals and the sixth mass extinction

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The loss of biological diversity as a result of the impact of the growing human population is one of the most severe global environmental problems, and probably the only one truly irreversible. Thousands of species and hundreds of thousands of populations of mammals (and all other life forms) are being driven to extinction every year. Current mammal extinction rates are increasingly higher than the "background extinction" rates prevailing in the Pleistocene, estimated at 1 mammal extinction per 5,000 species per 100 years (that is, 1 E/MSY). So, mammal species that become extinct in the last 100 years would take up to 7,000 years to disappear. But focusing exclusively on species extinction undermines the magnitude of the extinction crises. A sample of all mammals indicate that more than 32% of all species have declining populations, including both common and rare species. These estimates reveal an exceptionally current rapid loss of biodiversity indicating that a sixth mass extinction is already under way. This "biological annihilation" highlights the current magnitude of Earth's ongoing sixth major extinction event. It is still possible to avert the dramatic decay of biodiversity and the subsequent loss of ecosystem services intensified through conservation efforts. The window of opportunity is, however, rapidly closing.

51: Wolves for Yellowstone: predicting dynamics in time and space

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Wolf (*Canis lupus*) reintroduction to Yellowstone National Park is the most-celebrated ecological experiment in history. One of the outcomes of successful wolf recovery has been that predation is increasingly recognized as an ecological process that structures natural communities, and has been targeted as an important focus for conservation. Yet, the extent and magnitude of trophic cascades has been debated and few clear examples exist in terrestrial ecosystems, especially for behaviourally driven trophic cascades. I will review details of this debate for wolf recovery in Yellowstone National Park and conclude that as predicted by theory we see both temporal and spatial variability in predator-prey systems that likewise generate temporal and spatial variation in the expression of trophic cascades. Initially the consequence of wolf reintroduction was an interaction with elk (*Cervus canadensis*), the most-abundant ungulate in Yellowstone. More recently grizzly bears (*Ursus arctos*) and bison (*Bison bison*) have had an increasing role in ecosystem dynamics. Outside protected areas in western North America, however, humans have a dominant influence that overwhelms trophic cascades resulting in what appear to be bottom-up influences on community structure and function.

52^{E,HTA}: The underappreciated role of generalists in rodent-mycorrhizal dispersal networks

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Animals are often the primary dispersers of seeds and symbiotic fungal spores. Specialist species, that consume fruits or fungal fruiting bodies as their primary food source, are thought to play a more important role in dispersal networks compared to generalist species. However, dispersal networks are often based on occurrence data, overlooking the influence of animal abundance and inter-annual fluctuations in their abundance. We assessed the relative importance of generalist and specialist rodent species in the dispersal of mycorrhizal fungi in temperate forest. Using network analyses, we modeled the interactions of five rodent species and 34 mycorrhizal taxa over three years and across three forest types in northern New Hampshire. *Myodes gapperi*, a well-known fungal specialist, interacted more often with fungal taxa and carried higher spore loads compared to rodent generalists, making it the most important disperser of mycorrhizal fungi per individual. Nevertheless, during years when generalist species such as *Tamias striatus* and *Peromyscus maniculatus* reached high abundance, their relative importance in networks was equal to or greater than that of *M. gapperi*, particularly in forest types where *M. gapperi* was less common. Population increases of generalists were coincident with the germination of tree seeds following masting, a time when inoculation by mycorrhizal fungi is critical. Our findings suggest that although specialists play key roles in rodent-mycorrhizal dispersal networks, generalists play a heretofore underappreciated role.

53^{E,HTA}: Prescribed fire and thinning increases small mammal diversity while decreasing parasite loads in pine-oak woodlands

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Forestry management aims to increase habitat heterogeneity, manage game species, promote biodiversity, and improve stand health. While research on the effects of fire and thinning generally shows equivocal shifts for small mammal communities, research remains limited for the joint effects of how parasites and their hosts are impacted by habitat alterations. Parasites are important vectors of disease to both wildlife and humans, so characterizing the effects of management on host-parasite relationships is essential for determining whether altering disease dynamics is a reasonable management goal. To better understand host-parasite community responses to management treatments, we chose four sites representative of a gradient of pine-oak woodlands of the Cumberland Plateau including 1) open, grassland dominant, 2) sparse canopy woodland, 3) interlocking canopy woodland, and a negative control composed of a closed canopy forest. We characterized mammals and their parasites using standard diversity indices that we compared to vegetation composition and stand structure. We detected patterns in mammal and parasite prevalence and abundance at both temporal and spatial scales. However,

preliminary results suggest more frequently disturbed habitats harbor greater mammal diversity, evenness and abundances relative to less managed sites. Furthermore, parasite burdens tend to be highest in the control and less frequently managed sites. Taken together, these results suggest frequent planned thinning and fire management in pine-oak woodlands increase mammal diversity while decreasing parasite loads and transmission efficacy.

54^{HTA}: Hungry like the wolf: have coyotes experienced dietary release following apex predator extirpation?**

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The loss of apex predators frequently releases medium-sized mesopredators from competition, resulting in trophic cascades with widespread ecological impacts. For example, within the Pacific Northwest, historical extirpation of the gray wolf (*Canis lupus*) has been linked to the release of coyotes (*Canis latrans*), causing cascading effects in the interactions between wolves, coyotes, and foxes (*Vulpes vulpes* and *Urocyon cinereoargenteus*). Typically, mesopredator release studies focus on changes in population abundance. Despite hypotheses suggesting mesopredators can partially fill the dietary niche of vacant apex predators, it remains unclear if released populations experience any dietary change. Here, we test if mesopredator release results in cascading dietary niche shifts using museum specimens of the aforementioned canids. We quantified dietary niche using Dental Microwear Texture Analysis and analysis of stable isotopes from hair ($\delta^{13}\text{C}$ and $\delta^{15}\text{N}$). Coyotes and foxes were categorized as released from wolves by spatial and temporal proximity along a transect of Western North America. Mean dietary position did not change for coyotes that have undergone competitive release; however, dietary breadth increased towards space previously occupied by wolves. Similarly, both fox species showed no change in mean diet, yet had a reduction in dietary breadth near released coyotes. These findings suggest released mesopredators do experience cascading dietary niche shifts. Quantifying dietary shifts could better predict how mesopredator release cascades will alter trophic networks and energy flow in communities. This research was supported by a Grant-In-Aid of Research awarded to Brian Tanis in 2015.

55^{E,HTA}: Small mammal communities and habitat associations along an elevation gradient in southern California**

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Habitat associations along with competitive interactions play an important role in determining the composition and structure of small mammal community assemblages. These associations can mediate responses to climate change and vary across space, particularly by elevation, and through time. Therefore, there is a need for complete studies spanning an entire gradient. To improve our understanding of this relationship, we completed a comprehensive assessment of community assemblages and species habitat associations across an extensive elevation gradient spanning 2,500 meters in southern California. We used 10x10 trapping grids (15-meter spacing) with 12-inch Sherman live traps to survey heteromyid and cricetid rodents in paired sites in eight habitats along this gradient. We discovered fourteen species across the gradient with a mid-elevation peak in species richness and diversity. Canonical correspondence analysis, a form of constrained ordination, revealed strong relationships between community assemblages and key habitat metrics such as canopy cover, litter depth, soil hardness, and shrub and herbaceous cover. A greater understanding of community structure and habitat associations is critical to our understanding of how communities and species distributions change over time. This research was supported by a Grants-in-Aid of Research awarded to Aviv Karasov-Olson in 2016 and 2017.

56^E: A test of Eltonian niche conservatism for martens (*Martes* spp.) in the Pacific Northwest

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Niche conservatism – the retention of ecological traits across space and time – is an emerging topic of interest because it can predict species' responses to global change. The conservation of Grinnellian niche characteristics (e.g., species-habitat associations) has received widespread attention, but the conservation of Eltonian niche characteristics (e.g., consumer-resource interactions) remains poorly understood. Using a suite of stable isotope analyses, we explored Eltonian niche conservatism by comparing dietary niche overlap in American (*Martes americana*) and Pacific martens (*Martes caurina*) across the Pacific Northwest. We employed a paired design and quantified dietary overlap between species (*americana* vs. *caurina*) and geographical contexts (island vs. mainland) to assess the relative effects of landscape and phylogeny. We quantified pairwise dietary overlap in isotopic δ -space using multivariate permutation tests and standard ellipses. We then estimated proportional diets using isotopic mixing models and developed a novel test of niche overlap in proportional dietary space using utilization distribution overlap indices. We detected no dietary overlap between any marten populations in either in δ - or p-space, but both mainland populations specialized on terrestrial vertebrates while island populations exhibited generalist diets. Ultimately, we found no evidence of Eltonian niche conservatism, and our results suggest that landscapes, not phylogeny, mediate consumer-resource dynamics. These results question the efficacy of recently proposed carnivore-driven restoration efforts that are contingent upon dietary conservatism.

57: Rodent predation by the nocturnal-hunting letter-winged kite during resource pulses in arid Australia

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Acyclic predator-prey interactions have evolved in landscapes that experience resource pulses that are temporally unpredictable. This unpredictability results in consumers exhibiting non-cyclic population dynamics. Because of the acyclic nature of consumer outbreaks, many predators are nomadic such that predator-prey interactions occur irregularly. To understand the dynamics of such a system, I examined the numerical and functional response to rodent outbreaks by the letter-winged kite (*Elanus scriptus*) in the Simpson Desert, Australia; a region that experiences major pulses in primary productivity, driven by large rainfall events every 5-8 years. The letter-winged kite is unique in being the only night-hunting species in the family Accipitridae. It is a rodent specialist (rodents contribute >95% by frequency to its diet). Letter-winged kites irrupted in the area on only three occasions during 20 years of sampling (1999-2018) and remained for a maximum of 20 months. Each of the three irruptions occurred only during the peak of rodent population cycles. The dominant rodent prey species varied across the three periods being either the native plains mouse (*Pseudomys australis*) or the introduced house mouse (*Mus musculus*). Although present during one of the rodent outbreaks, the long-haired rat (*Rattus villosissimus*) was infrequently consumed by the kites. The bipedal spinifex hopping-mouse (*Notomys alexis*) was also captured infrequently even when abundant.

58: Evolution of dentary and scapular shape in foxes: are gray foxes (*Urocyon cinereoargenteus*) unique?

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We used geometric morphometric techniques to explore shape variation in the dentaries and scapulae of foxes. Dentaries and scapulae from 18 and 11 species, respectively, were photographed in lateral view at the Los Angeles County Museum of Natural History, Field Museum, SIU Carbondale Mammal Collection, and University of Kansas Museum of Natural History. We placed 12 homologous landmarks and edgels on each dentary, as well as 50 semi-landmarks along the margin of the angular process. Ten landmarks were placed on each scapulae with 20 semi-landmarks across the caudal and dorsal borders, and 30 semi-landmarks across the cranial border. We performed a Procrustes superimposition to align the specimens, followed by a canonical variates analysis, and principal components analysis. Dietary data were collected for each species and a principal components analysis was performed.

Canonical correlations were performed with PC scores from diet, scapula shape, and dentary shape of each species.

59:** Effects of climatic stress on morphological symmetry in bushy-tailed woodrats (*Neotoma cinerea*)

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Many species have ranges constrained by climatic tolerances. Life near the limits of tolerance is challenging and can have lasting sub-lethal phenotypic effects, including random, non-directional deviations from bilateral symmetry—termed fluctuating asymmetry—reflecting developmental instability caused by genetic or environmental stress. Although marginal populations may adapt to stabilize developmental pathways, we generally expect more stressed populations to display higher levels of asymmetry. I explored the effect of climatic stress on fluctuating asymmetry in the wide-ranging bushy-tailed woodrat (*Neotoma cinerea*) using geometric morphometric analysis of over 400 adult *N. cinerea* skulls available from natural history museums and originating from across the species range. I quantified fluctuating asymmetry over the midline of each skull using 3-dimensional landmarks, selected a species distribution model from a set of candidate models built from climatic variables, and compared the degree of asymmetry to climatic suitability from the selected model. I clarified the relationship between asymmetry and climate using additional models including temperature, precipitation, and habitat productivity. Preliminary analyses suggest that while overall climatic suitability does not affect asymmetry, extremes of temperature and precipitation have weak effects at the southern edge of the species range. Future work will explore the effects of other stressors, particularly low genetic variation, to determine whether they have stronger explanatory power for patterns of asymmetry. This research was supported by an Albert R. and Alma Shadle Fellowship awarded to Angela Hornsby in 2016.

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

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Whether Bergmann's and Allen's rules hold for *Peromyscus maniculatus* was examined for approximately 3,000 mice (primarily subspecies *artemisiae*, *bairdii*, *blandus*, *borealis*, *gambelii*, *gracilis*, *osgoodi*, *rufinus*, and *sonoriensis*). No evidence was found to indicate that their body size increased with decreased temperature. Contrary to expectation based on Allen's rule, ear length increases with altitude. Furthermore, it appears to be more related to precipitation than temperature. Likewise, tail length, foot length, and skull length appear to be unrelated to temperature, but affected by amounts of precipitation.

61^F: Unintended morphological effects of captivity in Mexican wolves (*Canis lupus baileyi*)

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Endangered species in captivity often originate from small founding populations and are introduced to a variety of novel stressors and selection pressures while concurrently being removed from many of the ongoing natural selection pressures of the wild, circumstances that may make captive populations prone to morphological divergence. Zoos can act as genetic reservoirs for rare and endangered species; however, changes among captive populations could hinder their contribution to conservation. To assess whether such changes occur unintentionally in conservation-based institutions such as zoos, we used 2D geometric morphometric techniques, examining these effects among captive, wild, and reintroduced Mexican wolves (*Canis lupus baileyi*). Principal component and linear discriminate function analyses indicate that captive lineages may be exploiting a unique region of morphospace uninhabited by wild wolves. Such changes appear to be cumulative, where additional captive generations grow increasingly dissimilar from wild populations. This trend is also apparent among reintroduced animals, suggesting that these changes are not due merely to plasticity. These results may be a function of the small founding

population or unintentional captive selection. Habitat losses have placed an increasing burden on zoos, where additional captive generations may be required before a reintroduction can be considered, potentially leading to an accumulation of changes. Such results may have implications for captive species management and conservation practices.

62: Postcranial morphological trends in Rodentia: a morphometric analysis of the appendicular skeleton

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Rodents are one of the most diverse groups of mammals, both in the quantity of species and the morphological disparity among its constituents. Rodents offer a great opportunity to study how evolutionary morphology may be biased by influences on variation such as development or selection on form/function. In particular, rodents are uniquely suited because of the changing and convergent functional demands across the diversity of locomotory forms, such as; semiaquatic, arboreal, fossorial, jumping, and gliding. Studies using the post-cranial skeletons are surprisingly uncommon even for questions addressing locomotion. This is not entirely unjustified as the overwhelming prevalence of preserved specimens in museum holdings have until recently retained only the skull and skin, and given the importance of the skull to ecological correlates it has been a useful structure for taxonomy, and the source of many morphological studies. In this study, we use geometric morphometrics to explore how locomotion has influenced the shape variation across the major post-cranial skeletal elements. In particular we focus on what features of morphology correlate with locomotion, the magnitude of convergence in morphology, and if changing locomotory mode influences the rate of morphological change. Our initial findings suggest that morphometric change largely matches a brownian motion model of evolution, as well as finding that the range of variation for certain generalized locomotory modes often matched that of more specialized classifications.

63: Modularity during sigmodontine radiation

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Studying the modularity is fundamental to understand the evolution of complex features, as the modular structure influences multivariate evolution. Here, we analyzed skull modularity patterns on a broad phylogenetic and taxonomically structured sample of sigmodontine rodents, the mammal clade with the greatest diversity and distribution in the Neotropics and adapted to a wide range of lifestyles. We used comparative methods and quantitative genetic approaches to investigate the presence of specific functional/developmental modules within-groups and between-groups in sigmodontine species along their phylogeny. Our database includes 35 cranial measurements taken from 2,897 specimens representing 53 species for all tribes of the subfamily. We found a clear association of within-species modularity patterns with the between-group divergence, with traits belonging to functional/developmental groups evolving in a correlated way among species more often than expected by chance. Particular traits (within bone measurements) of the face, including oral and nasal regions, are not only greater in terms of correlation within species but also evolve in a correlated way among species. Allometry seems to play a role on this result since those traits are the ones developing latter during ontogeny and contributing more to allometric size variation.

64: A Wisconsin bat curriculum for high school biology courses

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Citizen science engages members of the public by involving them in authentic research experiences at various stages from data collection through data analysis. Currently much of community and citizen science involves utilizing the public in the collection of scientific data. We want to expand this to include the interpretation, analysis, and sharing of the data with peers and a broader audience. Bats are receiving

much national and international attention with new threats such as white-nose syndrome and collisions with wind turbines. With the Wisconsin Bat Program, the Wisconsin DNR provides a national model involving the public in the collection of bat acoustic data that has produced copious amounts of data since 2007. In addition to the numerous walking, driving, and boating routes uploaded to the Wisconsin Bat Program site, five stationary bat detectors were deployed throughout the state. The stationary detectors provide both spatial and longitudinal data on Wisconsin bats by monitoring bats at multiple sites over multiple years. We are developing a curriculum that makes this data available for high school biology courses. We have identified high school biology teachers in the Milwaukee area to help pilot some of the modules in the curriculum. We will demonstrate some of the modules and how they line up with Next Generation Science Standards (NGSS) and ACT College and Career Readiness Standards (CCRS).

65: What is the best approach for training teaching assistants to make their labs more active?

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Active learning (AL) teaching techniques benefit all students and can close achievement gaps for under-represented minority, first-generation, and female students in STEM disciplines. However little is known about how to best train teaching assistants (TAs) to use AL. Specifically, will TAs feel more knowledgeable about AL and find AL more useful if they are presented with evidence for AL's effectiveness or if they are able to facilitate AL themselves? To investigate this question, we offered an AL workshop and split participants into two groups. The A group worked in teams to learn an AL technique with a workshop facilitator, then these teams modeled the activity with their peers acting as students. In the E group, facilitators modeled the activities with all TAs acting as students and spent significant time presenting evidence of AL's effectiveness. Pre- and post-workshop surveys were analyzed to assess TA perceptions of AL. Our preliminary results suggest E group participants reported greater knowledge of AL after the workshop than A group participants. However, A group participants found all of the AL techniques more useful than E group participants. These results suggest that actually *modeling* AL made them more useful to TAs than simply *experiencing* the same techniques as students—even with the accompanying evidence. Therefore, assembling an easily implemented toolkit of strategies transferable to any course will facilitate TA adoption of AL.

66: Early engagement of undergraduates in research, an avenue for science education reform?

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Building on previous science experiences and reinforced by college science courses, students often come to think of science as an accumulation of facts and scientists as purveyors of these facts, a notion that is fundamentally incorrect. Rather, science is a process for understanding the physical world and anybody can use this process, but it requires practice to be proficient. Further, these misconceptions about science underpin many issues that plague our field and reduce scientific literacy within our society. These results have led to calls for reforming science education through student-centered, inquiry based, and experiential learning methods. One potential solution is to support undergraduates in conducting authentic scientific research. Here we report on a two-tiered course designed to provide undergraduate students a chance to participate in research as college freshman and sophomores. In this talk, we will briefly outline course competencies and structure. With data from 7 semesters and 53 students, we will summarize our successes, failures and areas for improvement, as well as provide suggestions to faculty interested in designing their own research course. This experience has helped students refine their interests, expand their professional network and resume, and learn marketable skills while simultaneously advancing science. Our hope is that this early engagement in authentic research will enhance what they gain in traditional courses and better equip them to apply science in solving real-world problems.

67: Squirreling around for science 301: CURE implementation & scaffolding for upper level courses

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Course-based undergraduate research experiences (CUREs) enhance not only research skills of students, but also confidence in conducting research and ability to succeed in science. Although few researchers have examined the influence of extended or multi-year research experiences on the development of students as scientists, recent literature suggests there are differences in both cognitive and personal development between novice and experienced student researchers. In particular, extended or multiple research experiences are likely to play an important role in student development of science identity. We have begun implementation of an observational CURE in which students investigate tradeoffs between foraging and vigilance behaviors in sciurid rodents; here, we discuss development of advanced CUREs that scaffold into upper-level courses to provide a multi-year research experience. For example, upper level students used radio telemetry to investigate space use of sciurid rodents along habitat gradients on/near college campuses. Additional upper level students pursued risk-reward tradeoff research via camera traps and giving up density (GUD) trials centered on focal animals from the observational behavioral study. As part of a multi-institutional network, these advanced CUREs allow students to collect and analyze standardized spatial data from contributors at multiple institutions while revisiting and expanding on research questions developed earlier in their college careers.

68: Choose your own adventure: Does allowing students to participate in course development increase student motivation?

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While many instructors design courses with the goal of engaging students in learning activities that are interesting and relevant, most of these selections are made before the course begins. However, a wide body of research suggests that student motivation can be positively influenced by allowing choice and engaging students as partners in a learning community. Here, I report on the results of a semester-long experiment in allowing students to identify and select syllabus topics for an upper division undergraduate course. Students were involved in the process of topic identification, development, and selection at the beginning of the semester, and the resulting course syllabus was designed around their ideas. Student feedback was collected immediately after the topic selection and again at the end of the semester to assess affect; student views about science were assessed in a pre/post survey. In addition, course learning objectives were contrasted with those from a previous course to assess whether expectations were similar. Finally, impacts on instructor time and effort were assessed based upon the percentage of material overlapping with the previously taught course. This approach positively influenced student motivation and views about science, and maintained the rigor of previous instructor-designed coursework. However, much of the material needed to be developed for the course *de novo*, making this a more costly exercise in terms of instructor time.

69: Squirreling around for science 101: multi-campus implementation and piloting of a Course-based Undergraduate Research Experience

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Recently, Course-based Undergraduate Research Experiences (CUREs) have been proposed as a way to engage undergraduates in authentic research and teach core concepts using inquiry-based activities. Compared to traditional labs, CUREs may better enhance student intellectual independence and critical thinking because scientific outcomes are unknown. Here, we introduce a CURE to investigate tradeoffs between foraging and vigilance behaviors in sciurid rodents for use in introductory and non-majors biology classes. Through the development of a multi-institutional network, this project provides a framework for students to develop research questions, collect standardized behavioral data, and analyze broad datasets from student and class contributors at multiple institutions. One advantage of this approach is that it provides an entry point for instructors seeking to engaging students in authentic research experiences and data analysis across a wide variety of courses and levels of student expertise. We provide an overview of the collaborative creation of the project and materials, course-specific implementation of the project, and the broader educational network which unites students and classes across our many institutions.

70: Small mammal, vector, and pathogen data collection in the National Ecological Observatory Network

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The National Ecological Observatory Network (NEON) is a 30-year, large-scale research program that is designed to enable ecological discovery by providing open-access data generated by standardized sampling of a diversity of taxa and ecosystem variables. A key component of the Observatory is terrestrial organismal sampling intended to increase our understanding of climate change and land use impacts on phenology, demography, diversity, community dynamics, pathogen presence, and ecosystem function. This includes the long-term community dynamics of small mammals and their pathogens at 47 sites distributed throughout the United States and its territories. Standardized sampling at this combination of spatial and temporal scales for small mammals is unprecedented. Here, we outline the current small mammal sampling designs for NEON, including vector and pathogen data, and the rationale for these designs, and demonstrate how these and other NEON data can be accessed by the larger community (<http://data.neonscience.org/home>) to support individual research and education programs (<http://neondatakills.org/>).

71: March Mammal Madness: a successful story about science and social media

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Since 2013, the blog “Mammals Suck... Milk” has featured a virtual combat competition among 65 species of animals in a virtual tournament called March Mammal Madness, in honor of the NCAA College

Basketball March Madness Championship Tournament. The competition started as a thought experiment among colleagues and has become a pedagogical innovation that engages people from around the globe by creatively integrating scientific literature, original artwork, and digital technologies. Briefly, the winners of simulated animal battles are determined by a probabilistic function of the two species' attributes within a preselected and/or randomized habitat. Scientific literature is cited to substantiate likely outcomes should the two species encounter one another. Battles are “live-tweeted” by a team of scientists and battle summaries are available afterwards through various virtual media, including Facebook and a library guide created by Arizona State University. Throughout the multi-week competition, participants learn about biological concepts including inter-species interactions, how natural selection has shaped adaptations, conservation management, and the significance of both arts and sciences in education. Here, we summarize the success of the latest championship (#2018MMM) by estimating the potential impact of broadcasting research through social media and classrooms, and by sharing reactions from participants. Our estimates strongly suggest that more people are participating in the championship every year, likely promoting one goal of the competition to inspire awe for the natural world.

72: Field courses as general education science courses for non-majors

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General education science courses are intended to increase overall science literacy for students not majoring in STEM fields. However, it can sometimes be difficult to promote engagement in these general education students as the students do not see how the material relates to their major, may be focused only on checking off a box required for graduation, and may prioritize their other courses over the science course. Research on general education courses indicates that they can be improved by encouraging intrinsic motivation in the students enrolled. This intrinsic motivation can be supported through inquiry-based learning, creation of a learning community, independent work requiring self-determination, and high expectations on the part of the instructor. Here, I describe how I have used two field courses in Costa Rica as general education science courses. I explain how the travel and independent study aspects of these courses lead directly to the above components and created intrinsic motivation in non-science majors. Further, I provide assignments and comments from the students indicating how the field experience broadened their understanding and appreciation of science.

73^{E,HTA}: Down the rodent burrow: weasels exhibit evolutionary shifts towards smaller and more elongate body plans**

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Why some animals exhibit extremely elongate body plans has puzzled many people for centuries. In the carnivoran clade Mustelidae, body elongation has been suggested to be an innovation for the exploitation of novel Mid-Miocene prey and habitats, resulting in increased species richness of “elongate” mustelids. To further test this hypothesis, we quantified body shape using the vertebrate shape index (VSI), a metric that describes a continuum of body shapes and allows for examination of the underlying morphological changes that drive the evolution towards more elongate body plans, body size, and relatively limb lengths. We found that mustelid crown clades Helictindinae, Martinae, Ictonychinae, Mustelinae and Lutrinae exhibited shifts towards smaller, more elongate body plans with reduced limbs. Furthermore, we found that body elongation exhibited negative relationships with body size and forelimb length but not hindlimb length suggesting that more elongate species are smaller and exhibit relatively shorter forelimbs. This relationship between body elongation and forelimb length has not previously been described in mammals but follows the major trend exhibited by other vertebrate clades. Our results are the first to quantify body shape in mammals and confirm that weasels are, indeed, small and exhibit the most elongate body shapes. This extension of the body may have served as an innovation by facilitating the ability to exploit subterranean habitats and prey. This research was supported by a James Patton Award awarded to Chris Law in 2016.

74^{HTA}: The role of locomotor mode in lineage turnover and persistence among Indo-Australian rats and mice**

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Island colonization followed by in-situ adaptive radiation is thought to have generated the patterns of endemism we see on islands today. Nowhere is this more prominent than the Indo-Australian Archipelago (IAA), where four isolated biogeographic regions contain high levels of endemism. Classical views predict that, following the arrival of an ecological generalist colonizer, subsequent speciation generates more specialist forms, increasing the overall ecological and morphological disparity within the resulting clade. We used a time-calibrated phylogeny of 395 murids (Rodentia: Muridae), along with measurements of locomotor mode (i.e. arboreal, general, terrestrial, amphibious) to reconstruct the ancestral states at each instance of island colonization across the IAA. We used Bayesian methods to examine lineage-specific speciation rates associated with each locomotor mode. Results suggest that colonizing lineages are always terrestrial or general, and the transition to arboreality is both rare and unidirectional. However, arboreal species appear to persist in older lineages in the face of subsequent invasion by rapidly diversifying terrestrial lineages. Phylogenetic logistic regression shows that branch lengths are longer for arboreal species than for other locomotor modes, providing support for the arboreal persistence hypothesis. These findings suggest that the rare transition to arboreality allows some IAA murids to escape competition with newly arriving lineages. The association between locomotor and diversification modes holds exciting potential for future studies of both living and extinct lineages of mammals. This research was supported by a James L. Patton award to Jonathan A. Nations in 2017.

75: Reducing uncertainty in past/future range predictions: models and population genetics for a Mexican shrew

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Predicting the areas climatically suitable for a species in the past or future represents an important endeavor for basic and applied science. Models of species niches/distributions yield such estimates, but with substantial uncertainty. One major source of uncertainty corresponds to differences among Global Circulation Models (GCMs) of past/future climates. We outline and begin to test a way to use genetic data to identify the GCM/s that best predict a species' past distribution. We do so for a Mexican cloud-forest shrew tightly associated with cool/wet conditions (*Cryptotis mexicanus*). First, we applied a niche model to the climate estimated for the Last Glacial Maximum (LGM) by three GCMs and determined the areas predicted suitable. Next, we identified regions where the GCMs yielded divergent predictions (continuously suitable areas with high genetic diversity vs. those colonized post-LGM holding low genetic diversity). Then, we conducted field sampling in one such region (Sierra Juárez of Oaxaca) and sequenced the mitochondrial cyt-b gene for those samples and others across the species' range. Ongoing analyses of the sequences will allow determination of which GCM/s better predict current genetic patterns. Using the best-performing GCM/s will allow tighter, more realistic estimates of past and future suitability in this part of the Neotropics. This approach can be applied elsewhere to identify the most realistic GCM/s in a given region.

