Spring 2019

DIRECT AND INDIRECT EFFECTS OF ANTHROPOGENIC LAND USE ON BOBCATS (Lynx rufus) IN NEW ENGLAND

Rory Patrick Carroll
University of New Hampshire, Durham

DIRECT AND INDIRECT EFFECTS OF ANTHROPOGENIC LAND USE ON BOBCATS (*Lynx rufus*) IN NEW ENGLAND

BY

RORY P. CARROLL
B.S., State University of New York at Plattsburgh, 2013

DISSERTATION

Submitted to the University of New Hampshire
in Partial Fulfillment of
the Requirements for the Degree of

Doctor of Philosophy
in
Earth and Environmental Sciences

May 2019

This dissertation has been examined and approved in partial fulfillment of the requirements for the degree of Doctor of Philosophy in Earth and Environmental Sciences by:

Dissertation Director, Dr. Marian K. Litvaitis
Professor of Conservation Biology
University of New Hampshire

Dr. Thomas Foxall
Professor of Biological Sciences
University of New Hampshire

Dr. Erik A. Hobbie
Research Professor, Institute for the Study of Earth, Oceans, and Space
University of New Hampshire

Dr. Jan E. Janecka
Assistant Professor of Biological Sciences
Duquesne University

Dr. John A. Litvaitis
Professor Emeritus of Wildlife Ecology
University of New Hampshire

Dr. Rebecca J. Rowe
Associate Professor of Natural Resources and the Environment
University of New Hampshire

On 10 April 2019

Original approval signatures are on file with the University of New Hampshire Graduate School.

To Mom and Dad:

Thank you for teaching me the best lesson: that anything is possible with some initiative and grit;

And for always believing I'd get where I'm going, even when I didn't.

ACKNOWLEDGEMENTS

First and foremost, I want to thank the best advisor and mentor I could ever ask for, Dr. Marian Litvaitis. Thanks for seeing the scientist inside an old kid who spent much of life pretending he was an actor. You've taught me so much about how to survive and thrive inside and outside the academy. I'm excited to pay that forward to your academic grandchildren. I also thank my committee members for their time, guidance, and thoughtful input in all aspects of this project: Dr. Rebecca Rowe, Dr. John Litvaitis, Dr. Thomas Foxall, Dr. Erik Hobbie, and Dr. Jan Janecka. The formal and casual conversations we've had over the past several years have meant more to me than I can express.

Thank you to the lab technicians who brought their own unique experiences and skills to this project: Brittaney Buchanan, Amanda Cugno, Sarah Clements, and Casey Coupe. This work is better because of you. Thank you to the small army of collaborators and contributors who provided samples or consultation throughout the course of this study: Pat Tate, Dan Bergeron, and Ted Walski at NH Fish and Game; Chris Bernier, Amy Alfieri, and Nick Fortin at VT Fish and Wildlife; Laura Hajduk-Conlee and Susan Ingalls at the MA Division of Fisheries and Wildlife; Eric Jaccard and Florent Lemieux at the Quebec Ministry of Forests, Wildlife, and Parks; Kristy Pilgrim at the USFS Wildlife Genetics Lab; Julie Young at the USDA National Wildlife Research Center; Lauren Moulis at Squam Lakes Natural Science Center; Stephanie Durette at the Buttonwood Zoo; Katherine Doyle, Todd Fuller, and Jeff Podos at UMASS; Clark

Stevens; Melissa Bauer and the Kovach lab; Ryan Stephens and the Rowe lab; Andy Ouimette; Alexej Siren; Jeff Traynor; Dohnavin Wurst; Rocky D'Ambrosia; Dallas Huggins; Randy Shoe; and Tom Crews.

This work was generously funded through a National Science Foundation Graduate Research Fellowship (147766), grants from the USDA National Institute of Food and Agriculture McIntire-Stennis Project (233076 and 1009906), the NH Agricultural Experiment Station, and a dissertation fellowship from the UNH Graduate School. Additional funding came from awards given by UNH's Department of Natural Resources and the Environment, the Natural Resources and Earth System Science program, the New England Outdoor Writers Association, and the NH Federation of Garden Clubs.