76^{E,HTA}: The role of ecological opportunity and incumbency in Philippine "old endemic" rodent diversification (Muridae: Murinae)**

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The role of interspecific competition in macroevolution has been explored across multiple spatiotemporal scales. In competitor-deficient, spatially-limited systems, lineage and morphological diversification can proceed through diversity-dependent evolution, in which evolutionary rates are initially rapid but decline over time as niches are filled. However, if repeated invasion of the system by ecologically similar lineages occurs, the evolutionary response of secondary colonists may be inhibited because this lineage must compete for limited habitat with an “incumbent” lineage that has previously colonized and diversified in the system. Previous studies have failed to recover the signal of incumbency at continental scales, which may be too coarse to exhibit persistent inter-clade interactions. The importance of persistent competition warrants examination at the island scale, where competition for suitable habitat and resources should be most intense. To test for incumbency’s signature at this more limited spatial scale, we compared rates of lineage diversification and mandibular evolution of two clades of Luzon Island, Philippines endemic rodents: the Phloeomyini and Chrotomyini. We found that uniform constant-rate processes, rather than diversity-dependent processes, best describe the evolution of the two Luzon “old endemic” clades, and the secondary-colonizing Chrotomyini may exhibit higher rates of evolution than the incumbent Phloeomyini. Our results suggest processes other than incumbency and diversity-dependent evolution are responsible for evolutionary rates, even in systems where multiple colonizing lineages have been in prolonged spatiotemporal contact. This research was supported by an ASM Grant-in-Aid awarded to Dakota M. Rowsey in 2016.

77: Hox clusters molecular evolution provides hints for mammalian evolution

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Because of their crucial role in defining the identities of body axis in nearly all metazoans, Hox genes have long been great candidates to drive the morphological diversification of animals. Here we report on the molecular evolution of the Hox clusters in mammals. We characterized several vertebrate Hox clusters, screened for repetitive elements, identified conserved non-coding elements (CNEs) using a comparative genomics approach, and measured the relative rates of evolution of the mammalian sequences in comparison with those of other vertebrates and within mammalian lineages. To identify specific sites that had undergone statistically significant levels of either conservation or acceleration in focal clades we conducted a statistical test using phylogenetic information. Our comparative analyses successfully identified CNEs that are highly conserved throughout mammalian evolution, being present only in mammalian species. These CNEs likely arose on the stem mammalian lineage and possibly have had an important role in the early mammalian evolution, mainly in eutherians. In addition, we were able to identify CNEs restricted to some lineages, and these regions are good candidates to further study in details in these specific groups. Moreover, our analyses confirm one more time the value of comparative evolutionary genomics approaches in the study of molecular evolution of genomes.

78^E: Could a failure in a post-mating isolation protein allow hybridization in deer species in Texas?

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White-tailed deer (*Odocoileus virginianus*) and mule deer (*Odocoileus hemionus*) occur naturally in Texas. Hybridization is thought to commonly occur between these two species in the Trans-Pecos region and along the edges of the Llano Estacado. Given that hybridization occurs, perhaps the molecular mechanism that serves as a post-mating isolation barrier fails, allowing the two species to mate. One of the genes involved is zonadhesin (ZAN), a sperm protein that is crucial in species-specific binding of the

sperm to the egg during fertilization. ZAN is the only mammalian protein which shows species specificity across multiple taxa and may act as a potential post-mating isolation mechanism that prevents two species from interbreeding. If the ZAN pathway fails and no longer serves as a barrier for reproductive isolation, then presumably the sperm cell of one species can recognize the egg cell of the other species, allowing fertilization to potentially occur. The focus of this study is to evaluate ZAN, a candidate gene that acts as a post-mating isolation barrier, relative to gametic specificity. ZAN sequences will be analyzed for differences (nucleotide and amino acids) between hybridizing taxa and to determine if the presumptive failure of ZAN allows introgression to occur. Additional molecular markers will be utilized to develop a multi-locus genotype, which will determine the directionality and level of introgression (F1, backcross, multi-generation backcross) between the two species.

79^{E,HTA}: Identifying geographic variation in the Virginia opossum's diet using stable isotopes**

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Virginia opossums (*Didelphis virginiana*) noticeably expanded their range northward over the past century. Their success in colonizing new communities is often credited to their generalist diet. Despite this hypothesized adaptation, patterns in diet across their geographic range has never been examined. Because *D. virginiana* is found from Central America north to the Midwestern U.S. and New England, we used stable isotopes as a proxy for diet – nitrogen ($\delta^{15}\text{N}$) indicates relative trophic level while carbon ($\delta^{13}\text{C}$) informs whether C_3 or C_4 plants form the base of their food chain. We first established that opossum guard hair represents the lifetime diet of an individual by sampling captive opossums with well-recorded diet shifts from adolescence to adulthood. Hair samples from museum skins representing Central America, Texas, Gulf Coast, Midwest, and Northeast were evaluated using stable isotope Bayesian ellipses to determine niche width for each region. The niche width of opossums in the Midwest was similar in size to that of Central America and Texas, but the niche width in the Northeast was approximately a quarter the size of the other regions. Neither the year collected nor latitude explained variation in opossum's isotope values, suggesting abiotic or biotic forces are acting to shrink the niche in opossums in the northeast. Our results suggest that a generalist diet does not adequately explain the opossum's range expansion into the Northeast. This research was supported by a Grant-in-Aid of Research awarded to Lisa L. Walsh in 2017.

80: Demography of snowshoe hare population cycles at Kluane Lake, Yukon

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The spectacular ten-year cycles exhibited by the snowshoe hare (*Lepus americanus* Erxleben) populations across the boreal forests of North America has fascinated generations of ecologists. Using long-term (1977-2017) mark-recapture data, we tested for the influence of cyclic phase (increase, peak, decline or low) and season (fall to spring, or spring to fall) on the apparent survival, recruitment, and realized population growth rate of a cyclic snowshoe hare population in the southwestern Yukon, Canada. Monthly recruitment rate (f) varied across cyclic phases, with the highest recruitment during the increase phase (0.174 ± 0.003) and the lowest recruitment during the decline phase (0.058 ± 0.003). Monthly apparent survival (ϕ) varied strongly across cyclic phases with the highest survival during the increase phase (0.917 ± 0.003) and the lowest survival during the decline phase (0.819 ± 0.003); this translates to yearly survival rate of 35.4% and 9.1% during the increase and decline phase, respectively. Monthly realized population growth rate (λ ; the ratio of population sizes in successive months) during the increase, peak, decline and low phase was 1.091 ± 0.006 , 1.010 ± 0.006 , 0.877 ± 0.006 , and 0.942 ± 0.007 , respectively (or 284% annual population growth during increase and 80% annual decline during the decline phase). We present the demographic mechanisms underlying the phase-specific changes in the population growth rate and discuss the drivers of these patterns.

81^F: The influence of density dependence, weather, and human exploitation on beaver population dynamics

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Beaver (*Castor canadensis*) populations often exhibit density dependent regulation through the interaction of habitat quality and territoriality among neighboring colonies. Extrinsic variables such as weather can also influence population dynamics, and human exploitation has been shown to suppress beaver populations below carrying capacities. The cumulative effects from these factors likely influence short-term beaver population fluctuations, however the relative influence that they have remains poorly understood. Using nearly 30 years of colony survey data (1975–2002), we evaluated the relative influence that density dependence and extrinsic covariates had on inter-annual beaver colony fluctuations across 15 survey routes in Minnesota. We combined a density dependent population growth model with weather and human exploitation variables within a linear mixed effects model framework. Preliminary results suggest that density dependence influenced inter-annual fluctuations to a greater extent than weather or human exploitation, even after accounting for observer bias within the colony surveys. Beaver colony density dependence appeared to have a non-linear response, which we hypothesize is a consequence of using beaver colonies as a proxy for population size. This survey method does not account for colony size fluctuations that occur spatially and temporally among beaver populations. We posit that higher colony growth rates at lower densities is a function of increased juvenile dispersal rates due to the combined effects of population density and habitat quality.

82: Climatic variables, seasonality, and population demography of the big-eared woodrat in coastal-central California

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In arid and semi-arid environments, water is a limiting resource and changes in temperature and rainfall patterns can have profound impacts on small mammal populations. How small mammals will respond to the hotter and drier summers predicted for these already water-restricted environments remains unclear. To disentangle the seasonal effects of weather patterns on the survival probability (Φ) and recruitment rate (f) of the big-eared woodrat (*Neotoma macrotis*), we used Pradel's temporal symmetry models on a 21-year (1993-2014) biannual capture-mark-recapture dataset collected in semi-arid California oak woodland, an ecosystem with a cool, wet season (October-April) contrasting with a hot, dry season (May-September). Monthly Φ was higher in the dry season than in the wet season, whereas f was higher in the wet than in the dry season. For all tested covariates, an interaction with season improved the models, suggesting a seasonality effect. Although all covariates significantly affected both Φ and f , total rainfall with a one-season lag had the strongest effect on both Φ in the dry season and f in the wet season, suggesting that the big-eared woodrat may be threatened by the more frequent and intense droughts that are predicted throughout this species' distribution. However, the big-eared woodrat's only moderate response to temperature and rainfall variability during our 21-year study, and its positive response to hot, dry summers, may help it cope.

83: Paleoecology of a Pleistocene woodrat (*Neotoma*) midden and coprolites from the La Brea Tar Pits

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Rodents of the genus *Neotoma* have played an important role in paleoecological reconstructions of arid areas. Their nest-building behavior creates time-capsules of local vegetation and climatic conditions that may be preserved as middens for thousands of years. Further, their biotic responses to temperature change are evident through fecal pellet proxies of body size. We report the first coprolites from the La Brea Tar Pits Project 23 deposit and apply stable isotopes of carbon and nitrogen to investigate their paleoecological significance and diet record. The La Brea Tar Pits of Los Angeles, California, is world-renowned for its Late Pleistocene mammalian megafauna, including dire wolves, ground sloths, and saber-tooth cats, excavated from sediments of active asphalt seeps. Radiocarbon dates on midden-associated coprolites confirm woodrat activity at La Brea ~49,000 years before present. We tentatively identify these coprolites as *Neotoma fuscipes* by size/shape and the presence of teeth in other deposit grids. Fecal pellets were intermixed within a large clump of matted leaves, sticks, and seeds. Fecal stable isotopes are an increasingly common tool in mammalogy, and we employ them to reflect rapid resource use at the time of midden formation. We combine these isotopes with vegetation identifications, the community context of La Brea megafauna, and the current distribution of *Neotoma* in Los Angeles to better understand the species history from the Pleistocene to present.

84: Reproductively mediated effects of precipitation on populations of *Dipodomys ordii* and *Peromyscus maniculatus* in Utah

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During a 4-year period in the Uinta Basin, Utah, there was a direct correlation between precipitation in October and the monthly densities of small-mammal populations the succeeding March to June. This correlation was predominantly due to a plunge in population density that succeeded the absence of any precipitation in October 1976 at the commencement of a drought, and the 1980 surge in population density that followed intense precipitation in October 1979. Precipitation was below normal from August 1975 through March 1977 (except for 2 months). Population density distinctly declined from September 1976 to September 1977 and did not significantly increase until ample precipitation was realized in October 1979. Plausible causes of the proximate responses of the population densities of *Dipodomys ordii* and *Peromyscus maniculatus* to augmented precipitation are presented.

85^E: Quantifying forage characteristics for ungulates with remotely sensed data

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Recent advancements in remote sensing technologies have allowed wildlife researchers to assess vegetation characteristics (e.g., vegetation biomass, plant phenology) in ways that would have been traditionally time intensive and potentially cost prohibitive. Using remotely sensed metrics, such as the Normalized Difference Vegetation Index (NDVI), as a proxy for vegetation characteristics, however, hinges on the rarely tested assumption that remotely sensed data accurately represent on-the-ground vegetation. We tested the extent to which remotely sensed data reflects on-the-ground vegetation by comparing vegetation biomass calculated from coarse-scale NDVI (acquired via satellite-derived remote sensing) and fine-scale NDVI (acquired from modified point-and-shoot cameras) with measures of on-the-ground vegetation biomass in multiple habitat types. Habitat types included conifer forests, deciduous forests, grass-, forb-, and shrub-dominated areas across summer ranges and stopover sites for mule deer (*Odocoileus hemionus*) in the Wyoming Range, western Wyoming, USA. The relationship between biomass estimated on-the-ground and via camera varied between habitat type and individual site, which highlights the importance of calibrating relationships between remotely sensed and on-the-ground data in a specific study area. Verifying the assumptions of remotely sensed data in ecological studies will strengthen research intended to guide conservation efforts for species affected by climate, anthropogenic influences and variation in phenological patterns.

86^{E,HTA}: Viability of population viability analyses: a critical evaluation

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Population Viability Analysis (PVA) is an important quantitative tool in the management of imperilled mammals and bird species with applications ranging from research design, threat assessment, and development of management frameworks. Given the importance of PVAs it is essential that they are rigorous and adhere to widely-accepted guidelines; however, quality of published PVAs are rarely assessed. We evaluated the quality of 106 PVAs (71 mammal species and 32 bird species) published in peer-reviewed journals between 1990-2017. We hypothesized that PVA quality would be: (1) lower for studies using generic software programs; (2) would be higher for PVAs developed for imperilled species; (3) would increase over time; and (4) would be higher for studies published in high impact factors journals. Most measures of PVA quality were lower for studies based on generic programs. Surprisingly, conservation status of the species did not affect PVA quality. Impact factor positively influenced all measures of PVA quality except model quality. Contrary to our expectation, PVA quality generally declined over time, suggesting that quantitative literacy of PVA practitioners has not increased over time. Only 21.69% of the studies met our definition of high quality, which is troubling because poor quality studies may have misinformed conservation decision. We call for an increased scrutiny of PVAs, especially of imperilled species, by wildlife managers before using the results in conservation decision making.

87^{E,HTA}: Analyzing behavior and aggression in coyotes across contexts and urbanization gradients

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Animal behavior and personalities can be influenced by environmental pressures and have been linked to life history traits and fitness. Urbanization may cause behaviors of individuals or populations to change as environments can influence or create feedbacks with and among behavior, stress, and underlying genetics. Previous studies, predominantly in birds and small mammals, found differences in behavior between habitats and increased boldness and/or aggression in urban landscapes. Coyotes (*Canis latrans*) are a widespread, generalist carnivore that inhabit areas across developmental gradients. We hypothesized that there are differences in behavior between individuals and among coyotes using different urbanization levels. We recorded behaviors across five different contexts consisting of observational and manipulative components in a field and lab setting on 142 unique individuals (161 total) from 2014-2018. Coyotes inhabited Chicago Metropolitan Area's natural areas (forest preserves) in the suburbs, suburban matrix, and urban core. We recorded individual behavioral actions, assigned an overall and context specific aggression score, and had each observer assign a bold and aggressive classification, along with an aggression level. We found differences in behavior across individuals, contexts, and development levels. Some behavior classifications were more consistent with behavioral actions than others. Identifying and measuring possible behaviors, contexts, and landscape types that may influence behavior, particularly aggressive behaviors, is important to properly manage and prevent conflict between coyotes and people, especially in urban environments.

88: Altitudinal stratification of rodents along the Ibrahim River – Mount Lebanon riparian ecosystem: a case study

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The complexity and diversity of the components of nature, among which are geographical gradients, result in a nonhomogeneous distribution of biodiversity. Understanding this geographical variation in biodiversity generates significant bases for conservation efforts. A study was conducted on the altitudinal stratification of rodent species along Ibrahim River in Mount Lebanon, and their habitat preferences during spring and fall. Two hundred seventy baited Sherman live traps were distributed among eighteen sites, riparian and non-riparian. The vegetation characteristics of each site were described. Trapped individuals were identified, and their morphometric measurements were recorded. Signs of rodents encountered were documented, and a total of 2,850 trap-nights resulted in 256 trapped individuals

belonging to eight species, among them a new record for *Mus macedonicus* distribution in Lebanon. The highest density and species richness of rodents were recorded in the Eumediterranean zone and in mixed (oak-pine) forests, revealing the importance of diverse habitats in holding a vast diversity of rodents. However, the density and species richness of rodents neither differed between riparian and non-riparian habitats nor according to altitude. Nonetheless, more rodents were trapped in spring implying the high reproduction activity. This study represents a baseline for the geographical distribution and habitat preferences of rodents, hence shaping conservation efforts and future investigations on the impacts of anthropogenic and environmental changes on biodiversity in general and rodent diversity in particular.

89: To see or not to see: park attendance impacts on animal sightings in Glacier NP

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Ecotourism has been an expanding field for the last several decades, with more people visiting more parks and protected areas every year. This was especially true in Glacier National Park which saw a rapid increase in attendance from 1960 (650,000 visitors) to 1980 (1,700,000 visitors). The influx of visitors could influence animal response to humans. Animals may respond to human disturbance by avoiding areas with human activity and reducing sightings, or by becoming habituated to humans with a concomitant increase in sightings. Our study focused on examining if the 3-fold increase in attendance at Glacier National Park impacted the ranger reported sightings of 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*). We found a significant increase in sightings for all species when comparing the 1960s to the 1970s. However, the only species in which we found a significant relationship between attendance and sightings was in the coyotes. Coyotes exhibited a significant positive relationship with attendance in the 1960s, but this relationship did not extend into the 1970s. Our results suggest that the rapid increase in park attendance resulted in these species neither becoming habituated to humans, nor avoiding areas used by humans.

90^E: The effects of prescribed fires on bat occupancy in the Ozark Mountains of Arkansas

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Due to the recent spread of white nose syndrome in Arkansas, it is imperative that managers understand the effects their management techniques have on native bat species. Our research aims to determine the availability of insect prey, and spatial and temporal variation in occupancy of bat species native to the Ozark Mountains of northwestern Arkansas. To determine the effects of prescribed burns on bat species including *Nycticeius humeralis*, *Perimyotis subflavus*, *Lasiurus borealis* and *Lasiurus seminolus*, and their nocturnal flying insect prey, we deployed acoustic monitors and insect traps at 20 burned and 20 unburned sites that were visited twice, between April and November of 2017. We grouped *L. borealis* and *L. seminolus* due to acoustic similarity. We used single-season occupancy modeling to determine that the probability of detection increased with higher ambient temperature for all species, (ex. *N. humeralis*, $\beta=0.106$). The most supported model of occupancy probability included the interaction between burn status and forest basal area, with occupancy increasing with lower basal area at previously burned sites. Although insect biomass estimates were similar during the summer season, biomass was over 50% higher at unburned sites than burned sites during the fall foraging period. These data suggest that occupancy probability is higher in previously burned sites due to an increase in flight area. However, these burned sites may have a seasonal decrease in prey availability.

91^{E,HTA}: An experimental translocation identifies habitat features buffering the effect of camouflage mismatch in snowshoe hares**

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Strategies for conserving mammals affected by climate change are often designed at scales impractical for local land managers, leaving limited options for direct management actions to protect threatened populations. Among species experiencing well-documented declines in distribution and abundance due to

climate change is the snowshoe hare (*Lepus americanus*). This winter-adapted species experiences increased vulnerability to predation during periods of phenological mismatch: when early snow melt or late snow development leaves hares in white winter molt conspicuous against a brown background. To test hypotheses about the effects of camouflage mismatch on hare survival and persistence, we translocated 96 radio-collared hares to a site where hares had been recently functionally extirpated, and used known-fate models to estimate weekly survival between January and May of 2017. Survival was low across the 20-week period ($S=0.53$, $SE=0.11$), with predation by generalist predators being the dominant form of mortality. Hares that were mismatched with surrounding snow cover had lower overall survival rates ($\beta=-1.18$, $SE=0.48$), but this effect was spatially variable. Hares inhabiting larger patches of high-quality habitat (stands of *Populus* spp. and *Alnus* spp.) had higher rates of survival ($\beta=0.25$, $SE=0.1$). These findings point to particular habitat features that can be managed to buffer the consequences of phenologic mismatch and climate change on this vulnerable and regionally declining mammalian species. This research was supported by a Grant-in-aid of Research awarded to Evan Wilson in 2017.

92^{E,HTA}: Survey design for threatened and declining species

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Understanding shifts in species' occupancy and abundance is critical in threatened species management, allowing quantification of declines, identification of threatening factors, and guiding management efforts. For small mammals, detectability – the likelihood of finding a species or an individual animal at a site with a given effort, if it is present – varies with factors such as seasonal shifts in behavior and abundance, food availability, and moon phase. Interpretation of survey results should recognize these species-specific associations, which in turn can inform efficient survey design. Failing to account for changes in detectability can lead to erroneous inferences about the absence or abundance of a species in an area. We applied these principles to an Australian mouse species (*Pseudomys novaehollandiae*) that has suffered a catastrophic decline in the past 40 years. Interrogating a 40-year dataset and our own recent comprehensive surveying efforts, we tested factors affecting detectability and abundance. We found that season, time since fire and long-term rainfall patterns governed abundance, while season, moon phase, night of survey, and rain during the survey affected detectability. We retrospectively applied these findings to interpret historical survey data and identify priority areas for resurvey. Additionally, we compared the efficacy of box traps against camera traps for detecting the species, and developed guidelines for ideal survey design. Our methods are broadly applicable to survey design for other small mammal species.

93^F: Change and fragmentation of woody cover affects ocelot recovery in Texas

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Over the last 25 years, the Rio Grande Delta of southern Texas has become one of the fastest urbanizing regions in the United States. This region has productive agriculture and rangeland, while still retaining a distinction as a rich biodiverse region in Texas. Since the early twentieth century, conversion of woody cover for agricultural uses and human development has become one of the main drivers of the decline of ocelots (*Leopardus pardalis*) in the Rio Grande Delta. We classified LANDSAT imagery from 1984-2016 to quantify the rate of land cover change and used housing density scenarios to project land cover change until 2050 based on five landscape metrics. Woody cover increased from 13.7% to 15.9% since 1984; however mean patch area decreased while edge density, patch density, and Euclidean distance to nearest patch increased indicating fragmentation near the Rio Grande River. Rangeland and agricultural conversion were the leading causes of change in woody cover, which can potentially be attributed to rapidly expanding urban areas. By 2050, urban cover types will represent the greatest percentage (39.9%) of landscape cover and we project a loss of at least 1.5% of woody cover and 4% of rangeland and agriculture cover types. These results provide important information for predicting future woody cover fragmentation to focus efforts for connectivity of ocelot populations.

94^E: Habitat use and species interactions of reintroduced fishers in Washington State

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Habitat use patterns are affected by both resource requirements and species interactions, and two common species interactions that influence habitat use are competition and predation. Mesopredators exist in a unique situation where competitors and predators are often the same species. This is the case for fishers (*Pekania pennanti*), an endangered species in Washington. Fishers require structurally diverse forest, but also compete with and can be preyed upon by coyotes (*Canis latrans*) and bobcats (*Lynx rufa*). We examined the habitat use of a reintroduced population of fishers in the Cascade Mountains of Washington, assessing how landscape features and species interactions influence habitat use. Using camera detection data of prey and predators and telemetry data of fishers, we found that fishers select habitats based on forest conditions and prey availability. Stand age, proximity to young stands, and number of snowshoe hare (*Lepus americanus*) detections all increased the probability of fisher use. Bobcat and snowshoe hare detections were positively correlated, suggesting that fishers may experience a food-safety tradeoff in this system. Our data suggest that fishers may mediate this danger by avoiding bobcats temporally. Understanding habitat use of fishers in Washington will allow managers to manage lands to accelerate recovery and plan future reintroduction efforts.

95^E: Linking climate, diet, and distribution: stable isotope analysis of Great Basin rodent communities.

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In the Great Basin, rodent community distribution and composition has responded to both climate and anthropogenic land-use modifications over the last century. However, it is difficult to link community responses to dietary resources across space and through time. Stable isotope analysis of hydrogen (δD) can link climate to diet and distribution, as δD is correlated to elevation, latitude, and plant water-source (surface vs. ground). Analysis of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotopes reflect an individual's diet and trophic position. We measured $\delta^{13}C$, $\delta^{15}N$, and δD in the hair of five rodent species from a 1000-meter elevational gradient in the Toiyabe mountains of central Nevada, collected in 1930 (then) and 2010 (now). At the community-level hydrogen stable isotope ratios are negatively correlated with elevation, then and now. This is consistent with the expectation that precipitation will contain a greater proportion of heavy isotopes at low elevations than at high elevations. However, this community-level trend is not conserved at the species-level; within a species, hydrogen isotope signals correspond to the diet space estimated by $\delta^{13}C$ and $\delta^{15}N$. Additionally, we found that for some species, δD is more strongly associated with diet than habitat affinity (eg. xeric, mesic, generalist), especially in xeric adapted granivores. Furthermore, species' δD signals are not always conserved from then to now, which may reflect shifts in diet or elevational distribution over time.

96^E: Integrating camera trap data to estimate spatial ecology of mesocarnivores in south-central Oklahoma

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Mesocarnivores have important ecological roles as primary predators of food webs and significantly contribute to maintaining the health of the lower trophic levels. Various anthropogenic effects impact the viability of mesocarnivore populations; therefore, conservation is essential to maintain ecosystem integrity. My study was conducted at Oka' Yanahli Preserve (OYNP), located in south-central Oklahoma. Camera traps were used to capture images of mesocarnivores in the preserve over winter 2016 and summer 2017. Six remotely-triggered infra-red cameras were deployed for 4 weeks. After 4 weeks, cameras were moved to different, random locations. Half of the cameras were systematically baited by using canned mackerel. Mesocarnivore species identified from both seasons were coyote, raccoon, bobcat, Virginia opossum, and striped skunks. Results show the proportion of sites occupied and detection probabilities were higher for all species during winter than in summer (single species occupancy modeling). Overall detection probability was higher with baited camera traps in winter, but baiting had no overall effect on the

probability of detection for all species in summer. Temporal activity overlap was higher ($\Delta > 0.7$) for all species during winter than in summer (Circular Kernel Density Estimates). Intraguild predation could be less expected in this preserve as supported by our results. The data gathered from this research will be useful in future research, long-term monitoring efforts, and restoration of habitats of mesocarnivores in OYNP.

97: Diversification and species diversity in the mammal tree of life

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Mammals are a remarkably heterogeneous group represented today by over six thousand ecologically disparate species, including humans. Yet major differences in the living species diversity among radiations in the mammal tree of life remain poorly understood. Here we develop a time-calibrated molecular phylogeny of nearly all extant species to capture the role of among-lineage variation in diversification rates upon mammalian diversity today. Accounting for topological and branch-length uncertainty, we find broad signatures of rate-variable diversification at levels of rate-shifted nodes, named clades, and tree-wide time slices. Species-level (tip) diversification rates and their skewness explain clade species richness significantly better than does clade age, consistent with ecological factors regulating diversity not time alone. Faster diversification rates are found among mammals of lower vagility and higher latitudes, as linked to short-term dynamics of species turnover that manifest at shallow and deep time scales of the tree, respectively. The evolution of diurnality is related to rate up-shifts in lineages such as simian primates and ctenomyid rodents. Traits that promote geographic isolation appear central to the recent species diversification of mammals, while diurnality exemplifies niche evolution influencing modern tree shape.

98: Revisiting the phylogeny and taxonomy of South American cottontails, *Sylvilagus* Gray, 1867 (Lagomorpha: Leporidae)

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A recently published taxonomic framework for South American cottontail rabbits (Lagomorpha: Leporidae: *Sylvilagus*) by Diersing and Wilson (2017 [DW17]), while correct in some of its taxonomic conclusions (species status for *S. apollinaris* and *S. fulvescens*) was, however, incorrect in other conclusions; namely: their hypothesis that *S. andinus* and *S. brasiliensis* are conspecific. DW17 ignored substantial and substantive data—molecular and morphological alike—that contradicted their conclusions to instead excise *S. andinus* from *S. brasiliensis*. As a result, the taxonomic framework ensuing from DW17 is compromised. Here, we redress some of the omissions of DW17: we provide details of morphological characters of *S. apollinaris* and *S. fulvescens* that support the taxonomic decision of separating these from *S. brasiliensis*. We reiterate the distinctive nature of the characters that support the distinction of *S. andinus* from *S. brasiliensis*. We adduce data suggestive to the effect that—absent any type material—*S. defilippi* is at best a *nomen dubium*. We rectify additional taxonomic actions indicated in the synonymies of DW17, thereby addressing the taxonomic status of additional taxa, and provide morphological evidence of their distinctiveness.