Thank you to my NREN and NRESS colleagues, who gave me ample opportunities to teach and to learn. Thanks to Danielle Garneau whose passion and prowess for wildlife and teaching lit a fierce green fire in me. To the seven Cs: I would not be where I am today without your boundless love and support. Last but not least, to my raisons d'être, Abigail and Oscar: Thank you for providing the ultimate source of inspiration, friendship, love, and joy.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

ABSTRACT

DIRECT AND INDIRECT EFFECTS OF ANTHROPOGENIC LAND USE ON BOBCATS (*Lynx rufus*) IN NEW ENGLAND

by

Rory P. Carroll

University of New Hampshire, May 2019

Bobcats *(Lynx rufus*) are the most widely distributed wild felids in North America, ranging across the contiguous United States, southern Canada, and northern Mexico. In the New England region (NER) bobcat populations endured nearly two centuries of intense harvest pressure and land use change that nearly led to their extirpation in parts of the region. However, they are currently experiencing a population resurgence despite large-scale increases of anthropogenic impacts on the landscape in the last 60 years. In this dissertation, I sought to understand the resurgence of bobcats in the NER by studying several aspects of bobcat ecology in relation to human land use.

Bobcats present a unique system in which to study anthropogenic impacts on wildlife. The NER is near the northern edge of their range. Combined with their history of fluctuating abundance, this provides a dynamic demographic landscape. They are reclusive, typically avoiding human contact, but are also highly adaptable to varied habitats including human-dominated areas. Their habitat preferences can widely vary based on local conditions and biological factors. They are a wide-ranging and charismatic species with great public appeal,

which makes them an ideal umbrella or flagship species for regional conservation efforts and provides ample opportunity for engagement with public stakeholders.

Chapter 1 of this dissertation explores genetic patterns across the NER over the past 60 years. I compare genetic structure, diversity, effective population size, and gene flow between a historic (1952-1964) and a contemporary (2009-2017) time period. My results suggest that bobcat populations in the region are robust, but development and edge-of-range dynamics play a significant role in population structure. Chapter 2 compares the diet of bobcats in the NER between the same time periods. I found that historically, bobcats were highly dependent on lagomorphs but their diet diversified in the contemporary time period. In Chapter 3, I explore the effect of land use on bobcat stress levels using hair cortisol as an indicator of stress. Anthropogenic land use was a better predictor of cortisol levels in bobcats than their preferred undeveloped land cover types. Finally in Chapter 4, I integrate data from the first three chapters to explore how the genetic structure, diet, and stress physiology of bobcats in the NER interact with one another and with the landscape, particularly anthropogenic land use. I also developed a framework for further study to elucidate precise mechanisms that explain those interactions.

CHAPTER I

This is a post-peer-review, pre-copyedit version of an article published in Conservation Genetics for which I was the first author and was intimately involved in all aspects of the work. The final authenticated version is available online at: http://dx.doi.org/10.1007/s10592-019-01170-8.

HISTORY MATTERS: CONTEMPORARY VERSUS HISTORIC POPULATION STRUCTURE OF BOBCATS IN THE NEW ENGLAND REGION, USA

Introduction

Bobcats *(Lynx rufus*) are the most widely distributed wild felids in North America, ranging across southern Canada, through much of the contiguous United States and into southern Mexico (Anderson and Lovallo 2003; Hansen 2007). Throughout their range, current populations are stable or increasing (Roberts and Crimmins 2010), a trend that is also evident in New Hampshire (Broman et al. 2014; Litvaitis et al. 2015; Mahard et al. 2016). However, for the last 100 years, New Hampshire bobcats have encountered both historic and contemporary challenges, events that may have left genetic signatures in today's populations.

The demographic history of New England bobcats reflects the changes in land use that occurred in the region (Litvaitis et al. 2006). Widespread conversion of forests to agricultural lands with the arrival of European settlers in 1623, followed by farm abandonment in the 19th century, facilitated the range expansion of bobcats (Seton 1925). Within 10-15 years, abandoned fields had reverted to early-successional forests, representing about a third of the northeastern land cover during the first half of the 20th century (Lorimer 2001). Associated with this type of

habitat is a uniquely adapted fauna, with some of its species highly dependent on thickets for their survival (Litvaitis 2001; Foster et al. 2002). A notable example is the New England cottontail *(Sylvilagus transitionalis)* that thrives in thickets and has been regarded as a preferred prey item of bobcats (Litvaitis et al. 1984). Not surprisingly, bobcats in this region strongly prefer scrub/shrub habitat (Reed et al. 2016) and their numbers track lagomorph abundances (Litvaitis 1993, 2001; Litvaitis et al. 2006). Consequently, unusually large numbers of bobcats compelled bounty programs meant to reduce their populations. Trends in bobcat abundances can be gleaned from bounty records. For example, annual harvests in New Hampshire from 1915 to 1930 nearly quadrupled and eventually peaked at 421 bobcats in 1959 (Litvaitis et al. 2006).

However, early-successional forests are inherently ephemeral in nature and as these habitats progressed into closed-canopy forests, bobcat abundances declined in response to decreasing prey availability (Litvaitis 1993, 2001; Litvaitis et al. 2006). A precipitous decline in harvests in the 1960s and 1970s ended bounty programs in Vermont, New Hampshire (only 10 bobcats submitted for bounty payment in 1970; Litvaitis et al. 2006), and Maine. In New Hampshire, bobcats have been a protected species for more than 25 years, while in surrounding states of Maine, Vermont, and Massachusetts, and the Canadian province of Quebec strict hunting and trapping seasons have been imposed. As a result of these measures, bobcat populations are now on the rise (Broman et al. 2014; Litvaitis et al. 2015; Mahard et al. 2016).

It is likely that historical bobcat populations were well connected, and the only substantial barriers imposed were major waterways and the high peaks of the Green and White Mountains. However, since the time of historically high numbers of bobcats, urbanization and fragmentation have changed the northern New England landscape, and optimal bobcat habitat is now fragmented with populations separated by urban and suburban areas, and by major

highways and other transportation structures (Litvaitis et al. 2015). Because bobcats are a wide-ranging species, they are sensitive to human-induced alterations of the environment, and thus can be useful indicators of connectivity in fragmented landscapes (Crooks 2002; Riley et al. 2003; Serieys et al. 2014; Reed et al. 2016). Existing genetic studies focused on the effects of natural and anthropogenic barriers on bobcat population structure have been equivocal. Genetic differences among populations have been found across the Straits of Mackinac in Michigan (Millions and Swanson 2007), across the Midwestern Corn Belt (Reding et al. 2012), and in southern California, across the 10-lane Ventura Freeway (Riley et al. 2006) and across Interstate Highway 5 (Lee et al. 2012). On the other hand, populations in southern Illinois (Croteau et al. 2010) and southern Georgia and northern Florida (Reid 2006) appear to be genetically homogeneous.

Starting in the 1950s, a dramatic increase in the construction of state and national highways produced over 40,000 miles of interstate highways and many more secondary roadways throughout the United States (Luna 1971). Since then, each passing decade has seen an average 51% increase in national vehicle miles travelled, with New Hampshire, Maine, and Vermont, all being above the national average in per capita miles travelled (Cambridge Systematics, Inc. 1994).

By themselves, roads can represent barriers to wildlife (McRae et al. 2005; Lee et al. 2012; Serieys et al. 2014; Poessel et al. 2014), but it is traffic volume specifically that may be of greater importance in limiting animal movement. The effects are evident in increased road mortalities (Litvaitis and Tash 2008) and reduced genetic connectivity among populations (Riley et al. 2006; Ruell et al. 2012; Litvaitis et al. 2015). Roads represent structural challenges to bobcat dispersal and jeopardize functional connectivity.

Concurrent with road construction, urban centers also spread across the landscape. In 1990, New Hampshire's human population exceeded one million, and by 2010, had grown by an additional 15.7%, with the largest increases in southern and southeastern counties (U.S. Census Bureau 2018). During that same period, the population of Maine grew by about 7.5%, again with highest growth rates in southern coastal counties. Similarly, Vermont and Massachusetts recorded increases of almost 10% and 3%, respectively between 1990 and 2010 (U.S. Census Bureau 2018).