99^F: Taxonomic revision and distribution patterns of *Marmosa* mouse opossums in Colombia

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The genus *Marmosa* (sensu Rossi, 2005; i.e., excluding *Micoureus*) is not well characterized in Colombia because of its topographic complexity and underrepresentation in foreign collections. We therefore examined the specimens of the main Colombian collections in order to better study distributions and morphology of the genus. Previously identified craniodental characters, by Rossi and collaborators, allowed us to confirm only six species in Colombia: *M. isthmica*, *M. lepida*, *M. robinsoni*, *M. rubra*, *M. waterhousei* and *M. xerophila*. We documented the following range extensions: 1) *M. isthmica* is found in the inter-Andean valley of the Cauca River, 2) *M. robinsoni* is found in the Colombian Orinoquia, and 3) *M. waterhousei* is found in the Cordillera Occidental. We confirmed the first locality in Colombia where *M. robinsoni* and *M. xerophila* are sympatric (second overall), we confirmed two *M. lepida* localities mentioned in a previous study for the country, and we reassigned *M. zeledoni* as probable. Furthermore, for *M. isthmica* and *M. robinsoni*, we conducted analyses of sexual dimorphism, geographic variation between cis-Andean and trans-Andean populations and developed ecological niche models. We found that: 1) sexual dimorphism exists in both species, 2) there is geographic variation between cis-Andean and trans-Andean populations of *M. robinsoni*, and 3) a possible indication of competitive exclusion of *M. isthmica* by *M. robinsoni* (which corresponded to drier areas).

100^{E,HTA}: The continued increase in our knowledge of mammalian biodiversity

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Mammalian taxonomy is exceptionally fluid and continues to be in flux as new studies describe, split, and lump species based on the increased use of genetic data, novel field explorations, and revision of existing museum specimens. Based on our extensive literature review, the current number of mammal species as of 15 August 2017 was 6495 (96 recently extinct; 6399 extant), representing an increase of 1251 species since the third edition of the *Mammal Species of the World*, which listed 5416 species (75 extinct, 5341 extant). With this updated tally, the Mammal Diversity Database (MDD; mammaldiversity.org) was created to keep track of the rapid transformations in mammalian taxonomy through regular updates. Although the website is still being perfected, it is now live and gathering public feedback. The importance of the database is underscored by how many additional changes have occurred since that August 2017 cutoff date for inclusion in the version 1.0 of the taxonomy, which was made public on 6 February 2018. The next version of the MDD species list is currently at 6525 species (96 recently extinct; 6429 extant) as well as 24 extinct species being newly added because there is genetic data available for them. Ultimately, our goal is to bring the taxonomy of global Mammalia into the digital world of fully updatable databases, similar to online efforts already accomplished for other vertebrates. This research was supported by ASM funding awarded to Nathan Upham in 2016.

101^F: DNA barcodes for urban small mammals in the northern Andes of Colombia

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DNA barcode is a worldwide strategy that seeks to accelerate the description of life on earth while providing a powerful tool for species identification. However, accurate identification of species requires an initial reference DNA library associated to voucher specimens with detailed identifications. Although the DNA barcode strategy is based on the Cytochrome Oxidase Subunit 1 (COI) gene, its geographic and

taxon sampling is limited for mammals; on the contrary the Cytochrome-b (CYTB) gene, which is the preferred marker for mammalian systematics, has a denser sampling and provides a more detailed framework for species identification. Herein, we present the first DNA barcode library for mammals of an urban/peri-urban area of the northern Andes of Colombia. We obtained tissue samples from 94 specimens preserved in local museums and sequenced both COI and CYTB genes. We generated 72 new DNA barcodes for Colombia, 29 of which correspond to entirely new barcoded species. Our findings show that traditional barcode analyses using “distance-based” methods of COI data alone provide misleading species identifications, while our two-gene DNA barcode strategy using phylogenetic analyses increases the accuracy of identifications. Finally, two species (genus *Caenolestes* and *Chilomys*) evidenced elevated mitochondrial diversity which could correspond to examples of cryptic diversity.

102^F: Redescription and phylogenetic position of *Ctenomys dorsalis* Thomas 1900, an enigmatic tuco tuco (Rodentia, Ctenomyidae)

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Ctenomys dorsalis Thomas, 1900 is known only from its type specimen, a female preserved as skin without skull (except for the upper incisors) from an imprecise locality in the “Northern Chaco of Paraguay”. Here, we report additional individuals of this species housed, since the 1940s, at the Field Museum of Natural History (Chicago, USA). Based on these specimens, which fully match the original description of this rodent, we provide novel information regarding its phylogenetic position, external and cranial morphology, and distribution. The analysis of ancient mtDNA sequences supports the distinctiveness of this taxon and suggests its placement within the *boliviensis* group of *Ctenomys*. Our study highlights once more the importance of museum collections as repositories of biodiversity.

103^E: Estimating density of bobcats in midwestern landscapes using spatial capture-recapture models

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Spatial capture-recapture (SCR) models provide a rigorous analytical technique for inference that extends standard closed population models to include a spatially explicit model by accounting for the distribution of individuals in space. Spatial capture-recapture models rely on spatial information readily available with camera data and use distance between traps and animal activity centers to model spatially explicit (i.e., camera trap) encounter probabilities and have been used in population density estimation for a range of carnivores. We used Bayesian analyses to evaluate the utility of SCR models for estimating density of bobcats in an agriculturally dominated landscape of west-central Illinois. We deployed 50 camera stations over a 77-day period from 1 February–18 April 2017. We captured 23 uniquely identifiable bobcats 115 times and recaptured these same individuals 92 times. Our analyses revealed that densities ranged from 1.44–1.57 bobcats per 100 km² with a 95% posterior interval of 1.07 to 1.90. Variation in the state-space extending beyond trap arrays affect bobcat density estimates and should be sufficiently large to minimize encountering individuals with activity centers beyond the state-space boundary. Increased size of home ranges of bobcats across midwestern landscapes may necessitate the use of relatively coarser survey

grids in SCR models to account for frequent movements to and from the state space or whose core areas are positioned beyond camera survey unit boundaries.

104: Nest tree use by southern flying squirrels in fragmented midwestern landscapes

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Southern flying squirrels (*Glaucomys volans*; SFS) nest in naturally-formed cavities in snags and hardwoods found in mature, oak-hickory forests. Intensive forest fragmentation of the midwest United States limits the number of available nesting trees. We studied annual nest site selection patterns of SFS across fragmented landscapes of west-central Illinois. We used radio telemetry to examine nest tree use by 55 SFS (30 males, 25 females) captured during 2014-2016. Of 105 nest trees used by SFS, live trees and snags comprised 75% and 25%, respectively. Probability of diurnal nest tree use increased 1.08/1 cm increase in DBH and by 1.50/1 unit increase in the number of overstory mast trees between random and nest tree habitat areas (i.e., 300 m² circular plots). Similarly, probability of diurnal nest tree use increased 1.29/1 unit increase in the number of snags between random and nest tree habitat areas. Our results revealed no intersexual differences in patterns of nest site selection, which may reflect the tendency for SFS to compensate for reduced availability of key structural attributes (i.e., snags, overstory trees) across fragmented forests by exhibiting similar intersexual patterns of nest tree use. Use of natural cavities for denning is encouraging, but also underscores the importance of unharvested oak-hickory forests in contributing essential habitat to SFS populations in fragmented midwestern landscapes.

105^F: The role of *Cecropia* trees in the fitness of three-toed sloths in an agro-ecosystem

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Resource specialists depend on only a few resources for their persistence. Consequently, the dispersion and abundance of such central resources should affect the vital rates, and ultimately, viability of such specialized species. Neotropical forests feature high levels of biodiversity and interspecific competition and, thus, a large number of specialists. Few studies, however, have directly evaluated how the variation of key resources across a landscape affects the survival and reproductive output of tropical specialist. The three-toed sloth (*Bradypus variegatus*) is an arboreal folivore that selects for only a handful of tree species in Neotropical forests. At our site in northeastern Costa Rica, three-toed sloth select strongly for *Cecropia obtusifolia*. Taking advantage of a 5-year radio-tracking dataset of 54 three-toed sloths, we quantified the effect of *C. obtusifolia* density and forest cover on the fitness of three-toed sloths. While the amount of forest did not affect the survival or reproductive output of sloths, we found that the density (# trees/ha) of *C. obtusifolia* was positively related to both the survival and the reproductive success of sloths. Our demographic analysis of fitness potential indicated a population growth of three-toed sloth, at low densities of *C. obtusifolia* (0.7 trees/ha). Thus, while the density of this key resource influences some vital rates of three-toed sloths, only low densities are required to enhance viability of their populations.

106: Predicting movement distances in small mammals through an ecological and life-history trait-based approach

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Key ecological and life-history to predict terrestrial mammal movement distances were identified in previous studies, which combined sets of species with wide differences in ecological/life-history traits and studies of different durations. To build more robust and accurate models, we identify the main ecological

and life-history traits to predict maximum (dispersal) and mean (routine) movement distances of small mammals, taking into account the duration of studies and taxonomic group (subclasses Eutheria and Metatheria, and the order Rodentia). We gathered data on small mammal movement distances through a global literature review, and used seven ecological/life-history traits as predictor variables of movement distances. The strength of phylogenetic autocorrelation of movement distances among species was tested, and then, through a model selection approach, identified the main ecological/ and life-history traits to predict small mammal movement distances. For small mammals as a whole, and for Eutheria and Rodentia, home range size is the main predictor of maximum movement distance from long-term studies, but trophic level, gestation length, and body mass also contribute. For Metatheria, life-history traits and body mass are key predictors of movement distance. Data from short-term studies do not seem to be useful. Movement distances of small mammals can be more accurately estimated by defining the movement distance of interest (dispersal or routine), taxonomic group (Eutheria, Metatheria, or Rodentia), and avoiding short- term studies.

107: Fair tests of the habitat amount hypothesis: an example with small mammals

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Patch size and isolation are traditionally considered as main determinants of species richness in fragmented landscapes, grounded on Island Biogeography Theory (IBT). The Habitat Amount Hypothesis (HAH) is the more recent alternative: species richness could be predicted exclusively by the total amount of habitat surrounding sampling sites. However, tests may be biased towards HAH by the use of poor metrics of patch isolation, and because landscape variables are measured only within scale of effect for habitat amount. Here we compare the HAH, IBT, and patch isolation as predictors of species richness of forest-dependent small mammals in an Atlantic Forest fragmented landscape using two measures of patch isolation: considering all (overall) or only the nearest three (restrict) forest remnants within the scale of effect for each variable. Models with habitat amount or patch isolation alone were equally plausible, and both had more support than models with patch size and isolation (representing IBT), or patch size alone. Had we used only restricted patch isolation, we would have found support only for the HAH. The appropriate metric of patch isolation is critical for robust test of the HAH, which means that previous studies could be biased in favour of the HAH. Our results provide strong evidence for overall patch isolation over restricted patch isolation, which may offer simplicity to decision-making.

108^F: Roost characteristics of *Myotis septentrionalis* in the Kisatchie National Forest, Louisiana

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Roosts play an important role in ecology and evolution of bats and are used for hibernation, rearing of young, mating, social interactions, digestion of food and protection from the natural elements. Roost use by bats may be influenced by abundance and availability of suitable sites, abundance of neighboring food resources, different risks of predation, and body size of the bat and how that influences energy use. Because there are not enough caves for bats to use, we believe that *Myotis septentrionalis* are opportunistically using trees as suitable roosts throughout winter and summer seasons. We captured *Myotis septentrionalis* by mist-netting throughout the Kisatchie National Forest in central Louisiana. Upon capture, we attached a LB-2X transmitter (Holohil Inc.) to each bat and tracked it until the transmitter battery died, or until the bat could no longer be found. At each roost where a bat was found we quantified important roost and stand characteristics within an 18 by 18-meter plot from roost tree. We successfully

captured and tracked 29 *M. septentrionalis* individuals and characterized 101 arboreal roosts, and 187 random roosts for comparison. Little is known of winter or summer roosting ecology of the northern long-eared bat in Louisiana and results from our analyses will help improve our understanding of its status and assist with possible conservation management efforts in the future.

109: Teeth through time: quantitative mammalian dental morphology across the Cretaceous-Paleogene boundary

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Understanding an animal's diet is critical to understanding how it interacts with other organisms and its environment. Feeding behaviors cannot be directly observed in the fossil record, but may be inferred from dental morphology. We use three-dimensional quantitative dental morphology to characterize dietary ecology of mammals following the Cretaceous-Paleogene (K-Pg) mass extinction, aiming to understand patterns of change in mammalian diets in the wake of a severe ecosystem perturbation. In previous studies of post-KPg mammalian ecological diversification, focus has been on patterns of change on a large spatiotemporal scale, or only on the earliest aftermath of the mass extinction. We concentrated on dietary ecology in therian mammals after the K-Pg mass extinction on a restricted spatiotemporal scale: the latest Cretaceous and first ca. 1.2 million years [Ma] of the Paleogene in northeastern Montana. To predict diet from dental morphology, we used three dental topographic metrics, which quantify surface features of teeth that correlate to the use of different food types. In the first ca. 1.2 Ma of the Paleogene, mammalian diets shifted away from insectivory toward omnivory and plant-based diets, with early morphological disparity arising from immigrant taxa rather than local extinction survivors. However, the relationship between diet and dental topography of individual teeth needs to be further investigated, to better understand the relative contribution each individual tooth makes to overall tooth row shape descriptors.

110: Macroevolutionary trends in marine mammal evolution

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Cenozoic marine mammals include: Cetacea, Pinnipedimorpha, Sirenia, Desmostylia, *Kolponomos*, *Ursus maritimus*, *Thalassocnus*, and sea otters. The three most diverse groups are Cetacea, Sirenia, and Pinnipedimorpha, which span a wide range of size, ecology, and marine adaptation. Here, trends in diversity, size, and geographic distribution are explored. Diversity over time is greatest in Cetacea, followed by Pinnipedimorpha, then Sirenia. Cetacea and Pinnipedimorpha peak during the Middle Miocene. Sirenia peak in the Middle Eocene and Late Oligocene. Size trends indicate body mass has increased over the Cenozoic with the maximum occurring in the Holocene. This pattern is consistent among the groups despite their different phylogenetic relationships, and contrasting feeding ecologies between Cetacea + Pinnipedimorpha vs. Sirenia. Also, these trends are similar despite the contrast between fully aquatic Cetacea + Sirenia vs. semi-aquatic Pinnipedimorpha. Finally, both Cetacea and Pinnipedimorpha share an antitropical diversity distribution, with diversity in both concentrated at mid-high latitudes, contrasting to Sirenia which are primarily tropical to subtropical in distribution. This pattern in Cetacea and Pinnipedimorpha originated at the Eocene-Oligocene boundary, when polar ice growth was initiated, which established strong oceanic temperature gradients, as well as upwelling patterns that affected food resources which is related to their distributional patterns. In summary, marine mammals share many responses to geological and biological conditions, while have contrasting responses to others, mainly due to their feeding ecology.

111: Northward bound: Xenarthran evolution and the Great American Faunal Interchange

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Xenarthrans originated in South America when it was an island continent. Consequently, most of the evolutionary history and diversification of the Xenarthra occurred in isolation. This resulted in the only mammals with dermal armor, the extant armadillos and the extinct glyptodonts and pampatheres, and a wide range of body sizes, from the extant *Chlamyphorus truncatus*, at 120 g to the extinct ground sloth *Eremotherium laurillardii* with an estimated body mass of 3,960 kg. Dietary preferences are also diverse and include herbivorous (both browsers and grazers), obligate insectivorous and omnivorous adaptations. Despite their evolutionary isolation, the Xenarthra was the most successful of the endemic South American mammals to participate in the Great American Biotic Interchange, with representatives of each major clade participating. Sloths were the most successful dispersers, reaching both Caribbean islands as well as Central and North America. Historically, it did not appear that these Xenarthrans underwent an evolutionary radiation similar to many of the North American mammals that entered South America. Despite the historically low number of Xenarthran taxa known from Central and North America, recent research in the northern Neotropics has documented a number of new, closely related, extinct megalonychid sloths, indicating that within this family a radiation did occur. Further research on the fossil record in the northern Neotropics may also demonstrate that is also true for other Xenarthrans as well.

112: The relative abundance structure of megafauna from Natural Trap Cave, Wyoming (Late Pleistocene-early Holocene)

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Natural Trap Cave (NTC) is a well-known fossil locality in Wyoming that produces a diverse vertebrate assemblage from the Late Pleistocene to early Holocene (34–3k). This study examines changes in the relative abundance structure of NTC's large-bodied (>10 kg) mammals, excluding horses, using rank abundance curves (RAC). Abundance counts for 12 taxa were tallied from disarticulated, skeletal elements (N = 3256) over 50% complete, identifiable to the genus or species level, and collected from 1974–1979 by the University of Kansas, because of the robust provenance data and large sample size. Kurtosis and Wilcoxon Rank Sum tests were used to quantify changes in the shape of the RAC between four stratigraphic units found in NTC. Data analyses of the whole, megafauna assemblage and the ungulates from NTC is underway. However, the RAC for NTC's six carnivores (N = 1402) have a more peaked or convex-down shape (>3 kurtosis), reflecting a more stressed ecosystem, with no statistically significant change (p-value <0.05) in the shape of the RAC through the four-meter section. Given the numerous glacial and interglacial periods that occur during the Pleistocene-Holocene transition, these preliminary results are not unexpected. While the amount of time represented by NTC's four stratigraphic units are different, RAC generated from fossil assemblages record the relative amount of perturbations that occurred over the represented time period.

113: The influence of cross-trophic associations on community structure at the end of the Pleistocene

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Climate influences the structure of both mammal and plant assemblages across space and time, seen most clearly in the emergence of no-analog mammal and plant assemblages coincident with no-analog climates at the end of the Pleistocene. Prior work has examined separately the influence of climate on mammals and plants, without consideration of how these two taxonomic groups are integrated with and co-dependent on one another -- for habitat, dispersal, resources, and other important interactions. Including both assemblages within ecological models may be necessary to capture a fuller set of

processes influencing spatiotemporal changes in species distributions and community structure. In this study focused on assemblages occurring in eastern North America over the last 21,000 years, we used datasets of faunal and plant data from the Neotoma Paleocology Database and general dissimilarity modeling to examine whether including cross-trophic associations, in addition to climate, as predictors in community-level models improved the explained amount of assemblage variation across space and time. We found that including mammals in models of spatial plant assemblage structure influenced the amount of variation explained, and vice versa. We further explore the magnitude of this effect, and which components of the mammal or plant assemblages most strongly influenced variation in community structure.

114^{E,HTA}: How a climate-sensitive alpine mammal responds to climate change: The importance of microclimate and habitat**

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As temperatures have warmed over the last century, American pikas (*O. princeps*) have disappeared from parts of their range. The pika is an ideal indicator species for the effects of climate change because its alpine habitats are largely spared the confounding effects of other anthropogenic disturbances. Organisms may respond to climate change through various means including evolutionary and morphological adaptations, dietary shifts, or altering distribution. Populations along the trailing edge of the species' range (elevationally or latitudinally) are likely to show the strongest initial responses, as they tend to sit on the boundary of a species' ecological limits. Here, we examine body size and diet across *O. princeps*' North American distribution over a century of climate change, with particular emphasis at their southernmost distributional limit. Using museum specimens, stable-isotope analysis ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$), and contemporary field surveys, we estimate body mass and seasonal and lifetime dietary variation, and identify habitat factors that influence pika distribution. We find that pika populations over the past century have shifted upwards in elevation, but exhibit limited responses in their diet or body size across their range or through time. At the southern limit of their range, pikas have disappeared from warmer, low-elevation sites. Our results suggest that local temperatures are among the most important factors influencing pika distribution. This research was supported by a Grant in Aid of Research awarded to Marie L. Westover in 2016

115: A common species amidst climate change: the Great Basin Pocket Mouse (*Perognathus mollipilosus*)

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The conservation of rare and currently threatened species has traditionally taken priority over species that are common and, therefore, perceived to be more resilient to environmental change. However, initiatives to "keep common species common" are increasing, as the role of widespread generalists in stabilizing ecosystems becomes better understood. In that vein, we constructed an ecological niche model (ENM) of the Great Basin Pocket Mouse (*Perognathus mollipilosus*), one of the most common species found throughout the Great Basin. We employed maximum entropy ecological niche modeling (Maxent), utilizing bioclimatic variables derived from 800m resolution monthly climate models (PRISM climate group). We asked how climate suitability varied across the geographic range of *P. mollipilosus* and how climate change might impact its future distribution. We hypothesized that *P. mollipilosus*' geographic range is more tightly constrained by abiotic factors at the high latitude extent of its distribution than at the lower extent, which may exhibit greater influence from biotic interactions. This biogeographic pattern, exhibited by many species, is known as the North-South hypothesis. We found that a climatically trained ENM followed a latitudinal gradient, providing support for this hypothesis. However, when projected onto future climate change scenarios, we found an overall contraction of suitable area, rather than a northward shift.

This suggests the potential for major climate-driven reductions in environmental suitability for this currently widespread and common species.

116: Manic pixie dream squirrel: phylogeography of the colorful *Sciurus variegatoides*

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Central America is a region filled with an incredible amount of species within its relatively small area. Unfortunately, many such species in this region, including many mammals, have drastically little known about them or their relationship to Central America's constant geologic upheaval. One such species is the variegated squirrel (*Sciurus variegatoides*), which exhibits multiple, distinct pelage patterns across its range from southern Mexico to central Panama. Hypotheses for the variable pelage of *S. variegatoides* include possible adaptations to primary habitat and/or consequences of the variable climatic ranges seen in the region. Despite this, no studies have investigated this variation or these hypotheses using morphological or molecular means. Given this, we undertook a phylogeographic assessment of this species using phylogenetic analyses, morphology, and ecological niche modeling. Mitochondrial genomes of 49 specimens representing 14 subspecies were collected from museum specimens using capture hybridization, and cranial shape differences between subspecies and localities were assessed using two-dimensional geometric morphometrics. These data posit that there is less variation among subspecies than the intriguing pelage patterns would suggest but highlight the importance of the Nicaraguan Depression in driving diversity, even despite the lowland nature of this species. Understanding the evolutionary patterns in this species will add to the current, sparse literature of Central American mammal evolution and increase our understanding of the biogeographic patterns affecting species in this region

117^{E,HTA*}: Co-occurrence with two carnivorans results in differential occupancy for invasive raccoons in Japan**

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Since multiple introductions in the 1970's via the pet trade, the North American raccoon (*Procyon lotor*) has invaded most of mainland Japan. Responsible for agricultural loss and disease transmission, the raccoon has become a significant management problem. Although a mesopredator in its native range, the raccoon is an apex predator across much of Japan, thus posing a significant threat to ecological communities. We were interested in how raccoons interact with two resident carnivorans of similar body size and trophic breadth, the invasive masked palm civet (*Paguma larvata*) and the native raccoon dog (*Nyctereutes procyonoides*), in urban and rural areas. We used data from a 6-year (2010 – 2015) raccoon trapping effort in Kanagawa prefecture to build a multi-species occupancy model. The model estimates occupancy probability as a function of environmental variables, taking account of imperfect detection, and can predict occupancy of one species conditional on the presence/absence of another species over environmental gradients. Our preliminary results indicate that as forest area increases, occupancy for both raccoons and *N. procyonoides* is higher when the other is present and lower when the other is absent, while *P. larvata* shows the opposite relationship with raccoons. This challenges a popular theory that raccoons are competitively excluding *N. procyonoides* from suitable areas at coarse scales, although the exact nature of the local-scale interactions is still unclear. This research was supported by an ASM Grants-in-Aid awarded to Jamie M. Kass in 2017.

118: North American evolutionary drivers of diversification: jumping mice (Zapodinae) reflect the 'Pleistocene species pump' hypothesis

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Gaining new insights into the diversification of major groups remains an important challenge and can yield key insights for other fields such as conservation. Here, I aim to elucidate the timing of evolutionary events and major relationships of widespread jumping mice (Zapodinae) and clarify the role of Pliocene savanna expansion versus Pleistocene colonization-isolation (species pump) mechanisms influencing diversification across major bioregions of North America. I applied a combination of probabilistic approaches to address several interrelated questions about the biogeography and evolutionary diversification likely common across co-distributed taxa. Using range-wide and complete taxon sampling (130 individuals, eleven putative species) and fossil-calibrated multilocus phylogenetic analyses, I assessed the tempo of diversification and tested alternative models of speciation and extinction. This approach provided a spatiotemporal perspective to assess whether diversification rates have remained constant or varied across time. Finally, I used ancestral area reconstruction to explore alternative models of range evolution. When combined, these approaches identified strong correspondence with major Quaternary events with transitions between biogeographic realms and ecological shifts corresponding with significant signals of divergence. Biogeographical signals imply increased intensity of glacial-interglacial cycles throughout the Pleistocene strongly influenced diversification of zapodids. The high degree of genetic differentiation recovered appears to be spatiotemporally congruent with other co-distributed species, suggesting North America may contain more evolutionarily important diversity than currently recognized.

119^F: Geographic responses of cougars (*Puma concolor*) following the Pleistocene megafaunal extinction

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A core assumption of many ecological studies is the concept of niche conservatism, where a species' ecological characteristics remain consistent over time. Following Hutchinson, niches are presumably fixed in eco-space by a combination of abiotic tolerances and biotic interactions. Within this simplifying assumption, such ecological limitations are exemplified by the niches of meso-carnivores such as the cougar (*Puma concolor*), who were largely outcompeted throughout the Quaternary by larger-bodied felids – particularly the saber-toothed cats (*Smilodon sp.* & *Homotherium sp.*). Following the extinction of these more massive hyper-carnivores at the terminal Pleistocene (~ 11,500 kyrs), it is unclear if cougars shifted their ecological niche and began to occupy abiotic eco-space vacated by the extinctions of the mega-felids (i.e., meso-carnivore release). We employed the maximum entropy method of Ecological Niche Modeling analysis using felid occurrences from the Neotoma Paleocology Database and the Community Climate System Model (version 4.0) to test the hypothesis that cougars re-filled open mega-felid abiotic niche space. We quantified the degree of intra- and inter-specific niche overlap between cougars and the extinct mega-felids through time. We find that cougars did not appear to re-fill the empty niche space vacated by the mega-felids following their extinction. Cougars also show exceptionally low fidelity to their abiotic niche throughout the Holocene. Our findings suggest that biotic interactions may be the primary influencers that limit quality cougar habitat.

120^{E,HTA}: Biologgers and fecal cortisol metabolites: understanding the physiological limits of free-living arctic ground squirrels

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Little is known of the relationship between glucocorticoids and specific behavioral outcomes in free-living mammals. This is likely due to the challenges associated with simultaneously investigating both hormonal and behavioral traits in wild animals. In this study, we used collars affixed with accelerometers and light loggers to measure the above-ground overall dynamic body acceleration (ODBA), an index of activity-

specific energy expenditure, across the active season on free-living arctic ground squirrels (*Spermophilus parryii*). In addition, we measured fecal cortisol metabolites (FCM) to non-invasively assess adrenocortical activity of squirrels across their active season. Female FCM concentrations were highest during the mid-lactation interval and lowest during post lactation, while male FCM did not vary across the active season. Levels of above-ground activity were consistent with expectations of reproductive demand. Cold and wet weather, which is known to adversely affect conditions of thermal exchange, increased FCM and decreased above-ground activity levels in both sexes. Furthermore, when temperatures were lowest in the early season, weather had the greatest effect on both above-ground activity and FCM concentrations. Lastly, our results suggest increased FCM concentrations are associated with decreased above-ground activity and time spent above-ground in female but not male arctic ground squirrels. Collectively, this study furthers our understanding of how reproductive state and environmental conditions may interact to affect behavioral patterns and adrenocortical activity in free-living mammals.

121: Reduced hepatic detoxification in marsupial folivores following heat acclimation

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There is growing evidence that mammalian herbivore physiology may be directly impacted by ambient temperature, such that the toxicity of plant secondary metabolites (PSMs) is amplified at warmer temperatures. This phenomenon is known as temperature-dependent toxicity (TDT). More specifically, mammals demonstrate reduced liver function at warmer ambient temperatures, which results in a decreased tolerance for PSMs likely due to slower detoxification. Recent work has provided evidence for TDT in woodrats (or packrats; genus *Neotoma*), however little is known about TDT in marsupials, which differ from eutherians in both thermoregulatory physiology and dietary PSMs. Here, we determined the effect of ambient temperature on functional clearance time of an hepatically metabolized proxy compound for PSMs in two species of marsupial folivores, the common brushtail possum (*Trichosurus vulpecula*) and the common ringtail possum (*Pseudocheirus peregrinus*). We found a positive correlation between functional clearance times and ambient temperature in both possum species, after possums were exposed to temperature treatments (10°C, 18°C, and 26°C) for at least 7 days. Brushtail possums exposed to different temperatures for only 24 hours, however, did not show a difference in functional clearance times. Our results provide initial evidence for the commonality of TDT across herbivores from difference lineages, and could have critical implications for wild herbivores that will be or are currently experiencing a changing climate.

122^{E,HTA}: The influence of demographic, social, and environmental factors on chronic stress in free-ranging coyotes

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Living organisms regularly experience various forms of stress. While short-term stress can be beneficial or even vital for survival, chronically high levels of stress can negatively impact animal health and fitness. Exposure to stressors activates the hypothalamic-pituitary-adrenal axis and ultimately leads to the production of glucocorticoids (e.g., cortisol). Portions of the hormones that are produced are stored in keratinous tissues (e.g., hair) over time, thus chronic stress levels can be approximated by measuring the concentrations within such tissues. Assessing hormones through hair analysis can be especially useful for wildlife studies since hair concentration is robust against handling-induced stress. Coyotes (*Canis latrans*) living in proximity to people are exposed to a combination of natural and anthropogenic stressors. To determine which demographic, social, and environmental factors may induce chronic stress in coyotes, we analyzed hair samples (n=159) from forest preserve, suburban, and urban locations throughout the Greater Chicago Metropolitan area. Cortisol concentration was not directly correlated with urbanization level and there was a high level of inter-individual variation. The estimated percentage of hair lost due to sarcoptic mange, a parasitic mite infection, was the most significant predictor of chronic stress ($p < 0.001$). Season, coyote age, and coyote social status also correlated with hair cortisol concentration ($p < 0.05$).