Our study examined the effects of two major challenges (historic demographic bottleneck and recent habitat fragmentation) on the genetics of New Hampshire bobcats. We compared the genetic diversity, effective population sizes, and genetic structure of historic (1952-1964) and contemporary (2010-2017) bobcat populations. Bobcats typically breed in their second year (Hansen 2007); therefore, these populations are separated by at least 23 generations. We also identified the magnitude, direction, and potential barriers to gene flow. Our comparisons were greatly aided by the availability of historic skull samples collected and curated by the late Clark L. Stevens (Dept. of Natural Resources, UNH). However, because their collection was restricted to New Hampshire, comparisons with contemporary populations were only made within that state. Population structure and diversity in contemporary populations also focused on bobcat samples collected throughout the New England region (NER, Fig. 1-1), because political boundaries (i.e., state or country borders) are ecologically not relevant.

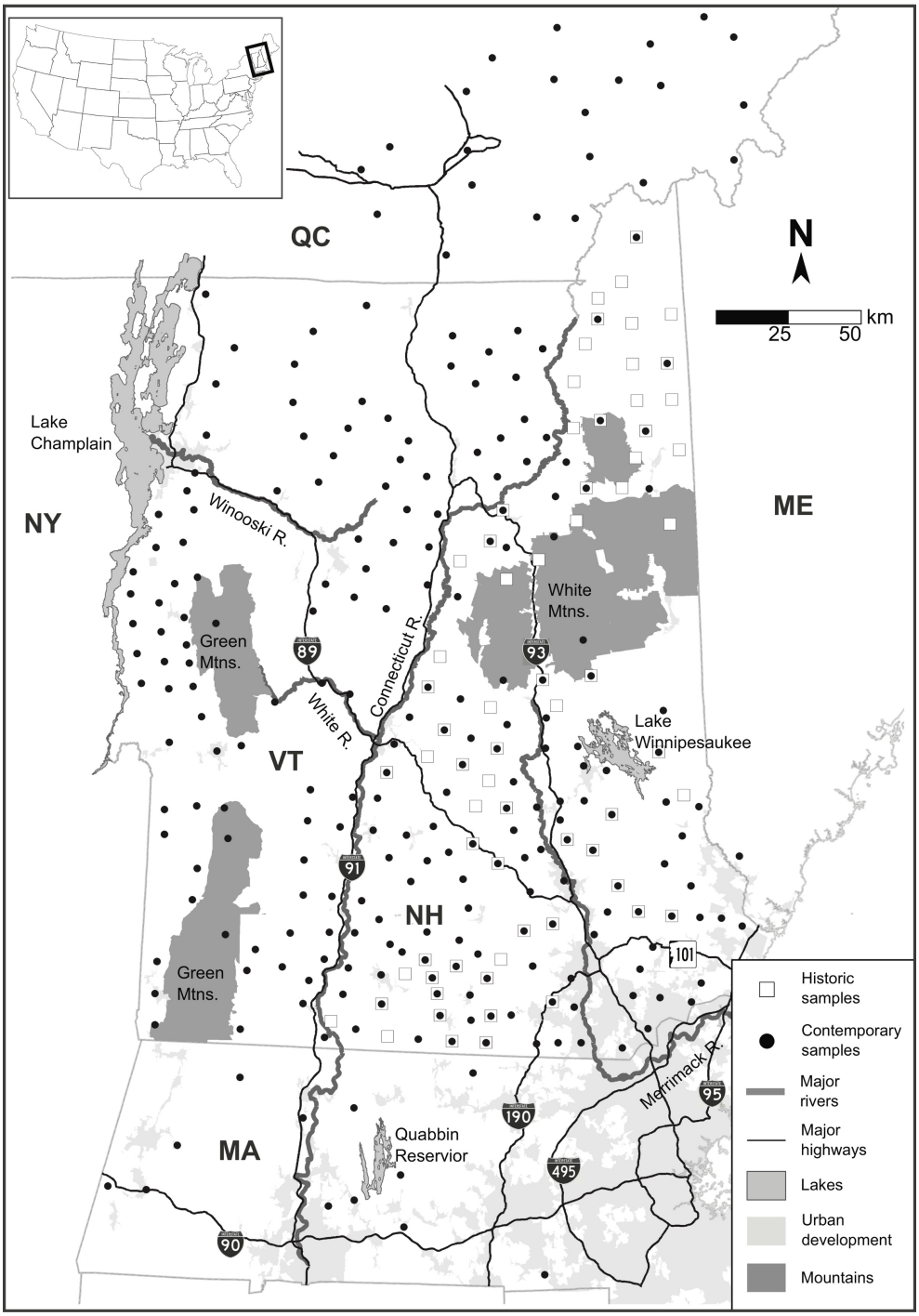


Figure 1-1. The New England Region (NER) encompasses all of New Hampshire and Vermont, as well as northern Massachusetts and southern Quebec, Canada. Sample locations represent centroids of towns where at least one bobcat was sampled. Contemporary samples were collected across the NER and historic samples came exclusively from New Hampshire.

Materials and Methods

Study area

The NER (Fig. 1-1) covers roughly 156,000 km^2 across New Hampshire (NH), Vermont (VT), northern Massachusetts (MA), and southern Quebec, Canada (QC). Currently, vegetation is dominated by second-growth forests that contain a mix of oaks (*Quercus* spp.), maples (*Acer* spp.), American beech (*Fagus grandifolia*), birches (*Betula* spp.), white pine (*Pinus strobus*), and eastern hemlock (*Tsuga canadensis*). Wetlands, scrub/shrub habitat, and agriculture make up a small percent of the landscape but are present throughout most of the study area. The Connecticut and Merrimack Rivers are the two major waterways bisecting the NER, the former along the NH-VT border and the latter through south-central New Hampshire. Other natural barriers are formed by the White and Green Mountains.