These findings will contribute to a greater understanding of urban wildlife endocrinology and have implications for managing healthy wildlife populations.

123^{E,HTA}: Metabolic costs of climate change in a temperate bat

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Bats are among the ~40% of endotherms that use daily torpor to conserve energy. Ambient thermal conditions influence the onset and duration of torpor, so a warmer climate could inhibit torpor use and impose metabolic costs on animals that rely on torpor for energy conservation. Thermal refugia may mitigate these metabolic costs under some conditions. To better understand this issue, we radio-tracked fringed myotis (*Myotis thysanodes*) to roosts in the Black Hills of South Dakota. We collected data on skin temperature and modeled the influence of weather on daily torpor patterns. Bats used torpor less on warmer days and were unable to mitigate their metabolic costs by selecting cooler roosts. Warmer temperatures are thus likely to impose metabolic costs on bats. Other prominent bat conservation issues—including white nose syndrome and migration—are also likely to be impacted by such metabolic deficits.

124^E: Bone strength of the metacarpal in pronghorn (*Antilocapra americana*)

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Human-made barriers influence the migration patterns of many species. In the case of the pronghorn (*Antilocapra americana*), a member of the Order Artiodactyla and native to the central and western prairies of the United States, the presence of fences may completely inhibit movement. Depending on the fence, a pronghorn will rarely decide to jump over it, instead preferring to crawl under or negotiate around it until it finds an opening. Although pronghorn having been observed to jump an 8 foot (2.4 m) tall fence in a previous study, some block, possibly physical, exists. We investigated the risk of breakage on the leg bones upon landing. Metacarpals of pronghorn and mule deer (*Odocoileus hemionus*), a routine jumper of fences that lives in relative proximity to the pronghorn, were collected during hunting season in 2016. Bones were tested using a 3-point bending apparatus (MTS 858 Mini Bionix II). Upon bone failure, the ultimate strength and deformation measurements were collected. A comparison of the two species shows that pronghorn may have greater bone strength in their metacarpals, however, mule deer showed more deformation before failure. This higher deformation could translate to more shock absorption upon landing. The strength of the pronghorn leg bone seems to be great enough to allow jumping which may support an alternative hypothesis that the jumping block may be psychological.

125: Evolution of litter size in North America's most common small mammal: An informatics-based approach

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Litter size is an integral life history trait that varies greatly in extant Mammalia. Despite an increasingly complete picture of life history variation across mammals at the macroscale, however, core ecological drivers of this variation are not well understood. This includes such simple questions as, "How do key climate variables such as temperature and seasonality shape litter size?" We investigated potential climate drivers of litter size variation in the North American deer mouse (*Peromyscus maniculatus*) across its extensive range by pairing new digitized biodiversity datasets (>400 literature records and >2,000 digitized museum specimens) with fine-scale climate data from the past century. We tested for correlations between *P. maniculatus* litter size and multiple climatic variables (temperature, precipitation, and seasonality collected at monthly- to annual scale) as well as female body size (head-body length)

using linear models. In addition, we examined whether litter size-environment correlations are constant across the entire range of *P. maniculatus*, or if that relationship itself varies by latitude and ecogeographic region. Finally, we compared the statistical precision and performance of literature-derived data to that of museum-derived datasets, and from these comparisons highlight further directions in use of digitized museum specimen data to address outstanding questions in mammalian life history research.

126: Trial translocation allows assessment of habitat suitability for the world's rarest marsupial, Gilbert's potoroo

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Establishing new populations through translocation is a widely-used procedure to improve the conservation status of threatened species. While measurement of critical habitat attributes such as food availability and abundance of shelters prior to any movement of animals can inform selection of translocation sites, detailed quantitative knowledge of these aspects of species biology is necessary to validate this approach. Gilbert's potoroo, discovered near the south coast of Western Australia in 1840, was last recorded in the 1870s, until 1994 when a colony of around 30 animals was discovered at Two Peoples Bay. The single population was extremely vulnerable to a possible fire event, so recovery planning gave the highest priority to the establishment of new populations. Closely-monitored translocations of a few individuals were used on two offshore islands with no prior record of the species to test the ability of the sites to support Gilbert's potoroos. On Bald Island, temporary release of two animals in summer resulted in both animals regaining lost weight within a month. On Middle Island, where the adjacent mainland was well outside the historic range of the species, four-week trials in summer and winter each involving four animals met the success criteria of 75% survival and loss of body weight of no more than 10%.

127^E: Individual detection of coarse woody debris using airborne LiDAR: implications for forest mammal habitat research

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Coarse woody debris (CWD) is an important habitat component for many forest mammal species. CWD detection and mapping would enhance mammal habitat research and management, but field-based CWD inventories are not practical for mapping CWD over large areas. Light detection and ranging (LiDAR) is a remote sensing technology that provides detailed information on three-dimensional vegetation structure that could overcome limitations of field-based inventories. Our objectives were to evaluate the ability of LiDAR to detect individual pieces of CWD and determine how site and CWD characteristics influenced detection. We acquired high-density (8 pulses/m²) LiDAR data in 2014 and measured 1,968 pieces of CWD at 189 field plots from 2015-2016. We filtered out canopy and sub-canopy returns using a height threshold based on field measurements of CWD and used height-filtered data to determine which field-measured pieces of CWD were visible in the resulting point cloud. Overall, we detected 23% of the individual pieces of CWD we measured. Larger pieces of CWD were more likely to be detected, with the majority of pieces ≥ 30 cm diameter or ≥ 11.1 m long detected. Canopy density, shrub density, and forest type did not influence detection probability. Our results demonstrate that airborne LiDAR can be used to detect CWD. We will discuss potential applications of our results for research and management of mammals that are associated with CWD.

128^E: Spatial ecology and landscape-scale behavior of coyotes in south Texas

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Despite repeated calls in the literature for further research into basic coyote (*Canis latrans*) behavior and space use, scientific understanding of these topics remains limited. Our goals were to quantify activity patterns and landscape-scale behaviors of coyotes, as well as correlates of these behaviors that may be of management significance. We captured a total of 16 coyotes between 2 capture events in December 2016 and April 2017 and fitted them with satellite-transmission GPS collars that record locations every 2 hours. We used autocorrelation functions to analyze the structure of coyote activity patterns. We used novel applications of kernel intersection methods to gain insight into the temporal dynamics of coyote space use and inter-individual interactions. We found that coyote movements exhibited strong diel periodicity with subtle differences between social strata. Territorial individuals exhibited strongly crepuscular behavior while transient individuals showed less stable rhythms. With our kernel methods, we were able to uncover behavioral responses to carrion deposition. Four territorial coyotes converged on a calf (*Bos taurus*) carcass outside of their territories, resulting in subtle changes in individual space use, but a sharp increase in inter-individual overlap. The dynamics of inter-individual interaction were markedly different from this event through the end of the study, 3 months later. This suggests that carrion deposition can have marked and lingering effects on coyote space use.

129^E: Molecular diet analysis of New York City coyotes

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Coyotes (*Canis latrans*) have expanded their range over the last 150 years due to the extirpation of the gray wolf and the conversion of forested land to agriculture and they are now inhabiting even the most densely populated cities in the United States. Coyotes are recently established in New York City (NYC), where they were first observed 25 years ago. They have the potential to impact the ecosystem through predation and competition by influencing the abundance and distribution of other species. Coyotes are omnivores that consume a wide variety of foods and can alter their diets in response to food availability. The NYC landscape is heterogenous, containing parks and other greenspaces of different sizes and microhabitats. This habitat diversity may influence the type of diet items available to coyotes. We examined whether diets differ between coyotes sampled at different parks throughout the city. Additionally, we compared the urban coyote diet to the diets of coyotes sampled in suburban and rural areas. We used next-generation sequencing of DNA obtained from coyote scats to identify vertebrates, invertebrates, and plants that comprise their diets. The molecular analysis allows us to identify items that cannot always be observed visually, such as anthropogenic food. Preliminary results suggest variation in diets among coyotes inhabiting different NYC parks as well as differences in anthropogenic food use between urban and non-urban coyotes.

130: Marking small mammals for individual recognition: a survey of practitioners use and perceptions of methods

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Crucial to the success of studies based on capture-mark-recapture (CMR) designs is the retention (i.e., permanency) and recognition (i.e., readability) of marks applied to individuals. Despite a variety of marking methods being employed in CMR-based studies, a review of their use is lacking. We conducted a literature review and an online survey of researchers individually marking small mammals (<100 g) to determine their beliefs, perceptions, and choices regarding marking methods. We received 93 responses to our online survey, with 74% of respondents having >5 years experience, and 61% respondents each marking >1,000 individual small mammals. Respondents believed that ear-tagging was the most preferable method in terms of efficiency to apply in the field, impact to the animals (i.e., survival, pain),

and their personal ethics, while PIT-tagging was the most preferable in terms of retention and recognition, and toe-clipping with regards to cost. Greater than half of the respondents indicated that they planned to use ear-tagging (78.2%) and/or PIT-tagging (66.7%) in future studies of small mammals. The primary factor influencing respondent decision regarding which marking method to use were ranked—in decreasing order—as impact to animals, retention, cost, personal ethics, efficiency, and recognition. Most respondents (80.0%) agreed that additional studies on the efficacy and impact of various small mammal marking methods are needed to help assess their costs and benefits for CMR-based studies.

131^E: Survival and cause-specific mortality in a hunted population of elk (*Cervus canadensis*)

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Adult female survival often is the most important factor influencing growth of ungulate populations. Increased understanding of survival and causes of mortality for adult females is fundamental for conservation and management. Our objectives were to quantify survival rates of female elk (*Cervus canadensis*) and determine cause-specific mortality. We predicted hunter harvest would be the leading cause of mortality and that hunters would harvest prime-aged animals in better condition than elk lost to other predators. We captured 452 female elk via helicopter net gunning in central Utah. Individuals were fitted with a GPS-transmitting collar that collected a location every 13 hours. When a mortality warning was received, we located collared individuals and determined cause of death within 48 hours whenever possible. We estimated survival using Kaplan-Meier method and Cox Proportional Hazard models within an AICc model selection framework. Survival was consistent across years, mean of 83.4% (SE = 1.7%) including harvest and 94.9% (SE = 1.1%) without harvest. Mortality occurred from human hunters (71.2%), other predators (12.0%), vehicle collision (2.4%), disease (0.8%), and unknown causes (10.4%). Neck circumference, body length, and loin thickness were negatively associated with survival suggesting that larger animals in good condition had lower survival. Individuals lost to cougar predation were younger and in below-average body condition. Hunters may be removing individuals that have a greater effect on population dynamics than other predators.

132: Second chances: replacement estrus in seasonally breeding Richardson's ground squirrels

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Richardson's ground squirrels (*Urocitellus richardsonii*) are obligate hibernators with a single annual reproductive season occurring immediately after emergence from hibernation. In a 25-year study of reproductive chronology in southern Alberta, the majority (82%) of females entered vaginal and behavioral estrus within 5 days of resuming above-ground activity and almost all were impregnated immediately, suggesting a strong advantage to rapid establishment of pregnancy even though females have had little opportunity to replenish mass and fat reserves post-hibernation. A few females (8%) did not become pregnant until they had been active for ≥ 10 days, raising questions of why impregnation is delayed and whether delay negatively affects reproductive success. Onset of estrus was delayed in females that emerged unusually early from hibernation or at unusually low body mass. Alternatively, some females entered estrus promptly but failed to mate due to inclement weather or mated but failed to become pregnant. If inclement weather was brief, females remained in vaginal estrus until weather improved. If inclement weather persisted, vaginal estrus ceased and females eventually entered a second estrus. Likewise, females that copulated on their first estrus but failed to be impregnated experienced a second estrus after a latency of 5-8 days. Whether estrus was delayed, prolonged, or replaced, females that mated ≥ 10 days post-emergence experienced high rates of successful reproduction.

133^{E,HTA}: Active space of grasshopper mouse vocalizations in relation to woody plant encroachment

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Vocal communication is a critical component of mate choice and territoriality in many animals. The efficacy of communication depends on signal transmission through an often-cluttered environment. Anthropogenic-induced changes in vegetation structure may impact sound propagation and thus habitat quality, but few studies have explored this hypothesis. In the American Southwest, fire suppression and cattle grazing have facilitated displacement of grasslands by pinyon-juniper woodlands. Northern grasshopper mice (*Onychomys leucogaster*) produce long-distance vocalizations to advertise their presence to rivals and potential mates and inhabit regions impacted by juniper encroachment. Here, we coupled acoustic recordings and physiological measurements of hearing sensitivity in the laboratory with sound transmission experiments in the field to estimate the active space of grasshopper mouse calls. We found that receivers are sensitive to loud (ca. 85 dB re: 20 μ Pa at 1 m) 11.6 kHz calls at 30 dB and that calls travel 30 m (range: 20 – 40 m). However, we found no effect of shrub encroachment on call propagation as juniper and grass density were inversely associated and both present barriers to a 9 cm mouse advertising at ground level. Our findings suggest that juniper encroachment does not affect sound propagation but may influence habitat quality through alternative mechanisms.

134^{E,HTA}: Food for thought: how personality affects seed choice in a guild of terrestrial small mammals

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Individual animals behave consistently differently from one another across contexts and under a range of environmental pressures. This behavioral variation among individuals is known as personality. Numerous aspects of behavior are influenced by an animal's personality, and the links between personality and foraging behavior have received recent attention – with a select number of studies considering the complex interactions that this may have with different trophic levels. In this study, we have examined the way that personality in a small mammal community can translate to other trophic levels, ultimately influencing forest structure and composition. We have done this by identifying links between personality and the essential processes of seed predation and seed dispersal. Using a large-scale, fully-replicated mark-recapture design, we have trapped small mammals from four different species, measuring behavior using a series of standardized behavioral tests. Then, in a field experiment using RFID readers (i.e. permanent readers able to scan microchips inserted subcutaneously in wild small mammals) paired with trail cameras positioned in the field, we have observed individuals predated and dispersing seeds in their natural habitat. A novel technique for tracking seeds has allowed us to recover the caches. Using mixed-effects models, we have explored how personality in small mammals influences decisions regarding seed predation and seed dispersal. To the best of our knowledge, our study is the first to address this question.

135^{E,HTA}: Grasshopper mice exhibit sex differences in call production and behavioral responses to playbacks

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Many animals produce vocalizations in a variety of social contexts, including mate attraction, territory defense, and alarm signaling. Understanding the function of acoustic signals requires quantification of receiver responses, which can be challenging in field settings and/or for inconspicuous animals. We designed a large indoor arena to measure phonotaxis (movement in response to sound) in northern grasshopper mice (*Onychomys leucogaster*), a species in which both males and females produce loud, long-distance vocalizations. Captive-bred animals from wild-trapped progenitors were given two days to acclimate, followed by presentation of one of three stimuli (silence, white noise control, or conspecific call) throughout the night over three consecutive nights in random order. We quantified phonotaxis and vocal responses using automated tracking and recording equipment. Our preliminary results (n=11 females, 8 males) indicate that males call more (= 10.5 times/ night) than females (= 2.1 times/night) under various experimental contexts ($F_{68,1} = 7.78$, $p < 0.01$). Males and females also exhibit opposing trends in phonotaxis; on average, females spent more time than males in the zone that broadcast conspecific calls. Our results indicate that long-distance vocalizations may have dual functions—mate attraction (males call more and females move towards the call) and announcing their location to potential competitors (both sexes call and males spend less time towards the calls to minimize conflict).

136^{E,HTA}: Behavioral responses to advertisement vocalizations among sympatric grasshopper mice (*Onychomys*)**

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Mating between heterospecifics can result in inviable offspring and drive the evolution of pre-mating reproductive barriers. In southern New Mexico, sympatric populations of grasshopper mice (genus *Onychomys*) produce species-specific long-distance advertisement vocalizations that differ in fundamental frequency. Hybrids are rare in nature and exhibit reduced viability in the lab, indicating the existence of strong pre-mating isolating mechanisms. In this study, we quantified behavioral responses (number of calls and response latency) to playbacks in the laboratory to explore the role of long-distance vocalizations in mediating reproductive isolation. We broadcast synthesized stimuli representing species-specific call parameters to captive-bred and recently wild-captured animals of all three species (northern; n=18, southern; n=20, and Chihuahuan; n=17) from Animas, NM. First, we found that a subset of individuals (n =15) did not call nor respond to playbacks, indicating substantial variation in the underlying mechanisms mediating call production and perception. Among the individuals that did respond (northern; n=15, southern; n=13, and Chihuahuan; n=12), we found no species or sex differences in responses to conspecific versus heterospecific playbacks. Interestingly, recently captured wild mice called less frequently with longer latencies compared to captive-bred animals. Our findings suggest that species-specific vocalizations in sympatry may be unrelated to reproductive interactions. Furthermore, vocal behaviors appear sensitive to social experience, suggesting a role for auditory learning and raising caution for extrapolation of laboratory findings to field settings. This research was supported by a Grant in Aid of Research awarded to Grace Griffiths in 2017.

137^F: Importance of rivers as migratory corridors for temperate bats

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Investigating landscape level movement patterns of migratory animals can often be challenging, yet this is a major component of an animal's life history and behavior. In particular, bat migration has historically been difficult to characterize, yet research in recent decades has progressed much in the field of bat migratory ecology. It has been largely accepted that rivers and other linear landscape features may be important migratory corridors for bats during both long and short distance migrations. However, this idea is primarily based on a handful of studies throughout the world, and recent studies have questioned the importance of linear features in bat migration, warranting further evaluation. The goal of this work was to assess the migratory behavior of multiple temperate bat species along a major river corridor by using seasonal directional passes as an estimate for migratory behavior. Count comparisons within species and across seasons demonstrated significant differences in directionality in one season for two species. However, repeatabilities estimated from generalized linear mixed effects models found the effects of season and species explained less than one percent of the variation of directional passes, potentially indicating an absence of season-specific movement patterns along the studied river corridor.

138: Vigilance of black-tailed prairie dogs (*Cynomys ludovicianus*) in urban and rural landscape contexts.

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We assessed the relationship between landscape context and vigilance patterns of black-tailed prairie dogs (*Cynomys ludovicianus*) in central Kansas. We studied five colonies, two in urban settings and three in rural settings, from 23 March – 20 April 2016, 31 August – 19 September 2016, 26 March – 12 April 2017, and 7 September – 17 October 2017. We measured vigilance in colonies by observing individuals for five minutes and recording the amount of time the individual spent vigilant or foraging. In addition, we counted the total number of individuals in the colony that were actively vigilant at ten minute intervals for

one hour. Generalized estimating equation (GEE) modeling indicated that urban locations and number of prairie dogs counted within a colony were negatively related to vigilance behavior. We observed that prairie dogs in rural colonies spent significantly more time vigilant than those in urban colonies during all seasons. Because prairie dogs in urban colonies may be habituated to disturbance and have a lower risk of predation, they may spend less time vigilant. Urban colonies also had a higher proportion of individuals foraging within the colony. These findings could be used to better understand factors that influence vigilance behavior and specifically the impact that encroaching urban development may have on black-tailed prairie dogs.

139: Estimating home ranges using different currencies and animals' perception about their environments

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Most researchers estimate home ranges using telemetry location estimates. With an appropriate estimator, this approach produces utilization distributions that can be considered to approximate probability distributions for where animals spend time. Essentially all home ranges estimated today use time as their currency. Estimating home ranges using other currencies, such as energy expenditure and importance of resources, provides insights into why animals use space as they do. Weighting each telemetry location by rate of energy expenditure at that time, estimated from travel speed using an equation in the literature, produces a new utilization distribution. For some animals, energy expenditure in their home range cores is higher, and in the home range peripheries lower, than time spent in those areas. Home range estimators have parameters that must be chosen to be appropriate to the biology of study animals and research technology. Choosing those parameters based on perceptual distances for sight, sound, smell and memory produce different utilization distribution yet, explaining different aspects of why animals use space as they do. I present data for fishers (*Pekania pennanti*) and black bears (*Ursus americanus*) to illustrate and to compare how using different currencies and perceptual distances affect utilization distributions, home range overlap, and home range cores. Techniques appropriate to the questions or specific hypotheses are needed to understand animal behavior and the potential for successful management.

140^{E}: Towards improved functional trait information for small mammals**

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Functional diversity quantifies the range of species traits in an assemblage. This dimension of biodiversity is increasingly being applied to mammalian conservation, biogeography, and community ecology. However, any conclusions drawn are only as good as the traits measured to quantify functional diversity. Here, we seek to improve functional trait information quality for non-volant small mammals (rodents and shrews) by identifying continuous measures of ecomorphological traits that reflect commonly used functional categories (e.g. diet group, environmental affinities). Specifically, we investigated the potential of a suite of cranial and dental measurements as indicators of diet, relative medullary thickness (RMT) of the kidney as a measure of habitat affinity (mesic-to-xeric spectrum), and hair density as a metric of thermoregulatory ability as it relates to species distributions. We sampled these traits from 32 Great Basin small mammal species using museum specimens. We found craniodental morphology and kidney RMT to reliably reflect traditional categorical groupings while also revealing finer-scale interspecific variation. Future applications of small mammal functional diversity should consider these simple yet informative continuous traits for environmental tolerance and diet. In contrast, hair density produced inconsistent results, suggesting that this trait alone cannot be used as a proxy for temperature tolerance. However, it may prove informative when assessed in conjunction with a suite of other traits related to thermoregulation. This research was supported by a Grant-In-Aid awarded to Brooks Kohli in 2016.

141^E: Processes driving small mammal community composition over the previous 17,000 years

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The importance of neutral and non-neutral processes on community composition is often debated. The relative importance of different processes can vary depending on the scale of sampling, species pool size, and nature of climate or habitat change experienced by a community. However, predicting which processes are important under specific scenarios is difficult, making it challenging to determine how species will assemble into communities as they respond to future climate change. Here, we assess the importance of climate and stochastic processes for facilitating the assembly of small mammals at Samwell Cave in northern California over the previous 17,000 years. We generated climate-based predictions of community composition at fourteen past time periods, and estimated potential community composition based on the species pool, which served as a neutral hypothesis. The neutral and non-neutral predictions were then compared to the fossil communities found at Samwell Cave in each of the time periods. Results suggest that community composition at Samwell Cave can mainly be attributed to climate, but mismatches between predictions and observations suggest that climate is not the only factor determining community composition. Climate predictions did significantly better at predicting species composition than stochastic predictions. Our results suggest that climate-based community predictions do fairly well at predicting past community composition, which will be important as we predict community change in the future.

142: The role of functional traits in mammalian community structure across the Pleistocene-Holocene transition

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The study of communities over time allows us to evaluate the degree to which ecological processes are affected by climate change and human activity. Such knowledge is critical to predicting how species will assemble into communities in response to future climate change. Recent work documenting the co-occurrence structure of communities over the past 300,000 years attributed a shift from aggregated (species that occur together more frequently than expected by chance) to segregated (species that occur together less frequently than expected by chance) species pairs in the mid-Holocene to human impacts. Here, we investigate the complex role of climate and species traits in the co-occurrence structure of mammals across the late Pleistocene to the modern. We find that the climate change and biodiversity loss at the terminal Pleistocene fundamentally changed species associations: extinct species were more likely to form significant, positive associations than surviving species. Moreover, the interaction strength of pairs that contained an extinct species was stronger for aggregations, but not segregations suggesting that the loss of the megafauna had differential effects on the co-occurrence of surviving species. Specific species traits, such as body mass or trophic interaction, declined in their importance or switched from promoting aggregations to promoting segregations amongst surviving species. We conclude that future climate change and extinction are likely to exacerbate these trends.

143: Impacts of a tornadic blowdown on small mammals inhabiting eastern deciduous forest in western Pennsylvania

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Tornados are common natural weather phenomena shown to highly influence ecosystem structure/function. A tornado struck the area of Ligonier, PA in 2012, creating a path of severe canopy damage 8 miles long. Thereafter, experimental forest management of blowdown areas was initiated, included salvage logging, no salvage logging, and control (unaffected forest). Our objective was to examine impacts of a tornadic blowdown and subsequent forest management on the small mammal assemblage in affected forest. The forest small mammal assemblage was composed mainly of *Peromyscus leucopus* and *Clethrionomys gapperi*, with 7 other species being trapped less frequently. Trapping success has averaged >30% per trapping season. More small mammals were found in the

blowdown area than expected. Species including *Microtus pennsylvanicus* and *Napaeozapus insignis* were found in the blowdown only during early succession. Small mammals in the blowdown area had lower body masses, skewed sex ratios, and lower reproductive activity compared to those in control areas. Age, sex, and body mass differences of the two most frequently trapped small mammals were seen in the salvage treatment compared to the other treatments. Although all of these mammals existed in forested habitat prior to the tornado, the added complexity of the ground cover seems to make the blowdown area one of opportunity for small mammals willing to occupy it.

144^{E}: Abiotic and biotic characteristics influencing community dynamics across the distribution of a rare kangaroo rat**

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Many factors, such as environmental filters (e.g., climate, habitat) or interspecific interactions (e.g., competition, facilitation), influence the structure of ecological communities. Understanding community dynamics for rare or threatened species is especially important because they are more vulnerable to extinction due to low abundance, genetic drift, or habitat loss. We sampled the rodent community and measured soil and vegetation characteristics at 35 sites across the historical range of the Texas kangaroo rat (*Dipodomys elator*), a rare and potentially threatened species endemic to north-central Texas. To investigate influence of abiotic and biotic characteristics on rodent community composition, we evaluated species co-occurrence patterns and the influence of different habitat characteristics on species distribution and abundance. The majority of possible pairwise species associations were random, although there were a few significant aggregations and segregations, particularly among heteromyid rodents (e.g., *Chaetodipus hispidus* and *Dipodomys ordii*). Moreover, we found evidence that soil composition and vegetation characteristics influenced rodent species distribution and abundance across the geographic range of *D. elator*. Our results suggest a stronger role for environmental filtering than biotic interactions on rodent community structure across the geographic range of *D. elator*. Together, these results should inform management strategies to promote biodiversity of small mammals in this region. This research was supported by a grant-in-aid of research awarded to John Stuhler in 2016.

145^E: Changes in South American bat biodiversity patterns along environmental gradients: a multidimensional problem

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Biodiversity patterns are often related to environmental gradients. Typical approaches to understand relationships between biodiversity and environmental gradients evaluate changes in species richness. However, different aspects of biodiversity may produce different patterns along the same gradient. Using other dimensions of biodiversity may provide a more comprehensive understanding of variation in biodiversity along environmental gradients. Moreover, changes in biodiversity along one gradient may vary with respect to other gradients. We hypothesize that changes in biodiversity along elevation gradients varies according to latitude. We examined changes in three dimensions of bat biodiversity across elevation gradients of 16 bat metacommunities that differ based on their latitudinal position in South America. We characterized biodiversity using 12 indices and used analysis of covariance to determine whether diversity changes along elevation were similar across different latitudes. Most metacommunities exhibit a decrease in biodiversity towards higher elevations. Decreases are more evident in the taxonomic dimension. However, these changes depended on latitude. Metacommunities at lower latitudes exhibit a more rapid decline in biodiversity with increased elevation than those at higher latitudes. Changes in biodiversity in the tropics are more related to phylogenetic and functional diversity whereas changes in biodiversity at higher latitudes are primarily explained by changes in taxonomic diversity. Our results suggest that generalization of elevation gradients of biodiversity can be facilitated by considering latitudinal position of the gradient.

146^F: Variation in space and time: examining conspecific and heterospecific density-dependent dispersal in woodland rodents

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Dispersal is a fundamental ecological process, and population density drives dispersal in many taxa. Conflicting examples of positive and negative density-dependent dispersal, however, leave little consensus regarding general effects of density on dispersal. Additionally, variation in heterospecific population densities are seldom considered when studying dispersal, despite potential interspecific effects of density on dispersal through interactions like competition. To address these issues, we examined how dispersal within a wild small mammal community is affected by naturally varying population densities at both local and regional scales. Using over 50 years of live-trapping data, we also investigated whether the direction and strength of these relationships vary over large time-scales. Numerous species within the community exhibited conspecific density-dependent dispersal. Deer mice (*Peromyscus maniculatus*), the most abundant species in the community, exhibited a decreased probability of dispersal with increasing local conspecific densities that was more pronounced in years of low regional conspecific density. The strength of this negative density-dependent dispersal varied through time, from very strong in some decades to absent in others. Preliminary results also indicate that heterospecific densities may influence the frequency of deer mouse dispersal. This work demonstrates that dispersal-density relationships may not be temporally static. It also suggests investigations of density-dependent dispersal might consider both local and regional population densities and that heterospecific density effects on dispersal may warrant more attention than they currently receive.

147^F: Trapping approaches for detecting rare small mammals

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Improving detection probabilities for rare species is critical when assessing presence or habitat associations. Our goal was to create a new small mammal trapping protocol that improved detection of rare species, such as the olive-backed pocket mouse (*Perognathus fasciatus*). We used three trap and bait types and trapped an area 4.4 times larger than the standard grid. We also assessed the effects of captures of non-target species on detection probability and occupancy of pocket mice. We found that bait and trap type selection varied significantly by species with pocket mice selecting strongest for Havahart traps baited with bird seed. Increasing grid size while maintaining a similar trap effort resulted in higher detection probability and occupancy estimates, although our analyses showed that grids can be smaller than ours. We were also able to demonstrate that with a combination of different traps and baits we were able to overcome the potential effect of non-target species (deer mice, *Peromyscus maniculatus*) on the detection probability of pocket mice. Our results show that simple changes to the standard small mammal trapping methods can dramatically increase the detectability of rare and elusive small mammals. These protocols can also yield better estimates of community composition, species richness and interactions, interaction strength, as well as energy flow in ecosystems.

148: Phylogenetic analysis of South American rodents of *Thomasomys* and *Microryzomys*

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e examined the phylogenetic structure in the Andean rodent genera *Thomasomys* and *Microryzomys* and uncovered patterns of evolutionary divergence. *Thomasomys* is a South American genus endemic to the Andes. Pacheco (2015) assigned seven species groups within the genus *Thomasomys*. Our analysis of *Cytb* shows that with some exceptions these groups form monophyletic clusters. All the specimens assigned to the cinereus species group formed a monophyletic clade. However, there appear to be

multiple distinct monophyletic clades within the cinereus group. The *baeops* species group also formed a monophyletic cluster. The aureus group members *T. aureus* and *T. princeps* were not sister to each other rendering the *aureus* group polyphyletic. Finally, *T. gracilis* does not form a monophyletic cluster with other *gracilis* members *T. andersoni* and *T. oreas*. In *Microrhizomys*, three unique clades were discovered suggesting the presence of a third species in this genus. More work is needed in both groups to discover the evolutionary history of these Andean rodent genera.

149: On the taxonomic status and distribution of African species of *Otomops* (Chiroptera: Molossidae)

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Free-tailed bats of the genus *Otomops* are poorly known, and most species are documented from a handful of widely scattered localities. Recently, two allopatric species of *Otomops* were recognized in continental Africa: *O. martiensseni* (Matschie, 1897) in the south, central, and west of Africa, and the new species *O. harrisoni* Ralph et al., 2015 in the northeast and in Yemen. We collected additional samples of *Otomops* in Kenya and Rwanda where the ranges of these taxa approach one another to clarify their geographic ranges and taxonomic status. Mitochondrial and nuclear intron sequences served to identify and delimit species; we also documented their echolocation call variation and ectoparasite complements. *O. martiensseni*, the southern African species, was documented in northern Kenya in Marsabit National Park. *O. harrisoni*, the northeastern African-Arabian species, was documented in southern Kenya and in a cave in Musanze District, Rwanda. Moreover, individuals of both species were found together at the Musanze cave, establishing them in precise spatial and temporal sympatry. Analyses of mitochondrial and nuclear loci identify no evidence of admixture between these forms, although available samples limit the power of this analysis. Echolocation call differences are also apparent among the three localities we analyzed. Our results corroborate species rank for *O. harrisoni* and establish a zone of potential geographic overlap spanning at least 800 km of latitude.

150^{E,HTA}: Glacial cycles drive rapid divergence between cryptic species of the field vole, *Microtus agrestis***

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Understanding the factors that contribute to the generation of reproductively isolated forms is a fundamental goal of evolutionary biology. Cryptic species are an especially interesting challenge to study in this context because they lack obvious morphological differentiation that provides clues to adaptive divergence between species. Isolation in refugial areas during glacial cycling is known to be important for generating genetically divergent populations but its role in generating reproductively isolated species is variable amongst different groups. We combine analysis of 35,434 single nucleotide polymorphisms (SNPs) with environmental niche modelling (ENM) to investigate genomic and ecological divergence in three cryptic species of the field vole, previously inferred to have diverged during recent glacial maxima. These cryptic species have high genome-wide divergence (pairwise F_{ST} values of 0.45-0.72), cluster by putative refugial origin, and show little evidence of gene flow. Accordingly, ENM reveals three areas as potential glacial refuges and that cryptic species differ in climatic niche, although there is some potential overlap between certain species pairs. These voles show rapid divergence driven by glacial cycles. Future investigation of the intrinsic barriers to gene flow between the field vole cryptic species is required

to fully understand what mechanisms contribute to reproductive isolation. In addition, the Portuguese vole shows on average high inbreeding coefficients and a shrinking climatic niche, and warrants future investigation into its conservation status. This research was supported by an American Society of Mammalogists Grant-in-Aid of Research in 2013.

151^{E,HTA}: The impact of introgression on mammalian evolution**

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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 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 the process of speciation. Here, I investigate introgression dynamics in multiple, independent North American meso-carnivores including 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 systems have subsequently formed insular and mainland hybrid zones. We use whole-genome sequences to contrast introgression dynamics between these systems. We discovered a hybrid origin for an insular endemic and evidence for biased introgression in both systems, some of which may result in the genetic swamping and loss of endemic populations. Ultimately, it appears that although the consequences of hybridization vary across time and space, introgression has created a lasting impact on the evolution of high-latitude meso-carnivores. This research was supported by a Grant-in-Aid awarded to Jocelyn P Colella in 2015

152^{E,HTA}: Phylogeographic assessment of the Heermann's kangaroo rat (*Dipodomys heermanni*)

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Heermann's kangaroo rats (*Dipodomys heermanni*; Rodentia: Heteromyidae) are endemic to California and primarily found in the dry, gravelly grassland and open chaparral habitats of the San Joaquin Valley. Current taxonomy (based on morphology and habitat use) recognizes nine subspecies within this kangaroo rat species. Current management practices of *D. heermanni* are based on these historical classifications; however, these classifications may not accurately reflect unique lineages in need of conservation. Using molecular and morphological data, we assessed the phylogeography of *D. heermanni* across its geographic range. Phylogenetic and network analyses of mitochondrial data from over 90 museum specimens (representing all nine subspecies distributed across the range of the species) revealed no substantial genetic differentiation within *D. heermanni*. Similarly, a geometric morphometric analysis of the cranium of over 200 adult *D. heermanni* museum specimens (again representing all subspecies across the geographic distribution of species) resulted in no apparent morphological differentiation. Our analysis indicates that recognition of all nine subspecies is likely unwarranted and that conservation and management practices of *D. heermanni* are in need of revision.

153: Conflict and consensus among datasets assessing relationships among southern brush-tailed mice, genus *Calomyscus* (Rodentia: Calomyscidae)

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At present 8 species are recognized in the genus *Calomyscus*, but the existence of as many as 14 unique clades are suggested by mitochondrial data. The genus is divided into two main clades. The southern clade includes *C. bailwardi* of central Iran, *C. hotsoni* of eastern Iran and southwestern Pakistan, and *C.*

baluchi, which is distributed along the Afghan-Pakistani border and well into both of those countries. Mitochondrial data suggest that the ranges of *C. hotsoni* and *C. baluchi* overlap in Pakistan, and the two may be hybridizing. Mitochondrial data also suggest that *C. baluchi* populations north of the Kurram River form a distinct clade. We subjected 20 samples to a ddRADseq protocol. Our results showed a strong separation between populations north and south of the Kurram River. Meanwhile, limited differentiation was detected separating true *C. baluchi* and *C. hotsoni*. A new, highly distinct, clade was detected that spans geographically disparate populations that include animals who exhibit various combinations of *C. hotsoni* and *C. baluchi* haplotypes and pelage color. Finally, the ddRADseq data uncovered clear evidence of a hybrid zone that involves *C. baluchi*, the new clade, and, potentially, *C. hotsoni*. The genus *Calomyscus* clearly exhibits a complex evolutionary history that is inadequately represented by current taxonomy.

154: Genomics of environmental adaptation in Douglas squirrels (*Tamiasciurus douglasii*)

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Landscape genomics can serve as a powerful tool for the discovery of adaptive genes underlying complex traits in forest ecosystems. Douglas squirrels, *Tamiasciurus douglasii*, are found in coniferous forests throughout western North America and possess a lifestyle and multiple morphological adaptations related to feeding on seeds from conifer cones. The north-south Cascade Mountains creates a forest ecotone with mesic coastal forests on the western side and dry interior forest on the eastern side. Douglas squirrels in these two forest types possess differences in multiple ecologically important traits, such as ventral fur color and body size. We investigated local adaptation to these different forest habitats by measuring phenotypic variation and performing ecological associations using Latent Factor Mixed Models (LFMM) between climatic variation and whole exome data along a 240-km transect. We found sharp clinal patterns in fur color and body size, but not in other ecologically important phenotypes, such as skull traits associated with bite force biomechanics. Furthermore, we found no population structure across the entire transect. Our gene ontology enrichment analyses of our top candidates from the LFMM results show molecular functions associated with tissue development, animal organ development, and anatomical structure morphogenesis. Our study sheds light on environmental adaptation in a forest mammal by identifying putatively adaptive genes that may have a role in body size differences.

155: DNA-based identification of small Neotropical rodent species using Oxford Nanopore's MinION real time sequencing technology

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DNA sequencing has been increasingly used in recent years for species identification given the challenges associated with morphological identification. Yet, traditional DNA-based identification requires processing samples in laboratory and the use of primers which are often absent for non-model organisms. The portability of Oxford Nanopore Technology (ONT) allows us to obtain genome-wide data *in situ* without the need of PCR-based amplification. We present a computational routine for rapid and accurate species identification using the MinION from ONT. We explored the yield and efficiency of the sequencing method based on library preparation using low-molecular weight DNA (traditional DNA extraction kits) and high-molecular weight DNA (modified phenol-chloroform DNA extraction). We sequenced each library in an independent flow-cell (FLO-MIN107, R9.5 chemistry) during its entire lifespan. After sequencing, we evaluated three methods to recover mitochondrial reads (for species identification) from total genomic DNA: BWA, Meta-aligner, and a novel in-house script based on BLAST. Our results show that although high-molecular weight DNA clearly improves the sequencing yield (almost by a two-fold), both libraries show an accuracy above 95% in the correct species identification. The computational routine herein presented (including our mtDNA extraction script) is a promising method for species identification both in laboratory and field conditions.

156^{E,HTA}: Does a textured coating alter bat activity at wind turbine towers?

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Large numbers of migratory tree bats are killed at wind turbines globally. Recent studies have predicted potential population-level impacts as a result, highlighting the need for strategies alleviating bat-wind turbine collisions. Research has shown bats active in close proximity to turbines, approaching and interacting with tower surfaces as if they provided resources, such as water sources and foraging opportunities. Evidence indicates that the smooth surface of the towers can be misperceived by bats as water, and it can also create an acoustic mirror that can enhance foraging success. We hypothesized that a textured coating would disrupt the smooth tower surfaces. Thus, the focus of our study was to determine if texture application would result in decreased bat activity in proximity to tower surfaces, which in turn would reduce collision risk. From May to September 2017, we used thermal cameras, night vision technology, and ultrasonic acoustic bat detectors to assess bat activity at two pairs of wind turbines in north central Texas. Each pair comprised a texture-treated turbine and a control, and bat proximity and behavior at towers were compared. In this first year of testing, we conducted 76 survey nights, observed 1030 confirmed bats on video, and recorded 1215 acoustic calls from 7 bat species. To fully assess the effectiveness of the texture coating, we will be repeating surveys from June to September 2018.

157^E: Immune function and hibernation energetics of four North American bat species with white-nose syndrome

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White-nose syndrome (WNS) causes substantial mortality in certain species of hibernating North American bats. The responsible agent is *Pseudogymnoascus destructans* (*Pd*), a fungus which causes increased arousals and energy depletion during the hibernation season. Elevated immune responses have been observed in torpid *Pd*-infected bats, but bat immunology remains under-studied. Tri-colored bats (*Perimyotis subflavus*) and northern long-eared bats (*Myotis septentrionalis*) suffer extensive WNS mortality, while gray bats (*Myotis grisescens*) and big brown bats (*Eptesicus fuscus*) are infected, but mortality is rarely observed. It is hypothesized that there is a difference in immune responses and/or hibernation metabolism between these species, resulting in interspecific variation in disease severity. Experiments were conducted at both the cellular and whole-bat level. Wing tissue cells were cultured and infected with *Pd*, and RNA-sequencing was used to assess differences between the above four species. Also, captive tri-colored bats were infected with *Pd* and tested for torpor energetics throughout hibernation. Results are currently being analyzed. This study has the potential to explain interspecific differences in WNS disease severity, which could assist in establishing treatment and conservation strategies for North American bats. In addition, we are pioneering a cell culture method to address WNS-questions without using live bats; this will allow researchers to address a myriad of questions, such as which western bat species might be most susceptible to WNS as it spreads westward. This research was supported by a Grant-in-Aid of Research awarded to Briana Anderson in 2017.

158^E: Deciphering the *Neotoma albigula* complex of southwestern New Mexico

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Neotoma albigula and allies are closely related woodrats widely distributed across the American Southwest and exhibit relatively high levels of geographic genetic structure. Recently, *N. melanura* (Bradley et al. 2016) was recognized based on nuclear and mitochondrial data. Previous survey work by Jones (2016) based on mtDNA identified two divergent clades of white-throated woodrats that converge along the eastern flanks of the Black Range in southwestern New Mexico. This study aims to resolve species limits and phylogeographic relationships within *N. albigula* and its allies in this region, and to characterize and explore the dynamics of potential contact zones between distinct lineages. The mitochondrial gene, cytochrome b (cytb), was sequenced for 68 specimens from the Museum of

Southwestern Biology for this study, with an additional 88 cytb sequences acquired from GenBank to provide greater geographic breadth of sampling. Bayesian phylogenetic analysis of cytb provided a basis for hypothetical species clades that were tested using sequences of 3 nuclear loci (BFIB, ADH, and MYH2). The mitochondrial tree suggests deep divergence, ~7% sequence divergence in cytb, of two populations of *N. albigula* that are now sympatric in southwestern New Mexico. Integration of mitochondrial and nuclear genes allows tests of existing infraspecific taxonomic hypotheses (e.g., subspecies) and we explore the evolutionary history, historical demography, and dynamics of introgression within distinctive lineages of *Neotoma albigula* of southwestern New Mexico.

159^E: Identifying immune response to WNS in a resistant bat species (*Eptesicus fuscus*)

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Since its arrival in 2006, white-nose syndrome (WNS) has had a devastating impact on bat populations in North America. Bats affected by WNS appear to die of starvation, possibly due to the increase in metabolic rate, and expenditure of fat reserves during arousals that occur during hibernation when little food is available. During hibernation, mammalian immune systems are generally suppressed; however, once susceptible bat species are exposed to the responsible agent of WNS, *Pseudogymnoascus destructans* (*Pd*), the immune system seemingly produces a partial immune response. Nonetheless, not all bat species are susceptible to this syndrome. Big brown bats (*Eptesicus fuscus*) have experienced relatively little population decline since the WNS debut, posing the question of how their immune systems combat pathogens. To investigate this, *E. fuscus* was inoculated with *Pd* and meloxicam (an anti-inflammatory agent) to suppress the immune system. This technique will expose whether this resistant species enhances, or suppresses, their immune system to fight the fungal pathogen. Immune responses of these bats will be measured by cytokine levels from blood and wing tissue from each bat before, and after, hibernation using RT-qPCR. Results have not yet been analyzed. With this research, we will obtain a better understanding of the immunological response against WNS in resistant bats and contribute our findings to the conservation of susceptible bats as the disease continues to spread west.

160^E: Does the petal fall far from the rose? Revealing the ontogeny of ungulate migration

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Seasonal migration often provides fitness benefits, although the ontogeny of this important behavior is poorly understood in terrestrial migrants. Migratory traits (e.g., migration route, characteristics of seasonal range occupied) may be transmitted from mother to offspring, resulting in matrilineal clusters where surviving female offspring establish ranges close to the range of their mother. The rose petal hypothesis describes these matrilineal clusters of related females, which may result in fine-scale genetic clustering and have implications for understanding behavioral constraints on the occupancy of seasonal ranges. Nevertheless, the mechanisms underpinning how this behavior develops, and whether landscape-scale population consequences follow, remain largely unknown. We aim to test whether migratory patterns are transmitted from mother to daughter and assess the population-level consequences of this behavior in a long-distance, terrestrial migrant: mule deer (*Odocoileus hemionus*). We will test the hypothesis that the establishment and occupancy of seasonal ranges is influenced by mothers passing their migratory routes and seasonal ranges to their daughters. Then, to reveal whether this behavior influences population dynamics and understand historical performance of matrilines, we will use genetic mark-recapture to quantify family-level population dynamics. The development and transmission of migratory routes and seasonal ranges across generations may influence the occupancy and spatial distribution of migration animals and, consequently, may have implications for harvest management and efforts to conserve migration for ungulates.

161^{E,HTA}: Density-dependent habitat selection in a fluctuating population of golden-mantled ground squirrels, *Callospermophilus lateralis***

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Investigating how habitat selection varies with fluctuating population density is a central theme in ecology. As density increases in high quality habitat and competition for resources intensifies, animals are expected to preferentially settle in lower quality habitat, where they are equally likely to survive or reproduce due to lack of competition. However, direct measures of fitness are rarely coupled with these decisions in free-ranging mammals. We utilize a long-term dataset to quantify density-dependent habitat selection and its fitness consequences in female golden-mantled ground squirrels, *Callospermophilus lateralis*, at a site in Colorado. We rank 5 habitat types (aspen forest, conifer forest, dry meadow, wet meadow, and willow community) in terms of use from 1996-2006 and perform use-availability analyses on two spatial scales: habitat composition of the home range compared to that available across the study area, and habitat type preferentially used within an animal's home range. We then quantify the relationship between habitat utilization and two measures of fitness (survivorship and reproductive success) to rank habitats in terms of quality. Preliminary results suggest that golden-mantled ground squirrels prefer dry meadow habitat during years of low density. By combining spatial and demographic data, we quantify whether settlement decisions change as density increases. This will further our understanding about the causes and consequences of changes in habitat use, providing insight to the fields of wildlife management and conservation. This research was supported by a Grant-in-Aid of research awarded to Jaclyn Aliperti in 2017.

162: Who succeeds in a biodiversity course?

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As university institutions turn their attention to increasing diversity and inclusion in STEM fields including biology, it is imperative that zoology do so in kind. A pilot mammal lab activity was conducted with summer students at the University of Michigan taking Introduction to Biology Lab to expose students to our museum collection, specimen-based research, and biodiversity centered on mammals. To evaluate how prior knowledge might be influenced by student demographics, we surveyed students before the 3-day lab to obtain demographic data along with knowledge of and interest in biodiversity. Our results suggest that students who grew up solely in urbanized areas are more likely to underestimate biodiversity. To evaluate the efficacy of the laboratory exercises, we also surveyed students after the lab. Seventy-four percent of students showed an increase in biodiversity knowledge after the lab. Students did not show varying levels of interest in zoology based on gender or cultural identity. However, first generation students had a significant drop in interest in majoring in STEM compared to their peers. We hope to continue examining how a student's background and identity influence their interest and success in biodiversity by expanding our surveys to other courses that emphasize biodiversity.

163^E: Bat to the future: an insight into island biogeography using fossil and modern bats

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The Caribbean islands have undergone dramatic changes throughout the Pleistocene and Holocene. Changes in sea level and climate have drastically affected the distribution of vertebrates. Bats (order Chiroptera) are the most diverse group of mammals on Caribbean islands where they can occupy a wide variety of niches. Recent studies have shown that the advent of humans on these island systems has drastically changed the landscape and altered the distribution of numerous vertebrate species, including bats. Understanding how species distribute themselves can help demonstrate the adverse effects of climate change and anthropogenic impacts. The Caribbean islands are an ideal study site for bats due to the large number of extinct and extant species that are found on the islands. This study highlights the use of morphology in understanding the distribution of bats in the Bahamas. I discuss the significance of using a widespread bat, *Tadarida brasiliensis*, which is found in the Bahamas as well as the West Indies and in

North, Central and South America. By incorporating fossils along with modern specimens, inferences can be made about the size and morphology of bats and predictions can be made about future populations. Furthermore, this can be used as a template to study other species of bats which have been collected from fossil sites in the Bahamas.

164^E: Investigating shifts in skull morphology and dietary preferences in North American deermice associated with wildfire

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Fires have become more prevalent in the U.S. over the last few decades, drastically changing habitats and impacting mammal communities. Studies on small mammals in the Yellowstone region indicate predictable community shifts associated with fire disturbances. Immediately following a fire, North American deermice (*Peromyscus maniculatus*) predominate in burned areas that were previously dominated by southern red-backed voles (*Myodes gapperi*). However, as post-fire succession progresses, relative abundance slowly shifts to favor *M. gapperi*. A new set of fires swept through our study sites in 2016, and in the 2017 field season *P. maniculatus* was restored to ecological dominance in newly burned areas. What is unknown is whether this dramatic ecological transition is correlated with, or possibly facilitated by, any dietary or morphological changes within *P. maniculatus*. For this project we investigated cranial morphology using geometric morphometrics and diet using carbon and nitrogen stable isotopes focused on comparing two groups: deermice collected in the years before the 2016 fire (pre-burn) and deermice collected the year immediately following the fire (post-burn). Results suggest significant differences in morphology based on the year a specimen was captured, but these shifts were not significantly related to the pre/post fire groupings. These results provide important insights into how the ecology of a dominant small mammal is impacted by fire succession and the degree to which dietary generalism facilitates early colonization post-fire.

165^E: Developing protocols to recover and amplify museum DNA in *Berylmys bowersi* and other murid groups

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Museum collections are libraries of taxonomic, phenotypic, geographic, and temporal genetic variation. Materials like skin, bone, and teeth are often the only source of genetic information from rare or logistically inaccessible specimens. With improving technologies, DNA can be extracted from ever smaller quantities of material, minimizing damage to the future scientific value of specimens. Due to degradation, DNA from such sources is broken into fragments no larger than several hundred base-pairs. Pervasive environmental DNA contamination is also inherent with materials stored in museum collections. As DNA quality can vary greatly even among contemporary specimens within collections, successful extraction and amplification protocols must be tailored to the target taxonomic group. A successful workflow was developed to recover and amplify DNA from dry adherent tissues (4-9 mg) of *Berylmys bowersi* (Muridae: Rodentia) in the collections of Field Museum of Natural History. *Peromyscus leucopus* and *Rattus norvegicus* from NIU museum collections were used to develop successful parameters for use in *Berylmys*. Primers were designed to amplify regions of ~200 and 385 base-pairs in mitochondrial genes cytochrome-b and cytochrome-oxidase subunit 1, and a ~180 base-pair region of the growth-hormone receptor nuclear gene. DNA yields were 0.69-4.0 ng/ul for *Rattus*, 18.2-45.7 for *Peromyscus*, and 0.76 - 6.03 in *Berylmys*. All three gene regions were successfully amplified in *Peromyscus* and *Rattus*, and both mitochondrial genes in *Berylmys*.

166^E: Modeling the effects of environmental predictors on small mammal assemblage structure in an isolated rangeland

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Population modeling informs us of predictors that influence the response of small mammal assemblages to environments experiencing an increasingly variable climate. To investigate the relationship among habitat structure, weather patterns, and species distributions and detection probability, we assessed capture success with abiotic and biotic predictors to better understand population dynamics seen across time. Small mammal capture-recapture data was systematically collected annually from 2010 to 2017 across 35 trapping locations throughout the isolated Texas Tech University native rangeland site. We evaluated ambient temperature, aspects of rainfall, nighttime illumination, and percent cover of vegetation functional groups. Using Akaike's Information Criterion, we applied information theory to evaluate biologically determined models and use model averaging to determine the relative importance of these predictors to small mammal population dynamics. Preliminary models indicate that weather, and in particular rainfall of the previous season, exhibits the strongest relationship with capture success. These models also suggest that the density of mesquite (genus *Prosopis*) in the rangeland affects capture success and diversity, thus raising questions into the effect of removing mesquite from the rangeland on small mammal abundance and species composition. These questions will subsequently prompt the design of further small mammal surveys which may inform us of how changes in the environment through time affect the structure and interaction of the community as a whole.

167: Does agriculture influence demography, development and activity patterns in California ground squirrels (*Otospermophilus beecheyi*)?

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California ground squirrels are widely distributed across the state of California, and the behavior and ecology of this native species was well-described more than 60 years ago. However, most studies have focused on northern or coastal California populations, where natural food resources limit population densities. In the Central Valley of California, most of the landscape is devoted to agricultural crops which subsidize the natural diet of ground squirrels. As a result, population densities are very high in the Central Valley, and this native species is considered an agricultural pest. We are assessing how anthropogenic food resources influence demography, activity and development of ground squirrels in three National Wildlife Refuges in the Central Valley. Each refuge is surrounded by farmlands and orchards, with variation in the proportion of acreage devoted to high energy (almond) and low energy (vegetable crop/alfalfa) foods. We used a mark-recapture method to intensively sample within populations from 2015-2017. We have captured and marked 542 unique squirrels, many of which are subsequently recaptured. Here, we present preliminary data emerging from this study, which suggest that Central Valley populations exhibit patterns of development and behavior unlike those described elsewhere. We infer these differences have arisen recently in the evolutionary history of this species, and are evidence of adaptive behavioral plasticity, which may explain the persistence of populations despite environmental stochasticity and human disturbance.

168: Evaluating potential effects of camera density on capture and recapture rates of bobcats

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Performance advances among remotely triggered cameras has prompted their widespread use in estimating density of elusive and mobile predators such as bobcats (*Lynx rufus*). Nevertheless, reliability of density estimates varies widely between species, due to heterogeneity in numbers and placement of camera stations among studies, and the ability to capture and recapture individuals across multiple

camera trap locations. We evaluated potential effects of camera density on capture and recapture rates of bobcats in agriculturally dominated landscapes of west-central Illinois. We deployed 31 camera stations during two sampling intervals (15 May–15 Jun 2016, 20 Apr–20 May 2017) over 1,800 trap nights. Our analyses revealed that effects of camera density on bobcat detection probability was marginally significant ($P=0.07$); maximum detection was associated with moderate camera densities (4–6 cameras/9 km²). Numbers of individual bobcats detected varied ($P = 0.04$) with camera density; moderate and high (8–10 cameras/9 km²) camera densities yielded greater ($P \leq 0.05$) numbers of individuals than lower camera densities (1–2 cameras/9 km²) and we detected no more than 4 individual bobcats at any 1 camera station. When photo-capture and recapture rates are a function of camera density, modifying camera trapping techniques by deploying moderate camera densities or repositioning cameras to more productive areas within survey grids may improve capture success in low density bobcat populations.

169^F: Influence of spatial alignment on photographic detection rates of bobcats at remotely triggered camera stations

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Trail camera performance is influenced by a wide range of factors, though no studies have rigorously evaluated potential sources of sampling bias (e.g., camera type, relative position of cameras) on overexposure (i.e., capturing the flash of one camera by another) events within paired camera station (i.e., 2 camera traps placed perpendicular to animal travel corridors) designs. We evaluated potential effects of camera type and relative camera position (directly aligned vs. offset from one another [i.e., staggered]) on wildlife photographs recorded and overexposure events across 48 camera stations deployed during summer 2017. Total number of wildlife photographs varied by camera model and alignment (model \times alignment interaction, $F_{2,42} = 5.56$, $P = 0.007$); Reconyx and Browning cameras detected more wildlife photographs at aligned camera stations whereas Moultrie cameras more wildlife photographs at staggered camera stations. Number of overexposure events varied ($F_{1,46} = 35.24$, $P \leq 0.001$) between aligned and staggered camera stations. Mean percent overexposure for aligned stations was 5.63 (SE = 1.02). We documented no overexposure events at staggered camera stations and no difference ($P = 0.95$) in numbers of exposure events across camera types. We recommend that future use of paired camera stations for research, inventory, or monitoring of elusive species consider staggering the placement of cameras to minimize overexposure events of target species, and evaluate seasonal effects (i.e., winter) on overexposure rates.

170: Small mammal isotopic analysis of consumer roles across an experimental prairie woodland mosaic

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As the Great Plains experience progressive environmental change including climate and anthropogenic effects, we still lack clear understanding of vertebrate community responses or how wildlife impacts local resources. Historically, prairies that dominated this region were maintained by frequent wildfire and megaherbivore grazing. Here, we investigate the roles of small vertebrate consumers within a landscape-scale fire manipulation experiment where fire suppression may cause habitat conversion, species turnover, and increasingly complex interactions across a mosaic ecotone. Using stable isotopes we test predictions that resource use will be significantly different between grassland and woodland, and dietary breadth will be greater in the more floristically diverse woody habitats, but more stable through time than within grasslands that experience frequent fire. We tested C and N isotopic ratios from fur and liver of dominant rodent species collected from treatments reflecting 1, 4, and 20 year fire intervals, and

compared signatures with dietary reference samples. Preliminary results indicate that species occupy different fundamental niche space. Interestingly, grassland rodents consume a broader diet and experience intra-annual dietary shifts compared with woodland species. Conversion to woodlands significantly narrows niche breadth of vertebrate consumers with woodland species relying on woody resources. Our analyses suggest that fire suppression, woody encroachment, and community turnover leads to a novel, narrow, and stable dietary niche by small mammals, possibly reinforcing persistence and spread of woodlands within historic prairies.