Development is highest in the southern portion of the study area, especially throughout eastern Massachusetts and southeastern New Hampshire, but low-intensity exurban development is widespread (Fig. 1-1). States in the NER have an average of 31% of their land area and 55% of their human population in the wildland-urban interface, both much higher than national averages (10% and 32%, respectively; Martinuzzi et al. 2015). There are numerous high-traffic volume roads crisscrossing the region, including Interstates 89, 90, 91, 93, and 95, as well as several federal and state highways.

Sample collection, DNA extraction, and microsatellite genotyping

Contemporary samples: Between 2010 and 2017, we collected muscle tissue samples from adult bobcats (n=236) in collaboration with state wildlife agencies and licensed sportsmen across the

NER. The Vermont and Massachusetts samples were collected from legally harvested bobcats (Vermont Fish and Wildlife Department unpublished harvest data, Massachusetts Division of Fish and Wildlife unpublished harvest data). Because there is no harvest season in New Hampshire, we collected samples from road-killed, nuisance, or incidentally-trapped animals (New Hampshire Fish and Game Department, unpublished data) and from 19 bobcats that were trapped and collared as part of a previous telemetry study (Reed et al. 2016). Tissues from legally harvested bobcats were imported from Quebec, Canada to the United States in accordance with CITES regulations (import permit #15CA00859/CWHQ-1; Quebec Ministry of Forests, Wildlife and Parks, unpublished data). All tissues were spatially referenced to town level (mean town area = 60.1 km^2) and assigned the coordinates of the town centroid. We extracted genomic DNA from muscle tissue using DNeasy Blood and Tissue Kits (Qiagen, Inc., Valencia, CA, USA).

Historic samples: A collection of bobcat skulls was used to obtain historic DNA samples. The skulls had been obtained from bounty animals submitted for payment during 1952 – 1964. The skulls had been bleached or boiled to remove soft tissues, both of which may lower the quantity and quality of amplifiable DNA (Lee et al. 2010). Each sample is associated with extensive information on collection locality and date, the physiological condition of each animal, sex, age, parasite load, gut content and for females, number of uterine pregnancy scars.