171: Mesopredator distribution, abundance and potential competition with the American burying beetle (*Nicrophorus americanus*) for carrion

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American burying beetles (*Nicrophorus americanus*, hereafter ABB) were once prevalent throughout the eastern part of North America but they have declined by nearly 90% in numbers and range. The ABB was listed as an endangered species in 1989 and following listing many hypotheses were developed to explain their range-wide decline. I investigated the carcass competition hypothesis that implicates increased competition between vertebrate scavengers and ABBs for appropriate-sized carcasses as a cause for ABB decline. Predators of medium size that occupy an intermediary trophic level (hereafter mesopredators) are potential competitors for carcasses. I used camera trapping to assess mesopredator abundances in different habitats at Fort Chaffee Joint Maneuver Training Center (FCJMTC) in western Arkansas because this area supports the largest known ABB population in the state. I examined mesopredator presence at random locations and at locations associated with ongoing ABB trapping efforts. Photographs examined so far show evidence of Virginia opossum, northern raccoon, coyote and bobcat activity. More photographs captured Virginia opossums in pine, lespedeza and shrub habitats while northern raccoons were photographed more frequently in bottomland hardwood habitat. I will use the random encounter model to obtain mesopredator density estimates and then examine relationships between mesopredator and ABB abundances across different habitat types. Assessing mesopredator abundances at a location where ABBs are present could provide evidence of interspecies relationships and insight into the ABB decline.

172^E: Status, distribution, morphology and genetics of *Sigmodon fulviventer dalquesti* in the Chihuahuan Desert Ecoregion

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The tawny-bellied cotton rat, *Sigmodon fulviventer dalquesti*, is a Texas endemic subspecies reported only from a single sampling near Fort Davis in 1991. The Texas Parks and Wildlife Department's Texas Conservation Action Plan designates *S. f. dalquesti* as critically imperiled within the state. The current population, and distribution of *S. f. dalquesti* is enigmatic. Additionally, the relationship between *S. f. dalquesti* and other *S. fulviventer* subspecies in Mexico, Arizona, and New Mexico is not well understood. The current state of knowledge of *S. f. dalquesti* systematics consists of morphological distinction from *S. f. minimus*, and a finding of mitochondrial cytochrome *b* divergence between *S. f. dalquesti* and *S. f. fulviventer* roughly equivalent to 100,000 years of divergence. To inform an accurate conservation assessment, a more complete understanding of *S. f. dalquesti* biology is required. We will conduct morphological and molecular phylogenetic analyses of the recognized *S. fulviventer* subspecies using existing specimens available in museum collections, as well as specimens obtained in planned field work. We will assess the population and distribution of *S. f. dalquesti* in the Chihuahuan Desert Ecoregion by Sherman Trap sampling transects in areas of the original detection in addition to other localities. Lastly, we will use niche modeling to predict *S. f. dalquesti* distribution. These efforts will improve our understanding of *S. f. dalquesti* biology, and inform future conservation management decisions.

173: Phylogeography of the African wading rat, *Colomys goslingi* (Muridae: Murinae)

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The highlands of central and eastern Africa have a rich diversity of endemic small mammals, though many are poorly known. The African wading rat (*Colomys goslingi*) is one such murine rodent from equatorial Africa. Although little is known of its ecological habits, it does appear to adopt an unusual foraging strategy of wading in shallow streams on stilt-like legs in search of invertebrate prey. Despite its interesting behavior and wide range extending from Cameroon to Kenya, only a handful of studies have ever attempted to sequence DNA from this species, and it has always been collected in the context of a phylogeny of dozens of African murines. 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. Here, we present intraspecific phylogenies from both mitochondrial and nuclear genes. Results show geographically structured genetic diversity and the possibility of an undescribed taxon. 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.

174: Assessing status of eastern spotted skunks (*Spilogale putorius*) in Oklahoma

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The eastern spotted skunk (*Spilogale putorius*) is currently listed as a Tier III species of greatest concern by Oklahoma Department of Wildlife Conservation and as an S2 (imperiled) species by Oklahoma Natural History Inventory. This species is thought to be found in Cross-Timbers, Mixed-grass prairie, Ouachita Mountains WGCP, and Ozarks regions; however, in each of these regions its trend in population size is unknown, due to its rare and secretive nature (ODWC 2015). Due to its rarity and elusive behavior, not much is known about their distribution in Oklahoma or demographics. Reconyx Hyperfire camera traps were deployed from January 2 through March 26 in the Ouachita National Forest (LeFlore County, OK), resulting in 5000+ pictures. Mammals most commonly surveyed included raccoon (*Procyon lotor*), grey squirrels (*Sciurus carolinensis*), white-tailed deer (*Odocoileus virginianus*) and deer mice (*Peromyscus spp.*). Spotted skunks were detected 6 times at 3 sites approximately 1000-4000 meters apart. Results from this initial survey will inform future surveys to be conducted through the next 2 years.

175: Small mammal, vector, and pathogen data collection in the National Ecological Observatory Network

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The National Ecological Observatory Network (NEON) is a 30-year, large-scale research program that is designed to enable ecological discovery by providing open-access data generated by standardized sampling of a diversity of taxa and ecosystem variables. A key component of the Observatory is terrestrial organismal sampling intended to increase our understanding of climate change and land use impacts on phenology, demography, diversity, community dynamics, pathogen presence, and ecosystem function. This includes the long-term community dynamics of small mammals and their pathogens at 47 sites distributed throughout the United States and its territories. Standardized sampling at this combination of spatial and temporal scales for small mammals is unprecedented. Here we outline the current small mammal sampling designs for NEON, including vector and pathogen data, and the rationale for these designs, and demonstrate how these and other NEON data can be accessed by the larger community (<http://data.neonscience.org/home>) to support individual research and education programs (<http://neondataskills.org/>).

176^E: Exploring the distribution of *Peromyscus maniculatus* in south Texas

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Peromyscus maniculatus is sympatric with *P. leucopus* throughout nearly all of the latter's range. In Texas, *P. leucopus* is known from almost every county. Although *P. maniculatus* is thought to occur across the entire state, records of *P. maniculatus* from the southern parts of Texas are spotty, often based on few specimens. Differentiating these two species in the field can be difficult; thus, the Texas distribution of *P. maniculatus*, especially in the southern parts of the state, is uncertain. Using museum specimens and 2D geometric morphometric techniques, we used a cranial landmark scheme to distinguish between the species across the southernmost distribution of *P. maniculatus* in Texas. To set a morphometric baseline, several specimens included in the analysis were genetically identified *P. maniculatus* and *P. leucopus*. Principal component and linear discriminant function analyses indicated that the genetically identified *P. maniculatus* clustered separately (with some overlap) from specimens of *P. leucopus* with 95% confidence. The majority of south Texas specimens previously identified as *P. maniculatus* clustered within the morphospace of the genetically identified *P. leucopus* specimens, indicating that these specimens were likely misidentified. These findings suggest that the southernmost range of *P. maniculatus* in Texas is more limited than previously thought.

177: Nematode assemblages provide a glimpse of mammal-helminth community dynamics within the central Great Plains

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Prairie grasslands are both a biological filter across North America, and constitute a heavily human-altered ecosystem. This is an exceptional, yet understudied region for investigating vertebrate community interactions, and how environmental trends influence host-parasite/pathogen dynamics. But, the fundamental biodiversity baselines that allow resolution of eco-evolutionary relationships are lacking. We present nematode data from small mammal sampling on Konza Prairie as a developing effort across the Great Plains. Eleven mammal species were captured across different experimental treatments (representing grassland and woodland assemblages) and prepared as museum specimens to accommodate comprehensive host-parasite biodiversity discovery. We identified four nematode taxa including two new species: *Protospirura muris* from the stomach of *Reithrodontomys megalotis*, *Microtus ochrogaster*, *Peromyscus leucopus*, and *Sigmodon hispidus*; *Pterygodermatites parkeri* from the small intestine of *P. leucopus*; *Syphacia obvelata* from the large intestine of *M. ochrogaster*, *Trichuris* spp. from the large intestine of *Neotoma floridana* and *M. ochrogaster*, and *Vexillata* n. sp. from the small intestine of *Chaetodipus hispidus*. *Protospirura* and *Syphacia* species are common in small mammals across the Holarctic, however Konza specimens are genetically divergent from elsewhere. We characterize *Vexillata* n. sp. and provide phylogenetic relationships among other nematodes. *Microtus* (grassland) and *P. leucopus* (woodland) are the major hosts of nematode diversity within this region. Both host-generalists and worms found only in grassland or woodland habitats indicate potential for community turnover across habitat transitions.

178^F: Requirements for handling skills in entry-level jobs in wildlife biology

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While students interested in non-academic careers in wildlife biology typically learn wildlife-related information through course content associated with programs in biology or environmental science, not all programs provide hands-on training in skills such as wildlife handling. Understanding which types of entry-level positions in wildlife biology are most likely to require handling skills can help university programs to prepare students for successful entry into the field. In this study, we examine how often

handling skills are desired versus required for entry-level positions in wildlife biology, and if requirements vary with job sector (government versus private or non-profit) or the taxonomic group on which a job is focused. To address these questions, we are reviewing postings for entry-level positions in wildlife biology (both temporary and permanent) listed on the University of Maryland's "Ecolog" listserv between January and May of 2017. Preliminary analyses suggest across job sectors and taxonomic groups, more than 50% of job postings advertised a preference for job applicants with experience handling wildlife, but less than 50% required such experience. Entry-level positions were more likely to both prefer and require handling experience in the private or non-profit sectors than in the government sector. Additionally, an examination of job postings by taxonomic group indicate handling experience was required more often in jobs working with mammals than any other taxonomic group.

179^F: Examining the effect of raptors on vole populations and soybean damage in cover-cropped fields

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Across the Midwest, farmers are increasingly planting winter cover crops in corn-soybean rotations to improve soil health. Though this practice has many benefits, it also can provide habitat for potential pest species, such as voles (*Microtus pennsylvanicus* and *M. ochrogaster*). Voles have been reported by farmers to damage soybean plants in cover-cropped fields, but there has been little scientific inquiry to help farmers address this problem. One possible method of vole control is to provide structure needed by raptors to hunt in agricultural fields. To test this hypothesis, we installed artificial perches at increasing distances from the edge of 8 fields in northwest Indiana. Once cover crops have been terminated in spring, and again in summer when soybeans are growing, we will live trap treatment and control sites in each field. We also will survey transects in each trap grid to assess severity of vole damage to soybeans. We will present preliminary results evaluating the effect of perch availability, distance to field edge, and time since cover crop termination on vole abundance. Secondly, we will explore the possible association between raptor perch availability and the percent of soybeans damaged. If there is a strong association between raptor perches and decreased vole abundance and subsequent damage, farmers could utilize perches to manage vole populations in cover-cropped fields.

180^{E}: Small mammal community dynamics and isotope ecology at Rancho La Brea: millennial-scale stability or change?**

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Despite the longevity of paleontological research conducted at the Rancho La Brea Tar Pits (RLB) in Los Angeles, California, there is no consensus on the environmental conditions and changes that occurred there during the late Quaternary. We examined small mammal (<3kg) fossils from three RLB deposits (Project 23 Deposits 1, 7B, and 14) of different mean ages spanning >50,000 to ~30,000 calibrated years before present (cal BP) and evaluated changes in their faunal composition and diet through time. Such changes are proxies for interpreting past environmental change since small mammals can effectively track environments due to their small home ranges, high abundance, and high taxonomic diversity. We evaluated taxon-specific presence, absence, and abundance through time by randomly sampling and identifying fossils from each deposit, and tracked dietary niches via stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope analysis of radiocarbon-dated dentaries from several taxa. Preliminary results show similar sets of taxa among deposits, although taxon-specific abundances vary considerably. Moreover, $\delta^{15}\text{N}$ becomes increasingly positive through time in some taxa including *Otospermophilus beecheyi* and *Sylvilagus audubonii*. These data suggest that directional environmental changes, including aridification, may have occurred at RLB between 50,000 and 30,000 cal BP. Further study of the small mammal faunas and their geochemistry will improve understanding of species-environment interactions and the

extent of late Quaternary paleoenvironmental changes that occurred in southern California. This research was supported by a Grant-in-Aid of Research awarded to Nathaniel Fox in 2017

181^E: Secondary sexual dimorphism in white-lined broad-nosed bats (*Platyrrhinus lineatus*)

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Examining sexual dimorphism is important for understanding selective pressures that influence behavior or fitness of a species in a given environment. For example, the presence of sexual dimorphism may indicate differences in breeding preferences, diets, or energy expenditures within a species. In bats, sexual dimorphism has been reported for many species, where females are consistently larger than males. We evaluated whether sexual dimorphism exists in the white-lined broad-nosed bat (*Platyrrhinus lineatus*), a species endemic to South America. We examined sixteen skull characters (i.e., eight cranial, six dental, and two mandibular) and fourteen external characters from 94 adult bats collected from two sites in eastern Paraguay (Reserva Natural del Bosque Mbaracayú and Yaguareté Forests). Measurements were made to the nearest 0.01 mm using digital calipers. Results from a MANOVA did not indicate any significant differences in cranial characters between males and females or between the two sites. However, we found significant differences between males and females, but not between sites, for external characters. Importantly, these differences manifested in seven of the fourteen external characters, with females consistently larger. Because adult females were generally larger than males, it is possible that these differences are related to differential costs between sexes related to reproduction and rearing offspring.

182: Post construction bat and bird fatality monitoring at a wind energy facility in south Texas

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Wind energy development has long been known to cause bird and bat fatalities; despite emphasis on understanding and reducing these impacts, there is a paucity of publicly available data in the Great Basin/Southwest region and Mexico. We conducted post construction fatality monitoring at a wind energy facility in south Texas near the border with Mexico for 12 months (March 2017-March 2018). 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. Turbines were searched weekly from spring through fall and bimonthly during winter. In addition to standard fatality searches, we conducted searcher efficiency and carcass removal trials. We found 238 bats and 78 birds. The majority of bat fatalities was *Tadarida brasiliensis* at 76%, and the majority of bird fatalities were *Colinus virginianus* and *Cathartes aura*, with 17% and 12% respectively. The majority of bat fatalities were found in August and the majority of bird fatalities were found in September. Additionally, we are working to estimate fatality rates for the site by megawatt and by turbine. Post construction mortality monitoring data are rarely published, so making these data publicly available is of the utmost importance toward reducing turbine-caused fatalities.

183: Morphological analysis of *Peromyscus truei* from a mtDNA contact zone

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Peromyscus truei (Pinyon mice) is one of the more common species of small mammals in the western United States, occurring from California and Oregon eastward into portions of Oklahoma and Texas. Mitochondrial cytochrome b data demonstrates that there are two subclades (eastern and western) within Pinyon mice; these clades differ by about 4.5% with very little intraclade differentiation. Pinyon mice from California, Nevada and western Utah belong exclusively to the western clade; whereas, mice from Texas, New Mexico, Colorado, northeastern Arizona and eastern Utah represent the eastern clade. To date we

have identified 11 localities in Utah from which both eastern and western clade mice can be collected at the same locality. The aim of this study was to use 38 craniodental and 4 external measurements to determine if Pinyon mice representing the eastern and western clades could be distinguished morphologically. Results of Principal Components Analysis indicate that mice from California and New Mexico are morphologically separable, but that mice of known mitochondrial haplotypes from Utah are morphologically intermediate. We hypothesize that our results indicate that Utah represents a hybrid zone between the eastern and western forms of Pinyon mice. The next step of our research will be to test this hypothesis using nuclear DNA markers.

184^E: First genomic evidence of wolf-dog hybrids from Oklahoma's latest Holocene

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The analysis of genomic data extracted from subfossil specimens that are morphologically “wolf,” housed at the Oklahoma Museum of Natural History revealed a haplotype network of individuals with mitochondrial DNA lineages of dogs, wolves, and wolf-dog hybrids. Therefore, we report the first record of wolves and dogs hybridized in this region of the southern Great Plains prior to the extermination of the wolf from the region. These specimens range in age from 100 to 400 years before present. The mitochondrial DNA extracted from ancient specimens revealed two dogs, two gray wolves, and wolf-dog hybrids. One dog is most closely related to ancient dogs from Alaska and Canada. The second ancient dog from Oklahoma is most closely related to Pueblo period dogs from the southwest, and belongs to a larger clade/branch that is represented by village dogs from across North and South America, as well as, domestic breeds. This clade, however, is dominated by ancient Native American dogs. Therefore, it is likely that this clade originated in Asia and was brought to the Americas; whereas, part of the group remained behind and are represented by domestic breeds present today. Based on agouti results, there was no admixture with coyotes for the coloration gene. The next phase of the project will focus on the haplotype networks of the subfossils from Oklahoma that were identified as wolf.

185: Managing an undergraduate research lab at a teaching-focused university

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The importance of research experiences for undergraduates is well-demonstrated. These experiences can help retain students, improve their soft skills, and prepare students for graduate or professional school. Professors at teaching-focused universities often have a strong drive to provide these experiences but may lack time and resources in comparison to professors at research universities. Herein, I report on my experiences running a primate behavior undergraduate research lab at Oklahoma City University, a small private university. Over seven years I have worked with more than twenty undergraduates on three projects. Students have assisted with research projects on wild squirrel monkeys in Costa Rica, orangutans at the Oklahoma City Zoo, and long-tailed macaques at a local monkey sanctuary. I describe how I have developed a model of student participation that efficiently uses my time and allows students to participate in research in a variety of ways tailored to each student's availability and interest level. Some tools I use include regular structured meetings, intentional mentoring, and careful choice of research projects. Students from my lab have been awarded grants and presented at national and regional scientific meetings. I present tips to help others build undergraduate research programs in the face of limited resources.

186: Rural communities in the boreal forest are habitat islands for little brown bats (*Myotis lucifugus*)

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Urban development is detrimental to many species; however, little brown bats (*Myotis lucifugus*) may be attracted to human settlements and may be a “synurbic” species. Buildings and human-made bat houses provide apparently high quality roosting habitat, which may be a limiting factor in the boreal forest, where trees are typically small and subject to a short fire interval cycle. In the boreal forest, there are relatively few urban developments in a matrix of wilderness and seemingly suboptimal natural roosting habitat. Given their potential attractiveness as roosting habitat, we asked whether isolated rural communities are islands of summer habitat for little brown bats in the boreal forest. To test this hypothesis, we investigated the relationship between little brown bat activity, foraging rates, and proximity to urban centres. We used acoustic detectors to monitor bat activity near three small, rural communities in Yukon, Canada, and characterized bat habitat with remote sensing data. Bat activity increased with proximity to community centers, but foraging activity did not, suggesting that communities were important as roosting rather than foraging habitat. Bats were also attracted to waterbodies and areas with relatively high densities of linear features (e.g. roads and transmission lines). Our study advances knowledge of little brown bat habitat requirements in the boreal forest, where little is known and better information is required to help identify habitats critical to their recovery.

187: Landscape drivers of site occupancy by remnant populations of arctic ground squirrels (*Urocitellus parryii*)

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Arctic ground squirrels (AGS) occupy alpine and lowland habitats in southwestern Yukon, Canada, where populations have been monitored since the 1970s. While alpine populations have remained stable, populations in low-elevation sites collapsed in the late 1990s and have yet to recover. Propelled by the region-wide collapse of AGS at low-elevation sites, the purpose of our study was to determine covariates associated with occupancy of remnant AGS populations. Using walking transects, we surveyed 155 low-elevation sites in eight study areas for AGS presence, and report a naïve site occupancy rate of 0.628 (SE = 0.040) with a detection probability of 0.884 (SE = 0.026). The presence of conspecifics was the most important covariate explaining AGS occupancy. Importantly, AGS occupancy increased with increasing habitat openness, and was positively influenced by the presence of linear features. Connectivity among colonies and availability of open habitat patches within the boreal forest are likely important factors for the persistence of low-elevation populations, which may be linked to predator avoidance. Shrubification of the boreal forest as a result of climate warming may be reducing AGS ability to avoid predators and persist. Anthropogenic disturbance, such as linear features, may enhance AGS habitat and population connectivity, suggesting that remnant populations in low-elevation habitats at the southern edge of their range are largely persisting in landscapes with a greater human footprint than more natural sites.

188^E: Isotopic ecology and body size in grasshopper mice after the Late Pleistocene megafaunal extinction

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During the Late Pleistocene extinction (LPE) 10-14ka, human invasion of the New World drove 100+ genera of megafauna extinct. Our study examined the ecological consequences of the LPE with respect to mammal community changes. We use a multi-proxy approach, exceptionally preserved fossils, and a fine-grained age model of Hall's cave in Texas to study effects of the LPE on body size and isotopic dietary niche of the grasshopper mouse *Onychomys*. We measured bone collagen carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) values to estimate isotopic niche widths over time using Bayesian-based spatial metrics. We also constructed a dichotomous key to identify specimens, which revealed some previously sampled

"*Onychomys*" were actually granivorous/insectivorous *Reithrodontomys* and omnivorous *Peromyscus*. *Onychomys* ranged from -12.4‰ to -19.4‰ $\delta^{13}\text{C}$ and 7.4 to 12.5‰ $\delta^{15}\text{N}$. We found the greatest average $\delta^{15}\text{N}$ values (12.0‰) in the oldest strata ~11.5ka, declining ~2‰ by ~7ka, which closely matches contemporaneous declines in other co-occurring small mammal taxa. We suspect this drop reflects a baseline shift in vegetation nitrogen due to climate. Post-baseline shift *Onychomys* are larger than the largest modern individuals, and bone collagen $\delta^{15}\text{N}$ values positively correlate with proxies of body size. This may indicate ancient *Onychomys* fed at a higher trophic level. Ongoing work will couple isotope data with novel ecomorphological measures to assess ecological shifts for more taxa after the LPE.

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

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Artibeus fraterculus is endemic to Ecuador and Peru. Most of its distribution is restricted to the west side of the Andes Mts, specifically throughout the Tumbesian ecoregion. Its habitat is mainly xeric forest and scrub and distributed from 0-1,600 m along the elevational gradient. Very little is known on the population genetics structure of *Artibeus fraterculus* and the effect of the Andes Mts on its distribution and as a potential barrier for its populations. Using UCEs (Ultra Conserved Elements), patterns of genetic divergence among populations of *A. fraterculus* from different locations along Ecuador and Peru were analyzed. A total of 1406 UCE loci were obtained in which all the individuals analyzed were represented. All of the UCEs were concatenated and a phylogenetic analysis from this data set was carried out using RaxML. In addition, to investigate population structure, the program Structure 2.3.4 was used. A phylogenetic tree was recovered that showed two distinct clades corresponding to the location of the populations at each side of the Andes. This result is part of ongoing research and is showing that apparently there is an effect of the Andes Mts as a barrier to gene flow for these two populations of *A. fraterculus*.

190^E: Evolutionary relationships among brush-tailed mice, genus *Calomyscus* (Rodentia: Calomyscidae) based on mitochondrial and nuclear data

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The brush tailed mice (genus *Calomyscus*) comprise a unique lineage of muroid rodents found in sparsely vegetated dry rocky areas in south-central Asia. At present, 8 species are recognized based on morphology, karyotype, and some mitochondrial data. Excluding the poorly known *C. tsołovi* from Syria, *Calomyscus* can be informally separated into 2 species groups: a northern group allied with *C. mystax* (4 recognized species), and a southern group allied with *C. bailwardi* (3 recognized species). We compiled and expanded the existing cytochrome *b* dataset across the genus and sequenced the nuclear interphotoreceptor retinoid-binding protein (*Rbp3*) gene across the range of the *C. bailwardi* group. Mitochondrial data in the genus suggest there are as many as 14 distinct clades present. Within the *C. bailwardi* group, mitochondrial data identify potential unnamed forms in south-central Iran, northeastern Pakistan, and northern Afghanistan. Nuclear data, however, are not fully in agreement with the *Cytb* tree. We discuss our results in light of *Calomyscus* taxonomy and biogeography.

191^E: Embracing uncertainty in distributional model development and estimations by considering circulation models

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There is wide use of ecological niche models (ENMs) to create expectations for where species may occur, have occurred, or will occur in geographic space. A common approach has been to obtain a set of environmental predictors with analogues available for forecasted and/or hindcasted estimates. These

predictors explain the variation in presence (sometimes absence) records using some model framework, such as generalized linear models and MaxEnt. Issues regarding specific aspects of model complexity and background data for the popular MaxEnt implementation have highlighted the need to better evaluate model structure and assumptions. There also are a bevy of studies that show the choice of environmental predictors influence expectations. We examined various outcomes based on circulation models that are used to generate or estimate environmental predictors. Specifically, we used EcoClimate data that represent various climate scenarios that were trained using various circulation models. We focused on taxa that occur in North America, generated sets of models for each species and compared current, past, and future geographic estimates under different circulation models. We found parameter values and feature selections varied for each species with respect to circulation models, although geographic estimates were generally consistent. Forecast and hindcast estimates could vary between circulation models that would invariably affect confidence in predictions and expectations. In some cases, forecasted estimates became highly dissimilar within different rates of climate change.

192: Atlatl saltation, a new ricochetel locomotion model; a quicker, safer way to escape from predators

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Eluding capture is the surest means to avoid becoming prey. Small mammals use saltatorial adaptations to maximize escape from predators in semienclosed to open environments where sudden positional changes are more effective than fleeing in a single direction. Saltation is a series of independent jumps; each longer than body size predicts. Saltators can also alter their midleap trajectories using their tails as rudders. Ecological niches dictate common saltator morphologies, even when these ricochetel species differ in biogeographic range and phylogenetic origin. Saltational adaptations include bipedal hopping, long tufted tails, large eyes and auditory bullae, elongated feet and hind limbs with proximal muscle bellies. This study examines saltatory adaptations among similar appearing forms by comparing saltation to the atlatl. This device increases human hunting efficiency by propelling projectiles farther and more accurately. Animals using this locomotion pattern are atlatl saltators. The body regions involved in these locomotor movements compare to atlatl components, but are analogous to an inverted atlatl. An atlatl saltator's foot corresponds to the atlatl projectile and launcher, the calcaneus to the atlatl spur and the lower leg to the atlatl handle. The knee corresponds to the human's wrist holding the atlatl. Knee straightening equals a forward wrist snap. In parallel, the animal uses large thigh muscles to move forward, while the human movement allows large trunk muscles to effect a corresponding atlatl movement.

193^F: Diversification of the kangaroo rat, *Dipodomys phillipsii oaxacae*

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The Phillips kangaroo rat (*Dipodomys phillipsii*) contains three subspecies, of which *D. p. oaxacae* is the one with the southern most distribution. A rodent endemic to Mexico, *Dipodomys phillipsii* is threatened in accordance with NOM-059, due to the change in land use and the destruction of its habitat. The limited knowledge of the genetic aspects of this rodent has hindered the establishment of effective strategies for its conservation. The objective of this work was to determine the diversification of *D. phillipsii* populations and estimate their genetic divergence based on mitochondrial DNA (cyt *b*). We performed maximum likelihood and Bayesian inference analysis. We recovered two different clades, one consisting of *D. p. perotensis*-*D. p. phillipsii* and the second by *D. p. oaxacae*, both have geographical consistency. *D. phillipsii* is a monophyletic group, with sympatric speciation. According to our estimates, the time of divergence between both clades (one that lives in the province of the Trans-Mexican Volcanic Belt and the other in the province of the Depression of Balsas), is 2.02 million years, while the divergence was 2.8%. Our estimates indicate that the diversification of *Dipodomys phillipsii* occurred during the Pleistocene, suggesting that climatic changes and the development of deserts may have influenced the genetic divergence of their populations.

194: Quantifying habitat structure relative to predation risk: characterizing the functional properties of concealment and detection

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Habitat structure that conceals prey animals also might reduce their ability to detect predators. Evaluating if or how animals select habitat to balance tradeoffs between concealment and detection is challenging because both properties 1) occur across a continuum of spatial scales, 2) must encompass a diversity of predator hunting modes, and 3) likely vary temporally, especially when vegetation is a primary component of habitat structure. We used an image laser scanner to characterize habitat structure and derive these two functional properties. We compared this approach to more traditional photographic methods, and we expected that the two would produce similar results when compared at a single spatial scale from the perspective predators in proximity to the prey animal. However, because LiDAR data permit evaluation of both concealment and detection across a range of spatial scales, we expected that integration across scales would alter tradeoffs between the two properties in habitats with more complex vegetation structure. Disentangling these functional properties of habitat can advance understanding of factors that influence perceptions of predation risk, and provide insight into how habitat structure affects predation and anti-predator behavior.