We extracted DNA from condylar processes of 84 adult bobcat skulls. Prior to DNA extraction, we sterilized samples by soaking in a trypsin solution to eliminate extraneous nucleic acids (Li et al. 2009; Li and Liriano 2011). After grinding the samples to a fine powder in a BeadBug tissue homogenizer (Alkali Scientific, Pompano Beach, FL, USA), we extracted DNA

by digesting the bone powder in a buffer containing 0.5M EDTA, 1%SDS, 10mM DTT, and 1mg/µl proteinase K, and concentrated the solution on Amicon Ultra-0.5 Centrifugal Filters (EMD Millipore, Billerica, MA, USA). Contaminants were removed using Qiagen MinElute PCR purification kits (Qiagen, Inc., Valencia, CA, USA). All historic samples were prepared in a dedicated, UV-light sterilized hood (AirClean Systems, Creedmoor, NC, USA). Designated pipettors with aerosol barrier filter tips were used, and negative and extraction controls were carried through at every step.

We genotyped contemporary samples at 20 fluorescently-labelled felid microsatellite loci (Table 1-1; Menotti-Raymond et al. 1999, 2005; Carmichael et al. 2000; Faircloth et al. 2005). We used a 1x concentration of Qiagen Type-it Microsatellite polymerase chain reaction (PCR) MasterMix (Qiagen, Inc., Valencia, CA, USA), 0.2 µM forward and reverse primers, and 3.0 µl DNA to a final volume of 12.5 µl. Initial PCR activation at 95°C for 5 minutes, was followed by 28 cycles of denaturation at 95°C for 30 s, annealing at 60°C for 90 s, and extension at 72°C for 30 s, with a final extension at 60°C for 30 minutes. For quality control, we duplicated 22% of contemporary genotypes. To assess the contemporary genotyping error rate, we divided the number of conflicting duplicated genotypes by the total number of duplicated genotypes, resulting in an error rate of 1.4%.

Due to the highly fragmented nature of our historic DNA samples, only the 10 loci with the shortest sequences (< 124bp; Table 1-1) were used in genotyping the historic samples. To increase amplification success for historic samples, we altered PCR conditions by reducing the annealing temperature to 55°C, increasing the number of cycles to 35, and allowing final extension for 30 minutes at 72°C. We calculated an error rate of 10.6% for historic genotypes. Due to this high error rate, we genotyped all 84 historic samples at least four times and only

included individuals in this study if at least two of the four replicates could be confidently genotyped and none of the replicates contradicted each other. While this significantly lowered our sample size from 84 to 59 individuals, this procedure ensured that only correct genotypes were used in subsequent analyses. For both time periods, PCR products were sent to the Yale Center for Genome Analysis (Yale University, New Haven, CT, USA), and visualized on a 3730xl DNA Analyzer (Applied Biosystems, Foster City, CA, USA). Genotypes were manually scored and binned using GENEIOUS v. 5.6.7 (Biomatters, Inc. Newark, NJ, USA).

Table 1-1. Microsatellite loci used for population genetic analyses of historic (1952-1964) and contemporary (2010-2017) bobcat populations. Loci with a null allele frequency greater than 0.05 in a given time period were excluded from all further analyses in that period. Reference: a. Faircloth et al. 2005, b. Menotti-Raymond et al. 1999, c. Menotti-Raymond et al. 2005, d. Carmichael et al. 2000.

Locus	Period genotyped	Period analyzed	Null allele frequency (Period)	Reference
BC1AT	Contemporary	Contemporary	-	a
BCD1T	Contemporary	Contemporary	-	a
BCE5T	Contemporary	Contemporary	-	a
BCH6T	Contemporary	Contemporary	0.02 (C)	a
FCA031	Contemporary	Contemporary	-	b
FCA045	Contemporary	Contemporary	-	b
FCA082	Contemporary	Contemporary	-	b
FCA126	Contemporary	Contemporary	-	b
FCA391	Contemporary	Contemporary	-	b
FCA523	Both	Contemporary	0.06 (H)	b
FCA740	Contemporary	Contemporary	-	c
FCA008	Both	Both	0.03 (C)	b
FCA023	Both	Both	-	b
FCA043	Both	Both	0.03 (C)	b
FCA149	Both	Both	-	b
FCA567	Both	Both	-	b
Lc106	Both	Both	-	d
FCA087	Both	Historic	0.06 (C)	b
Lc110	Both	Historic	0.05 (C)	d
FCA205	Both	Neither	0.08 (Both)	b