195^E: Static allometry in the dentary of *Glaucomys volans*

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We used geometric morphometric techniques to explore shape variation in a sample of 75 jaws of adult southern flying squirrels. We placed 10 homologous landmarks and edgels on each dentary in an effort to reflect functional aspects of the jaw. Procrustes coordinates were then analyzed using a principal components analysis. This analysis revealed significant shape variation associated with the position of the coronoid process and the area of the masseteric fossa. A regression of principal component scores against size showed that larger animals were characterized by posterior deflection of the coronoid process and had a relatively smaller masseteric fossa, a shorter horizontal ramus, and a posterior and ventral deflection of the angular process. Larger animals had a thicker ramus at the level of the molar tooth row, anterior deflection of the anterior tip of the masseteric fossa, and a clockwise rotation of the mandibular condyle. We estimated the mechanical advantage of both the masseter and the temporalis, and found no significant correlation between centroid size of the dentary and mechanical advantage of the masseter muscles. However, mechanical advantage of the temporalis was significantly negatively correlated with centroid size. Thus, mechanical advantage of the masseter was independent of size, while that of the temporalis decreased with increasing size.

196: Founder takes more: interspecific competition influences range and niche expansion of North American mammals into deglaciated areas

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An environmental change often triggers large shifts in species distributions that can be accompanied by expansions of their ecological niches. Species ability to expand their niches can be influenced by a diverse array of biotic factors, such as interspecific competition. The impact of interspecific competition on species niche shifts, however, is poorly understood, as it is difficult to separate from other biotic and abiotic factors. The previously glaciated areas of North America provide an excellent system to study range and niche shifts. Areas covered by large, continuous ice sheets during the last glacial period were virtually uninhabitable. As the climate warmed and the ice sheets contracted, species began colonizing the newly available niches. Previous studies have documented reduction of genetic diversity in the direction of expansion on an intraspecific level as the first colonizers filled available niches and prevented expansion of later migrants. I hypothesized that this "Founder takes all" rule may also apply to competing species: as one species expands into a new niche, it hinders later expansion of competing species. To

test my hypothesis, I compared range and niche overlap of more than 70 mammalian species pairs that represent potential competitors. In agreement with my hypothesis, I documented smaller range and niche overlap of congeneric species pairs within deglaciated areas in comparison with areas that were never glaciated during the last glacial period.

197: Isolation by marine barriers and climate explain areas of endemism in an island rodent

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The Indonesian island of Sulawesi is home to thousands of endemic terrestrial animal species. Phylogeographic studies of some of these taxa revealed concordant distribution patterns (areas of endemism; AoEs), suggestive of a shared evolutionary or ecological mechanism driving divergence among various terrestrial taxa. Generally, AoEs have been attributed to Pleistocene marine incursions, geological fault zones, and Sulawesi's history as an archipelago. We test the hypothesis that population divergences are associated with unsuitable climate spaces at the boundaries between these areas in an endemic murid rodent: *Maxomys musschenbroekii*. We sequenced mitochondrial and nuclear genes and hundreds of ultraconserved elements from individuals sampled across the island, which we used to build phylogenies and identify population structure. To test climate-related hypotheses, we used multiple regression to assess the extent to which genetic distances, over-land geographic distances, environmental distances (derived from ecological niche model resistance surfaces), and areas of endemism are correlated. In all three genetic datasets, we inferred phylogeographic structure that is geographically concordant with previously defined AoEs. Genetic distances were more strongly correlated with environmental distances than geographic distances. Population divergences within *M. musschenbroekii* are consistent with AoE definitions from other taxa. Stable areas of unsuitable habitat near AoE boundaries probably supplemented marine incursions in generating population structure within *M. musschenbroekii* and other co-distributed species.

198: Body size downgrading across the late Quaternary

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Since the late Pleistocene, large-bodied mammals have been extirpated from much of the Earth. While all habitable continents once harbored giant mammals, the few remaining species are largely confined to Africa. This decline is coincident with the global expansion of hominins over the late Quaternary. Here, we quantify mammalian extinction selectivity, continental body size distributions and taxonomic diversity over five time periods spanning the last 125,000 years and stretching ~200 years into the future. We also compile and analyze the global pattern of mammalian extinction over the Cenozoic as a baseline. Our results clearly demonstrate that size-selective extinction was already underway in by the late Pleistocene, that it occurred on all continents, within all trophic modes, and across all late Quaternary time intervals, with the degree of selectivity decreasing towards the modern. Moreover, the degree of selectivity was unprecedented in 65 million years of mammalian evolution and was not driven by climate change. The distinctive selectivity signature implicates hominin activity as a primary driver of taxonomic losses and ecosystem homogenization. Because megafauna have a disproportionate influence on ecosystem structure and function, past and present body size downgrading is reshaping Earth's biosphere.

199^E: Modeling the range-wide distribution of pygmy rabbits: implications for the sage-grouse umbrella

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Loss and degradation of sagebrush landscapes across the Western US has prompted large-scale land management aimed at conserving and restoring habitat for Sage-grouse (*Centrocercus* spp.), including designation of numerous types of habitat management areas (HMAs). The pygmy rabbit (*Brachylagus idahoensis*) also is a species of conservation concern due to its obligate relationship with sagebrush, and our goal was to evaluate the degree to which grouse-focused HMAs also conserve pygmy rabbits. We created an inductive species distribution model (SDM) for pygmy rabbits across their full geographic range. We acquired 18,586 records of pygmy rabbit occurrence from all range states, and after screening for reliability and independence, we retained 10,421 records for further analysis. We used the program Maxent to build models of varying complexity incorporating a diversity of environmental factors representing topographic, vegetation, fire, climate, and soil characteristics. We evaluated variation in subsampling distances, background extents, and regularization multipliers to build a model with the best performance. Environmental predictor variables were iteratively eliminated from model consideration, resulting in a parsimonious model that reduced the spatial and sampling biases. This SDM provides a foundation for evaluating overlap between pygmy rabbits and Sage-grouse HMAs. Additionally, the model of predicted habitat for pygmy rabbits can be used by land managers to prioritize locations for pygmy rabbit surveys and to identify areas for land management, conservation, or restoration efforts.

200: A guide to campus squirrels

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Squirrels, adored or resented, are a noteworthy part of the campus landscape for colleges and universities across North America. Faculty experts from 518 institutions of higher learning in the continental United States and Canada contributed data of species presence for the Family Sciuridae. Campuses do have squirrels! The modal count was 2 species per campus. Five or more species occurred at 23, or 4.4% of campuses (11 or 2.1%, when excluding *Glaucomys* sp.) The highest species count was 10, from Sierra Nevada College. Only 26, or 5% of campuses reported no sciurids. Representatives from all of the 14 North American genera were found on at least one campus. Most species were under-represented on campuses compared to their range and potential for occurrence. In most cases it appears that squirrels are an incidental emergent property of a campus's habitats, hazards, and opportunities. The Eastern gray squirrel, *Sciurus carolinensis*, is by far the most frequent campus resident (over 60% of campuses). The next four most common species are *S. niger*, *Tamias striatus*, *Tamiasciurus hudsonicus*, and *Marmota monax*. We consider which landscape and community characteristics of campuses typically accommodate some species while deterring or excluding others. Competitive exclusion between species is probable in many cases. Species profiles between campuses are analyzed in regard to geographic location, institution size, elevation, surrounding land use/ecosystem, and historical land use/ecosystem.

201: Mammal diversity is correlated with productivity, but decoupled from food resources, abundance, or habitat complexity

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The most commonly invoked mechanism for a climate-diversity relationship is the more-individuals-hypothesis (MIH), which predicts a cascading positive influence of climate on plant productivity, food resources, total number of individuals, and species richness. We test for a climate-diversity relationship and an underlying MIH mechanism, as well as testing competing hypotheses including positive effects of habitat diversity and heterogeneity, and the species-area effect along elevational gradients in the Colorado Rocky Mountains. We conducted standardized small mammal surveys at 32 sites to assess

diversity and population sizes. We estimated vegetative and arthropod food resources as well as various aspects of habitat structure by sampling 20 vegetation plots and 40 pitfall traps per site. Regressions and structural equation modeling were used to test competing diversity hypotheses and mechanistic links predicted by the MIH. We detected 3,922 individuals of 38 small mammal species. Mammal species richness peaked at intermediate elevations, as did productivity, whereas temperature decreased and precipitation increased with elevation. We detected strong support for a productivity-diversity relationship, but no support for the MIH mechanism. Food and mammal population sizes were unrelated to NPP or mammal diversity. Furthermore, mammal diversity was unrelated to habitat diversity, habitat heterogeneity, or an elevational area. A mechanism other than the MIH underlies the small mammal productivity-diversity relationship, which is functioning contemporarily or based on evolutionary climatic affiliations.

202^{HTA}: Ecological causes of intraspecific variation in the aposematic patterning of the striped skunk *Mephitis mephitis*

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Aposematic signals—bold warning colors and patterns paired with unpleasant defenses in prey species—are predicted to take on similar forms both across and within species facing the same predators, enhancing predator memory. Our study explored roles of various selective forces in shaping aposematic variation within the striped skunk, whose stripes can vary substantially both within and between populations. Specifically, we investigated whether coloration patterns are (1) no longer under intense selection due to fewer contemporary predators, (2) are shaped by different predatory threats, (3) are a compromise between conspicuousness up close and crypsis at a distance, (4) are impacted by predator desperation at times of prey scarcity, or (5) vary with humidity or (6) urbanization. Morphometric data were gathered for stripes from 700 *M. mephitis* study skins from across North America, and specimen stripe whiteness indices together with individual capture locales were compared to predation risk, landcover, temperature, and humidity maps utilizing ArcGIS. Specimens from regions of low predator risk showed high stripe variation, while specimens from high predator risk areas showed reduced variation, (H1). Additionally, stripe variation was greater in regions of predominantly raptor risk and reduced in regions of mostly mammalian predator risk, suggesting that variation reflects differences in predator type (H2).

203: How small an island? Speciation by endemic mammals (*Apomys*, Muridae) on an oceanic Philippine island

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Species richness is determined by three primary biological processes: colonization, extinction, and speciation. We investigated the influence of oceanic island area on speciation by small mammals, in the context of other land vertebrates. Extensive field surveys on Mindoro Island (9,735 km²) in the Philippines, followed by sequencing one mitochondrial and three nuclear genes for use in phylogenetic, population genetic, and coalescent-based analyses, and by morphometric analysis of craniodental data, documented an endemic clade of probably four species of *Apomys* (Muridae). The common ancestor likely arrived from Luzon Island across a narrow sea channel between 2.4 and 1.5 Ma. The four species occur allopatrically, with variation in their elevational ranges. This makes Mindoro the smallest oceanic island on which speciation by small mammals has been documented. A review of land-living vertebrates suggests that bats and large mammals require the greatest area for speciation, whereas frogs, lizards, birds, and small mammals have lower and similar minimum-area requirements. However, data are limited and research is needed to document the impact of island area on speciation. The existence of a lower limit implies that the biological processes that influence species richness do not operate equivalently

along a gradient of island areas: speciation within islands may not contribute to changes in species richness below some limit, unlike colonization and extinction, which operate at all island sizes.

204^{E}: Patterns of gut microbial diversity in two recent diverged lineages of California voles**

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To explore relationships between gut microbial diversity and genetic divergence of host taxa, I characterized phylogeographic variation in the gut microbiomes of two recently diverged lineages of the California vole (*Microtus californicus*). Samples were collected from nine populations of *M. californicus* that encompassed a contact zone between the northern and southern lineages of this species. Using sequence data from the bacterial 16S rRNA (V4 region), patterns of gut microbial community composition were assessed relative to predictions based on shared host ancestry (phylosymbiosis), changes in gut microbial composition in hybrid hosts (hologenomic speciation), and increased microbial dissimilarity with distance (dispersal limitation). My analyses revealed that gut microbial community structure in *M. californicus* was best explained by the geographic distances among host populations, as predicted by the dispersal limitation hypothesis. The relative abundance of several genera of bacteria (e.g. *Papillibacter*), however, differed between voles from pure parental lineages versus voles with mismatched mitochondrial and nuclear genomes, as predicted by the hologenome speciation hypothesis. Thus, while the gut microbiome of California voles appears to have been structured primarily by geography, individual microbial taxa appear to have been influenced by host genotypes. Future studies will focus on this subset of microbes to determine how they influence and are influenced by genetic differentiation of host lineages over multiple temporal scales. This research was supported by a Grant-in-aid awarded to D. Lin in 2017.

205^E: Understanding the population structure and historical demography of the *Neotoma fuscipes* in California

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Understanding how different populations responded to past climate change may allow researchers to infer how they will respond to future warming. Here, we investigate the historical demography of one ecologically-important species: the dusky-footed woodrat, *Neotoma fuscipes*. We generated SNP data, using the double-digest RADSeq protocol, for 79 individuals from two closely related species (71 *N. fuscipes* and 8 *N. macrotis*), from across their geographic distributions in California. We inferred phylogenetic trees to see how individuals clustered genetically, determined population structure using several different methods, and explored the correlation between geographic and genetic distances. Additionally, we built ecological niche models (ENMs) to infer current and past (last glacial maximum) environmental suitability. Preliminary analyses indicate a three-population model—two northern and one southern population—but these do not map onto the current clades identified among the two species. We detected significant isolation by distance, but results are not representative of a single cline. Lastly, ENMs predicted suitable environment present throughout the known range of *N. fuscipes* for current conditions, and a reduction of northern habitat in the past. Using these results and current knowledge about *N. fuscipes*, we will generate and test several phylogeographic hypotheses. By understanding the historical processes that led to the contemporary geographic distribution of biodiversity, we can determine the relative importance of different factors that shape biodiversity, now and in the future.

206: The slow gradual action of the Great American Biotic Interchange (GABI) on nematode phylogenies

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The Great American Biotic Interchange (GABI) is a large-scale zoogeographic event that illustrates the exchange of mammals between North and South America and their subsequent diversification. This phenomenon was accelerated by the connection of both landmasses during the Pliocene. Evidence of the exchange includes the extant distribution of xenarthrans, didelphimorph marsupials, cricetine rodents, and carnivores, as well as the distribution of fossils in the stratigraphic record and the coalescence of genotypes. Reconstructions of the causes of diversification, extinction and dispersion of groups of mammals during the Pliocene (and Miocene) invoke changes in climate patterns and interactions such as competition and predation. We posit that parasitism should be considered as another interaction. During GABI, parasites would have been exposed to naïve mammals, faced the extinction of their original hosts or experienced both. Thus, parasites would form new associations with disparate groups of mammals, deviating from the expected cospeciation and codivergence. We present as evidence the evolutionary analysis of two groups of nematodes: *Litomosoides* (Filaroidea) and Aspiroderidae (Heterakoidea). Each of these lineages is associated with endemic South American mammals and a few species are able to infect organisms of a North American origin (Cricetidae). The analysis of the phylogeny of these nematodes allows us to identify at least four events of host switching and two continental range expansions.

207^E: Alternative mRNA splicing of a gamete recognition protein promotes potential functional adaptation in mammalian reproduction

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The birth of new genes with novel functions serves as a major contributor to adaptive evolutionary innovation. Novel genes commonly arise from mRNAs of ancestral genes, protein-coding genes metamorphosing into new RNA genes, and RNA genes composed from scratch. Alternative splicing during mRNA processing may lead to neogenesis, the process of gene birth, and promote potentially functional adaptations, especially if expressed in the gametes. We characterized the molecular evolution of zonadhesin (ZAN), a large sperm protein that mediates species-specific adhesion to the egg's zona pellucida. Intra-species differences show the gene is evolving under strong selective pressures and undergoing molecular splicing events. In marine invertebrates, rapid molecular evolution of egg recognition proteins promotes pre-zygotic reproductive isolation in certain species. Herein, we examine the same molecular process in mammals and evaluate alternative mRNA transcripts present in 21 species and 9 suborders of mammals. Further, ZAN protein sequence divergence, with domain duplications unique to some species of rodents, produced dramatic species differences in mature ZAN polypeptide sizes. Alternative transcripts are present in all mammal species examined, however domain duplications are restricted to the suborder Myomorpha in Rodentia, possibly indicating molecular mechanisms involved in duplication events were initiated following the divergence of Myomorpha from the other rodent suborders. Alternative splicing during ZAN mRNA processing and domain expansions in some taxa may contribute to potentially functional adaptations for reproductive isolation.

208^E: Coyotes exhibit an immune response to *Rickettsia* spp. in Arizona: an update

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Rocky Mountain spotted fever (RMSF) is a tick-borne rickettsial infection that causes severe morbidity and mortality in humans and mammals. In 2003, RMSF was recognized as endemic in Arizona, and outbreaks affecting humans have occurred since that time. In Arizona, the primary vector for RMSF is the brown dog tick (*Rhipicephalus sanguineus*), which exhibits host specificity for domesticated dogs but will use humans as incidental hosts when infestations are extreme. Large numbers of free-roaming dogs with >20% seroprevalence are the primary risk factor for human RMSF infections in Arizona's affected communities. However, we hypothesized that a wildlife component is responsible for the maintenance and transmission of spotted fever group (SFG) rickettsiae. Last year, we reported serological evidence that coyotes (*Canis latrans*) have been exposed to SFG rickettsiae in Arizona. Here we provide additional evidence from a second field season, an updated seroprevalence estimate based on a more conservative cutoff titer, and molecular evidence of *Rickettsia* spp. in coyote tissue.

209^{HTA}: Effects of maternal and grandmaternal flea infestation on offspring quality in a desert rodent

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Parental effects may beneficially alter offspring phenotype if parental environments sufficiently predict offspring environment. As parasitism is a common stressor, parental infestation could reliably predict infestation risk for offspring. However, little is known about parasitism and transgenerational phenotypic plasticity. Thus, we investigated how maternal and grandmaternal infestation with fleas (*Xenopsylla ramesis*) affected offspring quality and quantity in a desert rodent (*Meriones crassus*). We used a fully-crossed design with control and infested treatments to examine litter size, pup body mass at birth, and pup mass gain before weaning for combinations of maternal and grandmaternal treatment. No effect of treatment on litter size or pup body mass at birth was found. However, maternal and grandmaternal treatment significantly affected pre-weaning body mass gain, a proxy for sexual maturation, in male pups. Pups gained significantly more weight before weaning if maternal and grandmaternal infestation status matched, regardless of the treatment. Thus, pups whose mothers and grandmothers experienced similar risk of parasitism, either both non-parasitized or both infested, would reach sexual maturity more quickly than those pups whose mother's infestation status did not match that of their grandmothers. These results support the contention that parents can receive external cues, such as risk of parasitism, that prompt them to alter offspring provisioning. Therefore, parasites could be a mediator of environmentally-induced maternal effects and could affect host reproductive fitness across multiple generations.

210^E: Impacts of a plague-induced bottleneck on genetic diversity in black-footed ferrets (*Mustela nigripes*)

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Genetic diversity is a primary concern for small populations. For black-footed ferrets (*Mustela nigripes*), problems of low genetic diversity are compounded by, and have contributed to, increased mortality due to sylvatic plague (caused by the bacteria *Yersinia pestis*). Our study looks at the impacts of a plague-induced bottleneck on genetic diversity in a self-sustaining population of reintroduced black-footed ferrets in Conata Basin and Badlands National Park, South Dakota. We use microsatellite genotyping to compare genetic diversity post-plague to pre-plague data collected in the same population. In addition, we examine the spatial consequences of the bottleneck by detecting genetic clusters on the landscape. Our results indicate that although all alleles have been maintained in the population, heterozygosity has dropped from 0.43 in the pre-plague population to 0.26 in the post-plague population. Our results support

three genetic clusters, one consisting primarily of ferrets in Conata Basin, one of ferrets in Badlands National Park, and one of several smaller colonies in the area. These results provide insights into the effectiveness of plague and population management strategies and highlight the need for increased consideration of genetic diversity when employing techniques such as translocation. Understanding the impacts of plague on black-footed ferrets will provide insights into the impacts of disease epidemics on endangered species and will increase understanding of the connections between disease ecology, genetic diversity, and endangered species management.

211: Towards understanding the role of small mammals in the transmission of Lyme disease in Virginia

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Larvae and nymphs of many species of ticks select small mammals, reptiles, and birds as hosts. Since 2011, we have examined more than 1000 small mammals of 10 species and collected a small tissue sample as well as all visible ticks; rates of infestation range from 18 percent in harvest mice to 53 percent in meadow voles. Identification of immature ticks is challenging and requires molecular or genetic methods beyond classification as being from the genus *Ixodes* or another genus. *Ixodes* ticks include *I. scapularis*, the species that transmits the Lyme disease-causing bacterium *Borrelia burgdorferi* to humans. Of the approximately 2300 ticks collected from small mammals, 491 were identified as *Ixodes* spp. ticks, and the over 80% of these collected from short-tailed shrews (*Blarina*) suggests an important role in the Lyme disease cycle. Recent samples of *Blarina* tissues from eastern Virginia have a *Borrelia* infection rate over 50% percent and *Blarina* tissues from museum specimens collected from the 1970s to 1990s have a 56% percent infection rate. Tissues from museum specimens from elsewhere in Virginia indicate the widespread presence of *Borrelia* in *Blarina* for more than a century, with a positive sample from Virginia Beach collected in 1911. Further testing is being completed to identify the specific *Borrelia* spp. in *Blarina* over time.

212^E: Immunogenetic variation and potential pathogens of New England's imperiled and nonnative cottontails

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Evaluating immunogenetic variation of wild populations can provide valuable insights into functionally significant genetic diversity of imperiled species. Coupling genetic data with potential ecological drivers supports further understanding of the processes that maintain adaptive diversity in natural systems. This information is especially valuable for species facing conservation challenges of global relevance, including habitat loss and fragmentation, population decline, or species invasion. Here, we investigate immunogenetic diversity and parasites/pathogens of New England's native and nonnative cottontails. The New England cottontail (*Sylvilagus transitionalis*; NEC) is an imperiled native species that is part of an ongoing reintroduction effort, whereas the eastern cottontail (*S. floridanus*; EC) is an introduced congener that is thriving regionally. We utilized next-generation sequencing technologies to capture immunogenetic diversity and potential parasites/pathogens within and across New England's NEC and EC populations. Specifically, we target genes of the major histocompatibility complex (MHC), which are critical to the vertebrate immune response, and host-associated bacteria. Preliminary findings indicate that NEC MHC genes display limited diversity within and across populations, that MHC variation within the NEC captive breeding program is reflective of naturally-occurring diversity, and that cottontails are host to a suite of bacteria that are of potential disease concern. This knowledge is of direct value to ongoing NEC conservation efforts and advances our understanding of adaptive variation and its potential ecological drivers across wild populations.

213: Examining parasite distributions using niche models and patterns of host occurrence

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The geographic extents and ranges of species tend to be set by a collection of factors, including their evolutionary history. Ecological niche models (ENMs) use abiotic factors to estimate relationships among variables that best explain patterns of occurrence data. These ignore potential biotic interactions and evolutionary dynamics that may facilitate or impede occurrence at broad or fine scales. For parasites that specialize in a particular host, biotic interactions are key to diagnosing realized ranges, but for parasites that are or can be generalists, biotic associations would be more complex and could reduce the effect of host in range dynamics. To examine these relationships, we constructed a series of ENMs for suite of chipmunks (Genus *Tamias*) in western North America, and modeled occupancy patterns of four parasites (two lice and two pinworms). We predicted that host occurrences from areas with low suitability would be more likely to have a parasite. Further, we tested whether evolutionary lineages of parasites are geographically or environmentally constrained while considering host ranges. Our initial results indicate that parasite occupancy was not entirely dependent of host suitability at the site of collection. Estimated ENMs for individual lineages within parasites found mixed results of niche conservatism. Overall, biogeographic patterns of parasites are a complex association of host and environmental limits that may be difficult to assess at broad scales without detailed survey information.

214: Ecosystem services provided by bats, a XXI century update

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Although it is known that bats provide ecosystem services across the globe, very little has been done to implement, incorporate into policy and practice, and mainstream them. Here we discuss what we know about ecosystem services provided by bats in the light of recent technology such as transgenic crops, economic value, unaccounted-for transboundary ecosystem services, United Nations conventions protecting migratory species, and multisectoral mainstreaming of ecosystem services for the benefit of industry, ecosystems, and local populations. Many insectivorous bats consume millions of insects in the Mexico-U.S. border region, but the reciprocal service depends on the conservation of these populations on the other side of the border. Transgenic crops may temporarily reduce insect damage but insects are effectively nullifying their effect by evolving resistance. Bats are part of the solution as biological controls of insects, as they have done for many millions of years. Bats pollinate many ecologically and economically important plants. The genus *Agave* is one of the most useful plants to humans as sources of fiber, food, drink, and more, and is primarily pollinated by bats. After 25 years of trying, today the tequila and mezcal industry is joining forces with the conservation movement to protect the nectarivorous bats that pollinate agaves. It is time to quantify, document, and mainstream ecosystem services provided by bats

215: The skin we're in: Physiological consequences of white-nose syndrome for cutaneous respiration in bats

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White-nose syndrome (WNS) has caused devastating declines of hibernating bats throughout North America. The disease is caused by skin infection with the fungus *Pseudogymnoascus destructans* (Pd), and is associated with pathophysiological consequences during hibernation. While we have a basic understanding of WNS pathophysiology, the influence of Pd invasion of the wing on gas exchange has received little attention. Using sophisticated respirometry techniques we separated cutaneous from pulmonary respiration of euthermic and torpid bats and addressed three hypotheses: 1)WNS-tolerant/resistant (*Eptesicus fuscus*) and WNS-susceptible (*Myotis lucifugus*) bats differ in their reliance on cutaneous respiration; 2)Cutaneous respiration is disrupted in Pd-infected bats; and 3)Pd-infected bats exhibit increased energy expenditure and evaporative water loss because of increased reliance on pulmonary respiration. We found that cutaneous respiration made up 16% of total respiration in control *M. lucifugus*, and only 8% in *E. fuscus*. When euthermic, Pd-infected *M. lucifugus* exhibited an 85%

reduction in cutaneous respiration compared to control bats. However, there was no effect of Pd-infection on cutaneous respiration of *E. fuscus*, nor torpid *M. lucifugus*. Lastly, euthermic Pd-infected *M. lucifugus* exhibited higher levels of energy expenditure and evaporative water loss compared to controls. Our results highlight the extraordinary physiology of bat wings and suggest that any effort to treat WNS should carefully consider the implications of topical anti-Pd agents for wing physiology and cutaneous respiration.

216: A multi-pronged approach to the conservation of bats affected by the disease, white-nose syndrome

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In the past several decades, widespread population declines, species extinctions, and biodiversity loss due to the rapid emergence of infectious diseases has highlighted the critical need to identify protocols and working solutions for affected populations. However, this process has been complicated by the need to make critical decisions in novel systems where information regarding the ecology of newly emerging diseases is often not readily available. In 2006, the emergence of white-nose syndrome (WNS), caused by the fungal pathogen, *Pseudogymnoascus destructans* (*Pd*), in North America, and resultant rapid and severe nature of WNS-driven declines in bat populations, prompted a coordinated effort among researchers and managers to work towards conservation strategies for affected bat populations. We developed a model synthesizing current available strategies for managing WNS, and highlight several case studies where research can be used to inform conservation strategies. As *Pd* continues to spread and progress in North America, we identify critical questions and steps required to develop a management plan for protecting bat species affected by WNS.

217: 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. 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, recent acoustic-based studies in Saskatchewan, Canada and modelling based on fatality data from wind energy facilities in Ontario, Canada suggest that fatality risk is correlated with landscape features, such as distance to forest and proportion of water and cropland. This knowledge can be used in siting future developments.

218: Reducing wind turbine-related bat fatalities

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In the U.S., wind turbines are estimated to kill hundreds of thousands of bats annually. Because bats are long lived and have only 1–2 pups/year, the current rate of fatality may not be sustainable. For example, a recent study indicated the hoary bat (*Lasiurus cinereus*) population may decline by 90% in the next 50 years assuming no change in wind energy development. Yet, the industry is expected to grow from 90 Gigawatts (GW) in 2018 to nearly 225 GW by 2030. Thus, developing and implementing solutions to reduce the impact of wind turbines on bats is imperative; not only to address the current situation, but to account for the projected buildout of installed capacity. Two primary impact reduction strategies include 1) slowing the rotational speed of turbine blades during periods of high risk (aka curtailment or operational minimization), and 2) using ultrasonic acoustic deterrent technology to discourage the presence of bats

near the rotor-swept area. Currently, the former has been proven effective but expensive, and the latter unproven but cheaper. As a result, there is limited on-the-ground implementation. However, ongoing research is yielding promising results towards more cost-effective solutions. I review our current understanding of the effectiveness of these impact reduction strategies, discuss recent developments to optimize these strategies, and recommend next steps for future research.

219: Managing forests and other bat habitats in the age of white-nose syndrome

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In the 1990's, many wildlife managers and research biologists became concerned about the impacts of forest management practices, particularly harvesting, on bats. This sparked a large body of research on the effects of forest management practices on bat foraging and roosting habitat use worldwide. Much has been learned over the past decades including the range of variation in response to forest management based on forest type and ecomorphological differences among bats, as well as how we can use forest management practices to improve habitat for bats. Bats currently are facing many more dire threats than they were 25+ years ago, including disease and wind energy development. Conserving and recovering bat populations in the face of these threats, particularly white-nose syndrome, requires many tools including habitat management. I review and synthesize much of the literature on the effects of forest management on bats and suggest ways in which forest management practices such as thinning, prescribe fire, artificial roost structures, roost creation, and creation of early successional habitat can be used to improve habitat for bats as well as the caveats of using these techniques. I also discuss the importance and management of other habitat types that have received very little study including cliff faces, talus slopes, boulders, and rock shelters which may represent important winter refugia for some bat species affected by white-nose syndrome.