We used program MICROCHECKER to detect null alleles, allelic dropout, or stuttering (VanOosterhout et al. 2004). We excluded loci where the frequency of null alleles was greater than 0.05. We calculated deviation from Hardy-Weinberg Equilibrium (HWE) and linkage disequilibrium for each locus in GENEPOP v. 4.2 (Raymond and Rousset 1995), and determined significance using a sequential Bonferroni correction ($\alpha = 0.01$; Rice 1989).

Population genetic structure and gene flow

We used three methods to identify population structure: two Bayesian genetic methods (GENELAND and STRUCTURE) and a non-genetic multivariate model, sPCA. We used all available loci for each time period (17 for contemporary and 8 for historic bobcats; see Results for details). Because historic analyses had fewer loci and were exclusively within New Hampshire, we conducted an additional analysis of population structure including only contemporary New Hampshire bobcats. To create an equal comparison between the two populations, we used 8 loci (the 6 common loci plus FCA126 and FCA391) and only included 59 randomly selected individuals to match the sample size of the historic dataset.

Genetic structure: We initially assessed genetic structure using the GENELAND package (Guillot et al. 2005) as implemented in R statistical software (R Core Team 2019). This program uses genetic and spatial data to inform Bayesian population assignment and performs exceptionally well when the focal species is highly mobile and barriers to gene flow are permeable (Safner et al. 2011). We used the correlated allele frequency model to test for the optimal number of spatial genetic groupings (*K*), with potential *K* values ranging from 1 to 15. Because only the town of origin was known for each individual, we calculated the average size of towns in the study area

and set the spatial uncertainty in GENELAND to the radius of a circle equal in size to the mean town area (4.5 km). We executed 10 independent runs with 200,000 MCMC iterations each and thinning set to 100. We determined *K* from the run with the greatest log posterior density and repeated this procedure with *K* fixed at the optimal value.

We used STRUCTURE (Pritchard et al. 2000), a non-spatial Bayesian clustering algorithm, as an additional determinant of population structure and to determine each individual's estimated proportion of ancestry from the inferred clusters (Q values). We used a hierarchical approach following Coulon et al. (2008) in which each cluster inferred from the data was run through the algorithm independently until no further subdivision was evident. We completed 10 independent runs of 200,000 MCMC iterations after a burn-in of 100,000. We used the admixture model with correlated allele frequencies and allowed K to vary from 1 to 10. We used STRUCTURE HARVESTER (Earl and vonHoldt 2012) and CLUMPP (Jakobsson and Rosenberg 2007) to process the results. As suggested in the STRUCTURE software documentation, the optimal K value for each run was determined using log-likelihood plots, Delta K (Evanno et al. 2005), and biological relevance of results. We mapped individual Q values to determine spatial patterns in subpopulation structure.

Spatial principal component analysis: We validated Bayesian genetic structure results using an alternate method of assessing population structure not reliant on a genetic model. Spatial principal component analysis (sPCA; Jombart et al. 2008) uses an ordination-based multivariate approach that makes no assumptions about genetic equilibria. This method may be better at detecting the more clinal (as opposed to discrete) population clustering patterns present where isolation by distance (IBD) is evident (Jombart et al. 2008). We tested for IBD with a Mantel test

in the R package ade4 (Dray and Dufour 2007) using 100,000 randomized permutations. sPCA analysis was completed in the adegenet package in R (Jombart et al. 2008) using a saturated network with inverse distance weighting. The lagged scores of the first two global principal components were retained and groupings were determined using a K-means clustering algorithm. The potential number of clusters (K) was allowed to range from 1 to 15, and the optimal K value was selected using the cubic clustering criterion (CCC) in JMP Pro 13 (SAS Institute 2016). Similarity between GENELAND and sPCA results was assessed using R^2 values from contingency analysis.