220^F: Foraging activity of *Peromyscus leucopus* in relation to exposure to different levels of light pollution

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Light pollution increasingly encroaches on natural areas. Increases in night-time light may affect nocturnal animals because it aids visual detection of prey by predatory species. Research suggests wild rodents in light polluted areas may behave differently than conspecifics from darker locations. We monitored nightly giving-up densities (GUD) at 16 foraging patches each at four locations in central Oklahoma that experience different levels of light pollution. We created a multiple linear regression model to predict mean GUD from eleven nights of data collected between the full moon and new moon in November 2017. We found mean GUD varies with illumination from the moon, light pollution, % low vegetative cover, % canopy cover, and humidity ($F(6, 35) = 33.35, R^2 = 0.85, p << 0.001$). Light pollution and changes in moon illumination had the strongest impact on model prediction ($r = 1.65, p << 0.001; r = 0.08, p < 0.001$). Mean GUD trended higher at sites experiencing the highest levels of light pollution while patch use at these sites was lower than at sites experiencing lower levels of light pollution.

221^E: The Eastern woodrat's response to size of novel objects

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Eastern woodrats (*Neotoma floridana*) build nests or dens from locally-available objects such as sticks and leaves. If novel objects are available, Eastern woodrats will frequently incorporate them into the nest. Little is known however, about the features of novel objects, such as size, shape, or luster, that result in choice by a woodrat. Other researchers have attempted to examine selection of novel objects by Eastern woodrats in terms of central-place foraging theory, suggesting that the size of the object selected would vary with the distance the woodrat had to carry it. We attempted to eliminate distance as a variable and examine selection only for size of a novel object. Thirty-six woodrat nests with an obvious above-ground component were used in the study, which was conducted in central Louisiana. Eight groups of three

tinfoil-wrapped balls (1 large, 1 medium, and 1 small) were placed in a circle at fixed compass directions and 1 m distance from the center of each nest. Each nest was sampled twice. A total of 301 balls were incorporated into woodrat nests or missing. Eastern woodrats selected the large balls more than would have been expected based on their availability and the smallest size balls less than would have been expected. Medium-size balls were used proportionately to their availability.

222^{E,HTA}: Chiseling away dogmas of saltbush specialization and investigating local diet shifts in *Dipodomys microps*

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Dipodomys microps, the chisel-toothed kangaroo rat, is a desert rodent generally considered a saltbush specialist. The natural diet of *D. microps* is thought to consist mostly of *Atriplex* species (saltbush), a C4 plant, and sparing amounts of C3 plants, throughout most of its range. We predicted that environmental factors over the past century have caused *D. microps* to favor the inclusion of more C3 plants as they increase in abundance. To test the hypothesis of saltbush specialization and determine whether there has been a shift in diet over time, we analyzed hair samples of museum specimens (n=66) for carbon stable isotopes. Over time the representation of saltbush in diets of *D. microps* has declined markedly. C4 in the diet of individuals collected 1912-1917 was on average 44.0% , compared to 31.7% from 1973-1978 and 24.3% in those collected 2008-2017. Of particular interest is the low percentage of saltbush reliance by all individuals, suggesting this species may not be a true obligate *Atriplex* specialist. Based on plant abundances from associated field notes, individuals from areas with low amounts of *Atriplex* averaged a diet of 4.5% saltbush while individuals from areas classified as medium-high *Atriplex* averaged 24.9%. We conclude that *D. microps* is not a dietary specialist on saltbush and that it incorporates this plant into its diet based on availability. This research was supported by an Undergraduate Honoraria awarded to Sydney Rae Stephens in 2018.

223^F: Use of enclosure space by long-tailed macaques at Mindy's Memory Primate Sanctuary

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This study investigates how eleven male long-tailed macaques (*Macaca fascicularis*) at Mindy's Memory Primate Sanctuary in Newcastle, Oklahoma use their enclosure space. The results of this study will allow future macaque habitats to be designed for optimal efficiency. The trend toward naturalistic environments has shown promise in terms of behavioral benefits for animals such as primates. Providing the most stimulating habitat that encourages natural behaviors is essential for the well-being of captive animals. We collected data on differential usage of ground, platform, firehose, stump, warm house, and enclosure wall space. In addition, we compared enclosure space use patterns between former pet macaques and former lab macaques. Data were collected via narrated video recordings of fifteen minute focal follows. We hypothesized that overall the monkeys would prefer the platforms and firehose to the ground, and when comparing the monkeys based on their backgrounds, we hypothesized there would be no difference in enclosure space use. A 2x7 mixed ANOVA demonstrated no significant difference between former pet and former lab monkeys. There was a significant difference in the use of structures although it was not in the direction we hypothesized. All of our results are being shared with the primate sanctuary in order to enhance how captive macaques utilize their habitat.

224: Effects of plant composition, vegetative structure, and demography on fine-scale movement patterns of small mammals

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Small mammals serve as important consumers and prey in most terrestrial food webs. Wholesale changes in the composition of plant communities in which small mammals live could influence many

behaviors, including exploratory and foraging movements. We examined the influence of extrinsic factors such as grassland type (non-native-species dominated vs. native-species dominated) and intrinsic factors such as species, age, sex, and reproductive status on movement paths of small mammals in south-central Iowa, using fluorescent powder-tracking. We measured path tortuosity to understand how small mammals perceive and respond to physical features of their habitat. We also compared the dominant growth structure (grass, forb, or both) and density of plants immediately adjacent to movement paths with random locations in the same habitat patch to determine whether they were selecting paths based upon the structure of available vegetation or simply wandering at random. Grassland type, species, age, sex, and reproductive status did not help predict path tortuosity. However, small mammals differentially selected movement paths covered by grass over those covered by forbs or mixed vegetation and they overselected areas of lower-density vegetation compared to higher-density areas. This strategy could ensure that small mammals are able to adapt to various grassland habitats, regardless of the plant species present, a wise approach given the historical inclination of humans to modify native vegetative communities for agricultural uses.

225^F: Effect of reproductive status on social burrow construction in *Peromyscus polionotus*

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A long-standing goal in biology is to understand the conditions under which animals perform costly actions for the benefit of others. Though inclusive fitness has been invoked to explain cooperation between kin, the persistence of cooperation between unrelated individuals remains unclear. Studies of burrowing behavior in the oldfield mouse (*Peromyscus polionotus*) suggest that unrelated individuals coordinate burrowing in pairs, but only invest full effort when burrowing with the opposite sex—presumably in anticipation of shared reproductive interests (e.g. familial burrow construction). Biparental care, coupled with social and genetic monogamy in *P. polionotus* further suggests that individuals align burrowing efforts with joint reproductive efforts. Here, we assessed the impact of reproductive investment on social burrowing behavior in *P. polionotus*. We ran burrowing assays in sand enclosures to compare the behavior of male-female pairs that had successfully reproduced (i.e., mated) with that of male-female pairs that had not produced offspring (i.e., unmated). Unmated males burrowed more frequently than mated males, suggesting males exhibit high burrowing initiative in the presence of a female to encourage future mating. Further, mated animals of both sexes engaged in longer burrowing bouts than unmated animals. This suggests that established mates coordinate burrowing investment. Together, these results indicate that mating status modulates burrowing behavior in *P. polionotus*, highlighting reproduction as an important context for coordinated effort between unrelated individuals in a social species.

226: Burn severity and extent influence space use and post-fire survival in an endangered small mammal

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Altered fire regimes and drought are important drivers of disturbance events in forests worldwide. Understanding how disturbance events such as fire influence space use, post-fire dispersal, survival, and settlement is key. The Pinaleno Mountains in southeastern Arizona, USA experienced three increasingly catastrophic fires in 1996 (2,600 ha), 2004 (12,029 ha), and 2017 (19,604 ha), threatening the continued persistence of the endangered Mt. Graham red squirrel (*Tamiasciurus fremonti grahamensis*). Previous modeling revealed that individual red squirrels rarely used locations where burn severity was moderate or high (only 2.8% of 10,805 locations). In summer 2017, the 19,600 ha Frye Fire disproportionately impacted remaining red squirrel habitat; 31% of high-elevation forest experienced moderate - high severity burn, and 95% of available red squirrel territories were affected. In the absence of updated data on vegetation and forest structure, we developed probability of landscape use and connectivity models based on data immediately available post-fire (topography and burn severity) to predict areas that may still support red squirrel persistence. We used mountain-wide post-fire census results for model validation. We investigate how recent fires have influenced red squirrel habitat connectivity, home range size, post-fire settlement patterns, and survival. Our results show how severe and frequent disturbance events present conservation challenges, particularly for small mammals with site fidelity. These efforts

support and inform continued conservation efforts for one of North America's most endangered mammals.

227: Establishing a mainland population of New England cottontail (*Sylvilagus transitionalis*) in Rhode Island

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The New England cottontail (*Sylvilagus transitionalis*; NEC) is a species of great conservation concern in the northeastern United States. They have declined with the subsequent loss of early successional habitat and habitat fragmentation. In Rhode Island, they have nearly disappeared, and extensive surveys of thousands of fecal samples have only documented their presence at four mainland locations. The drastic decline in the regional distribution of NEC precipitated the establishment of a captive breeding program in 2011. From 2012 to present, captive bred NEC have been released on Patience Island in the upper Narragansett Bay of RI to establish a wild breeding colony. In 2016, 40 NEC trapped on Patience Island and born in captivity were released at the Great Swamp Management Area (GSMA) in West Kingston, RI. The GSMA has been managed for early successional habitat four times in the past from 1995 to 2018 and has adjacent habitat in different successional stages. In 2018, 16 NEC were translocated from Patience Island to the GSMA. Nine of the 16 animals were fitted with Global Positioning System collars and seven animals had traditional Very High Frequency collars. The animals are being tracked to determine habitat use and compare the efficacy of two types of GPS collar technologies from Telemetry Solutions and Lotek Wireless. The re-establishment of NEC populations will be critical to their restoration efforts.

228: Apparent competition in a semiarid savanna: reducing predation pressure on a rare ungulate through pastoralism

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Predator restorations often result in apparent competition, where co-occurring prey experience asymmetric predation pressure driven by predator preferences. We examined whether, how and why apparent competition reorganizes prey communities following restoration of lions to a semiarid savanna, and how livestock production alters this indirect interaction between predators and their prey. Three lines of evidence supported the hypothesis that Jackson's hartebeest (an ungulate of conservation concern) were suppressed via apparent competition. First, hartebeest exhibited an Allee effect where they were exposed to lions, but displayed negative density-dependent population growth where they were protected from lions. Second, spatial overlap between plains zebra (the primary prey of lions) and hartebeest further exacerbated lion predation on hartebeest. Finally, hartebeest were killed preferentially by lions, whereas zebra were killed by lions in proportion to their abundance. Given the suppression of hartebeest populations by lions, we then tested whether glades (nutrient-rich hotspots created by abandoned corrals) could manipulate survival of hartebeest via their influence on the spatial distribution of zebra. Zebra aggregated at glades and survival of hartebeest increased when there was no glade within their home range, suggesting that corrals may be located on the landscape away from hartebeest territories to create refugia for this species of secondary prey. Our work demonstrates how integrating apparent competition theory with spatially-explicit data on predation can improve conservation efforts in multiple-use landscapes.

229^E: Swimming against the tide: a unique mammal may be more exceptional than we ever imagined

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Many rodent species are successful and widespread due to their ability to exploit a diversity of habitats. The salt marsh harvest mouse (SMHM, *Reithrodontomys raviventris*) employs a different strategy, thriving exclusively in coastal wetlands. It is the only mammal species entirely restricted to this habitat type, and is found only in the San Francisco Estuary. SMHM are adapted compared to sympatric species; they can swim and climb well and drink saline water. However, conservation of this endangered species is hampered by a poor understand of its ecology. Over the past 4.5 years we investigated SMHM ecology using live-trapping, radiotelemetry and a diet preference study. The results of our study revealed that SMHM are even more exceptional than researchers and managers believed. Unlike many rodent species, SMHM populations exploded during drought periods, and plummeted during wet years. Radiotelemetry efforts showed that this species utilized tidal wetlands (their historical and assumed preferred habitat type) in a similar way to anthropogenically managed wetlands, and utilized virtually all microhabitat types. Finally, defying conventional belief, SMHM did not most strongly prefer pickleweed (*Salicornia* spp.), but more commonly chose a variety of non-native plants. This study has revealed that the SMHM is an even more extraordinary rodent than was previously believed and that a variety of conservation/management strategies may be effective for this unexpectedly adaptable species.

230^E: Determining habitat suitability for the conservation of a native ecosystem engineer

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The southeastern pocket gopher (SEPG, *Geomys pinetis*) is an ecosystem engineer native to Georgia, Florida, and Alabama. While the species is important for the functionality of the ecosystem, SEPG population decline has been severe enough to list them as a species of greatest conservation need in all 3 states and state threatened in Georgia. Preserving the species habitat is critical for long-term restoration and management; however, there are questions about specific vegetation characteristics influencing species habitat suitability. Our objectives were to determine vegetation characteristics that are associated with SEPG occurrence at both the home-range scale (900m²) and local-landscape scale (1-km² sites). To address those objectives, we surveyed 182 1-km² sites across the range of the species to assess species presence and vegetation attributes. At the home-range scale, we have found significant differences in vegetation characteristics such as percent ground cover of grasses ($p=0.0024$) and forbs ($p<0.0001$) between occupied and unoccupied patches. Total basal area and percent ground cover of woody vegetation were not statistically significant. Additional analyses will concentrate on local-landscape scale vegetation characteristics between occupied and unoccupied sites. These results will form the basis for a management-decision tool to prioritize habitat manipulations and inform future decisions concerning habitat with the most potential for reintroductions.

231: Black-footed ferret reintroduction in Kansas

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Black-footed ferrets (*Mustela nigripes*) have been extirpated throughout much of their historic range, largely due to habitat alteration and prairie dog eradication efforts. Since 1991, thousands of ferrets have been reintroduced to federal, state, Native American tribal, and private lands. These reintroductions have been possible only through collaborative conservation and scientific efforts by government and non-government organizations. Discoveries and improvements have been made in captive breeding, pre-

release conditioning, disease management, land management, and post-release monitoring, among others. Disease remains a threat to re-introduction efforts. In 2007, black-footed ferrets were reintroduced to private lands in western Kansas. Since that time, ongoing population monitoring has been supported via collaborative efforts among private landowners, U.S. Fish and Wildlife Service, Association of Zoos and Aquaria accredited zoos in Kansas, non-profit organizations, employees of the state wildlife agency, universities, private companies, and other volunteers. The value of these partnerships are highlighted.

232:** Characteristics of habitat used by fishers (*Pekania pennanti*) during reproduction in the southern Sierra Nevada

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Many wildlife species rely on attributes of trees during daily activities and fundamental parts of their life cycle; some elements of great value to forest-dwelling wildlife take extensive time and multiple ecological processes to develop. The fisher (*Pekania pennanti*) is a carnivore of conservation concern in western North America that uses forest structures with specific features (e.g., cavities) as refuges. Prior to this study, little was known about denning habitat at the southernmost extent of the fisher's range. We documented female use of microsites and structures during reproduction and characterized den habitat selection at 3 spatial scales in the southern Sierra Nevada. Between 2007 and 2015, we confirmed 45 females at dens during ≥ 1 reproductive season and located 95 natal and 206 maternal dens. At the microsite scale, females used tree cavities almost exclusively. At the structure scale, females used live hardwoods (51%), live conifers (23%), and conifer snags (21%). Females chose California black oaks (*Quercus kelloggii*) most frequently (55%), followed by white fir (*Abies concolor*) and incense cedar (*Calocedrus decurrens*). Habitat selection analysis suggested that large California black oaks, large snags, dense canopy cover, high stand density indices, decay, greater slope and lower elevation predicted den habitat. Conservation of potential fisher denning habitat in this region could focus on retaining large structures, especially California black oak, with long-term plans to replace decadent trees. This research was supported by a Grants-in-aid awarded to Rebecca Green in 2011.

233^E: Leaving more than a legacy: museum collection reveals small mammal climate responses in Ethiopian Highlands

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A new objective has emerged in the wake of the vast body of evidence supporting climate change: to identify the degree to which natural communities stand to be affected by it. In response to rising global temperatures, ranges of many small mammal species have shifted poleward or higher in elevation. Efforts to quantify such spatiotemporal responses are often impeded by the prerequisite for historical datasets substantial enough to account for decadal climate oscillations, and as a result, few studies for small mammals have been realized. By comparing data collected from a recent 2015 survey led by W.T. Stanley to the "Chicago Daily News Abyssinian Expedition" led by W.H. Osgood between 1926 and 1927, we assessed the influence climate change had on small mammal communities in the Simien Mountains of Ethiopia over a period of approximately 90 years. While some results of this historic expedition were later published in 1936, abundance and elevational distribution data never were published. By virtue of Osgood's specimen collection, journal entries, and field notes deposited at the Field Museum of Natural History, we were able to extract the information needed to support our analyses. Preliminary results indicate that five of the nine (56%) species that were documented by both surveys displayed upward shifts from their former ranges. This study illustrates the growing potential of invaluable data concealed within historic museum collections.

234^F: Spatially explicit genetic analysis is essential for guiding management decisions of a threatened kangaroo rat

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Comprehensive studies that document the abundance, distribution and evolutionary potential of imperiled species are vital for conservation management. The Texas kangaroo rat (*Dipodomys elator*) is a threatened rodent found in five counties in north-central Texas. Since 2015, we conducted surveys across the historical range of *D. elator*. Here, we report typical population genetic measures obtained via a reduced representation next-generation sequencing approach. We analyzed sequence data from 36 individuals using STACKS. To account for computational stochasticity, we varied the minimum locus stack depth to provide both liberal and conservative population genetic estimates. Both datasets reveal some population genetic structure within *D. elator* and show little evidence that the population conforms exclusively to the isolation-by-distance model. This suggests other factors, such as geographic or anthropogenic barriers, isolation-by-resistance or isolation by some other source playing a role in the genetic substructure of the population. Moreover, there is a large sampling hole or area where no samples were available in the center of the *D. elator* distribution, making population genetic inferences challenging. We posit that though traditional population genetic estimates such as heterozygosity and *F*-statistics offer some immediate insight to the management of the species, we stand to gain more from a spatially explicit perspective. Thus, incorporating models that focus on aspects of the physical landscape is critical for evaluating the evolutionary potential of this threatened species.

235^{HTA}: Fine scale field-derived resistance surfaces depict landscape connectivity in a desert-dwelling rodent

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Landscape genetics (LG) permits to evaluate the effects that the landscape has on microevolutionary processes (e.g. gene flow). Remarkably, LG studies are underrepresented for deserts ecosystems, whereas rodents have been proposed as an ideal group for LG research. Parameterization of resistance surfaces (RS), a means to evaluate connectivity in LG, has been based on hypothesized arbitrary costs, frequently assuming a linear relationship between landscape variables and genetic distances. Here we evaluate the relationship between landscape elements and individual-based genetic distances for the kangaroo rat *Dipodomys merriami*, a desert-dwelling rodent in northern Mexico, by using an optimization framework for RS that makes no *a priori* assumptions regarding scale and direction of the resistance relationship. We used field-collected and remote-sensed data to develop environmental surfaces of our study area, and assessed genetic diversity, population structure, relatedness and genetic dissimilarity between individuals. We determined landscape factors affecting gene flow by fitting mixed-effects models using Akaike's information criteria to evaluate model fit and optimize parameters values for individual and composite RS. Our findings suggest that vegetation cover best explains the genetic connectivity, and illustrate optimal humidity and temperature values that influence gene flow across the arid environment for *D. merriami*. Notably, to our knowledge this is the first LG study for a rodent species in a Mexican desert ecosystem.

236: Genetic diversity and hierarchical population structure within a recently fragmented metapopulation of imperiled cottontails

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An understanding of genetic diversity and population structure is important to conservation of declining species within fragmented habitat. These issues become critical for small, isolated populations, where stochasticity is a driver of genetic change and population extinction. In eastern New York and New England the endemic New England cottontail has declined as a result of habitat loss and fragmentation. As a species that exhibits metapopulation dynamics, habitat fragmentation can have profound implications for persistence where populations are small or isolated. We assessed genetic diversity, population structure and effective population size of New England cottontails in New York, a purported stronghold for the species, using 9 microsatellite loci amplified from live-caught and non-invasively collected genetic samples. We identified hierarchically structured genetic clusters that displayed little evidence of ongoing connectivity. We observed low genetic diversity based on allelic richness and the presence of private alleles within two populations, and all populations had critically low effective population sizes (< 50). Observed trends were consistent with reported trends for the declining, state-endangered Maine-New Hampshire metapopulation, and not indicative of a genetic stronghold within New York as previously suggested. Instead, the small and isolated populations observed here are suggestive of an ongoing breakdown in metapopulation functionality and an immediate need for human intervention to create habitat and improve connectivity among New England cottontail populations.

237: Rooting out population genetic structure of a destructive, invasive species in Texas

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Feral swine (*Sus scrofa*) are a widely distributed invasive species that are ecologically destructive and cost the United States' economy >\$1.5 billion annually. Further, management efforts are complicated by anthropogenic factors such as translocation and harvest. Population genetic analyses have recently been conducted in California and Florida, states with large feral swine populations, to elucidate patterns of dispersal and expansion. However, in Texas, where abundance is greatest, genetic structure has not been described at a state-wide scale. To fill this knowledge gap, we conducted a population genetic analysis in Texas, genotyping 579 feral swine sampled throughout the state with a high density SNP array. We estimated the number of genetic clusters (K) using snapclust, a hybrid method that integrates geometric methods and genetic model-based approaches, and visualized the geographic distribution of supported clusters. Our analysis produced biologically interpretable results across a range of clusters from 2 to 13. K2 revealed a broad split between long-established populations in the southeast part of the state from newly-emerging populations in the northwest. As K increased to 13, localized divisions in genetic structure were progressively revealed. Comparisons of our results with those from California and Florida suggest different landscape attributes or rates of translocation are shaping the spatial scale of population genetic structure in Texas.

238: A population genomics approach to estimating migration with small sample sizes and genetically similar populations

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Quantifying the movement of individuals among subpopulations can be difficult when subpopulations are closely related or sample sizes are small. We developed a population genomics approach that can resolve migration rates under such challenging conditions. Specifically, we conducted a supervised analysis with ADMIXTURE using a leave-one-out (LOO) approach in which we iteratively queried the

genetic origin of a single individual while all other individuals served as reference samples for the subpopulation in which they were sampled. Using observed allele frequencies within each subpopulation, we then simulated parental populations, descendants of migrants, and grand descendants of migrants. In a permutation framework, we repeated the LOO analysis with the simulated dataset. By comparing the assignment of observed individuals among respective populations to parallel distributions generated from the simulated dataset, we were able to classify observed individuals as residents, migrants, descendants of migrants, and grand descendants of migrants. We applied this method to evaluate migration rates of feral swine (*Sus scrofa*) among subpopulations in Missouri. We documented high rates of translocation among subpopulations and introductions from exogenous sources. Using Bayesian models to evaluate the influence of environmental and sociological covariates on translocation rates, we found translocation rates were positively associated with the number of cervid farms, frequency of wildlife hunting citations, and the availability of public land.

239: Chromosome-level assembly and annotation of the black-footed ferret (*Mustela nigripes*) genome

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The black-footed ferret (hereafter BFF) narrowly avoided extinction in the 1980s to become an oft-cited example of the benefits of intensive management, research, and collaboration to save a species and reintroduce it to nature. However, the BFF remains at risk of extinction due to a high susceptibility to disease and multiple fertility challenges. Several of these features are indicative of inbreeding depression, likely related to the small number of founders, gradual gene diversity loss, and possible fixation of deleterious alleles. To better understand the possible links between specific genes and infertility in the BFF, we generated a *de novo* assembly of a male BFF using 10X Genomics linked-read sequencing technology. This resulted in a highly contiguous *de novo* assembly (contig N50 size = 152 Kb; scaffold N50 size = 13.8 Mb) with ~70% of the assembly consisting of phased reads. This assembly was then further scaffolded through hybridization with an optical map (BioNano Genomics), resulting in a four-fold increase in scaffold N50 size (58.1 Mb) and a completeness index of 96% based on evaluation of 4,104 single-copy orthologues. Finally, we scaffolded this hybrid assembly into chromosomes using 3D genome sequencing (Hi-C). This resource provides an unprecedented opportunity to characterize the genomic features that limit reproductive function in this endangered species and thereby understand the link between reduced heterozygosity and reduced male fertility in mammals.

240: Hidden diversity of African house bats (*Scotophilus*, *Vespertilionidae*): insights from multilocus phylogenetics and lineage delimitation

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The genus *Scotophilus* contains 20 currently recognized species ranging throughout Africa and Southeast Asia. Among the 10 species recognized from continental Africa, systematic relationships remain poorly understood. Taxonomic uncertainty regarding names, suggestions of polytypic species complexes, and undescribed cryptic diversity all contribute to the current confusion. To gain insights into the systematics of this group, we inferred single locus and multi-locus phylogenies and conducted lineage delimitation analyses using seven unlinked genes for specimens from across Africa. Recent collections from Kenya allowed us to carry out population-level analyses for the diverse assemblage of East African *Scotophilus*. Multi-locus coalescent delimitation methods indicated strong support for three recently named lineages thought to be restricted to Kenya and Tanzania; it also uncovered two new distinctive lineages at present known only from Kenya. Subsequent taxonomic assessments that integrate these genetic data with phenotypic, distributional, and/or ecological traits are needed to establish these lineages as valid species. Nevertheless, as many as 15 *Scotophilus* species may occur in continental Africa, 10 of these in Kenya

alone. Our analysis highlights the importance of population-level surveys for the detection of cryptic diversity in understudied regions such as the Afrotropics.

241^F: From trash to treasure: techniques for reconstructing mitochondrial genomes from highly fragmented historical DNA

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As the importance and prevalence of genomics grow, so do the number of tools for obtaining, refining, assembling, and interpreting genetic data. With the wide variety of programs available, there is a need for the development of well-tested pipelines that join these tools together to carry raw data to a finished product. In particular, the *de novo* assembly and analysis of repeat-dense mitochondrial genomes for non-model organisms without references continues to be problematic for researchers working with rare species that have few sampled specimens. To address this issue, we aim to test and compare two different iterative-mapping software packages (MITObim and GRAbB) using mitochondrial and ultra-conserved element (UCE) sequence data derived from historical samples of tissue and skin obtained from rodents in the subfamily Sigmodontinae (Rodentia, Cricetidae). By benchmarking the effectiveness of these tools using metrics, such as wall time, average coverage, and read length, we can develop a best-practice guide for future assemblies.

242: Cracked teeth and broken bones: insights into Pleistocene carnivore paleoecology

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Prone to serious injuries while capturing large prey as well as in battles over resources, large mammalian carnivores lead exceptionally risky lives. Two recent studies of broken teeth and skeletal trauma in Pleistocene carnivores highlight the hazards and inform our views of pre-human ecosystems. In the Pleistocene, large carnivore species richness was greater than now and likely intensified interspecific competition and top-down effects. In support of this hypothesis, large Pleistocene carnivores display elevated tooth fracture frequencies that are argued to reflect greater carcass utilization (bone-eating) in response to competition. To better understand the relationship between prey availability and predator tooth wear, tooth fracture frequencies were quantified across a range of extant gray wolf populations that varied in predator:prey ratio, including a longitudinal study of Yellowstone National Park gray wolves as the number of elk declined between 1998-2017. Results confirm that dental wear and fracture increase with higher predator:prey ratios and greater carcass utilization, thus corroborating the hypothesis of tough times for carnivores in the Pleistocene. A second study of skeletal trauma in sabertooth cats and dire wolves at Rancho La Brea reveals species-specific patterns of skeletal injuries that reflect their distinct hunting modes, pursuit vs. ambush. Sabertooths have twice as many injuries as dire wolves, and trauma is focused in the shoulder and spine, as opposed to the neck and limbs in dire wolves.

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**CENTENIAL CELEBRATION AND 99TH ANNUAL
MEETING OF THE AMERICAN SOCIETY OF
MAMMALOGISTS**



Please join us 28 June to 2 July 2019 in Washington, D.C. for the Centennial Celebration and 99th Annual Meeting of the American Society of Mammalogists. The conference will be held at the Hyatt Regency Washington on Capitol Hill. Learn about the latest advances in the study of mammals and interact with researchers and educators specializing in these fascinating animals. Come celebrate 100 years of modern mammalogy and enjoy everything that the DC area has to offer!

The scientific program will include contributed oral and poster presentations as well as symposia, plenary speakers, and workshops. A full social agenda is planned including fieldtrips to local attractions, the opening social at the Hyatt Regency, the annual Run-for-Research around the National Mall, the picnic at the National Zoo, and closing social and awards ceremony at the National Museum of Natural History. Hotel room 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 2019 meeting, contact the program director, Cody Thompson (mammal.meetings@gmail.com); local co-hosts, Jesus Maldonado (maldonadoj@si.edu), Don Wilson (wilsond@si.edu), and Neal Woodman (woodmann@si.edu); or meeting planner, John Murray (jsmurray@k-state.edu).

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