Gene flow: We determined gene flow among subpopulations using coalescent theory in a Bayesian framework implemented in MIGRATE v3.6 (Beerli and Felsenstein 2001). This program has typically been used to estimate gene flow patterns in the distant past ($4*N_E$ generations ago), however Samarasin et al. (2017) found that MIGRATE provides the most accurate estimates of recent migration rates, provided that recent reductions in connectivity are not severe and F_{ST} values are relatively low. Both conditions are true for bobcats in the NER. Our parameters, following the recommendations in Beerli (2013), were as follows: a Brownian motion model for microsatellite data, a constant mutation rate, starting values for θ and migration rate estimated using F_{ST} for each dataset, and a MCMC of 5,000 recorded steps with a sampling increment of 100 and a 10,000 step burn-in.

Genetic diversity, effective population size, and bottlenecks

We calculated global HWE and genetic diversity metrics for each time period overall, and for each subpopulation identified by population structure analyses. To account for

differences in sample sizes (especially for contemporary subpopulations which varied widely), we rarefied diversity metrics to match the smallest group sample size. We used HP-RARE (Kalinowski 2005) to calculate rarified allelic richness (A_R) and private allelic richness (A_P) per locus. We calculated number of alleles (A), rarified observed heterozygosity (H_O), and rarified expected heterozygosity (H_E) across loci in GENALEX v. 6.5 (Peakall and Smouse 2012). We used GENEPOP (Raymond and Rousset 1995) to estimate inbreeding coefficients (F_{IS}) for each group. We calculated effective population size (N_E) for each time period and subpopulation using the linkage disequilibrium method implemented in LDNE (Waples and Do 2008). We also split each time period into two groups to examine short-term trends within that period. There was a documented dramatic population decline after 1959 (Litvaitis et al. 2006), so we split the historic period into pre- and post-decline groups (1952-1959, 1960-1964). Contemporary samples were binned into four-year groups (2009-2012, 2013-2016). We excluded rare alleles (< 0.05) from the analyses and estimated confidence intervals using the jackknife on loci option. Estimates of effective population size assume discrete generations. Bobcats violate this assumption, hence N_E values reported here are likely inflated from the true values (Jorde and Ryman 1995). However, each group is similarly susceptible to violations of this assumption, and we use the results solely for relative comparisons between groups. Lastly, we tested for bottlenecks using the Wilcoxon ranked test under a two-phase model in the program BOTTLENECK (Piry et al. 1999). The program detects recent bottlenecks (i.e., excess heterozygosity) by simulating heterozygosity for a dataset's given allelic diversity and comparing those simulated values to the actual value. We ran 1000 simulations and, following the recommendations of Peery et al. (2012), we compared results using a range of values for both mean size of multi-step mutations (σ^2 = 12, 16) and proportion of multi-step mutations (p_g = 0.7, 0.8, 0.9, 0.95).

Results

We successfully genotyped 295 individual bobcats (historic n = 59; contemporary n = 236) at 20 felid microsatellite loci for contemporary bobcats and 10 for historic bobcats. MICROCHECKER found no stuttering or allelic dropout at any locus. Seven loci (BCH6T, Fca008, Fca043, Fca087, Fca205, Fca523, Lc110) showed evidence of null alleles (Table 1-1). Significant effects on genetic parameters can occur when null allele frequency is large (> 0.1; De Meeûs 2018). Therefore, we excluded four loci with a null allele frequency greater than 0.05 from all subsequent analyses (Fca087, Fca205, and Lc110 for the contemporary population and Fca523 and Fca205 for the historic population). As a result, we retained 17 loci for contemporary analyses and 8 for historic analyses, with 6 loci in common between time periods. After sequential Bonferroni correction ($\alpha = 0.01$; Rice 1989), no loci deviated significantly from HW expectations in the historic samples. However, for contemporary populations, Fca043, Fca082, and Fca567 were not in HWE. All historic loci pairs were in linkage equilibrium and only one pair (BCE5T and Fca126) was significantly out of equilibrium in the contemporary population.

Population genetic structure and gene flow

Historical versus contemporary genetic structure in New Hampshire: GENELAND revealed two historic subpopulations (Fig. 1-2), with the White Mountains region defining the border between the two. STRUCTURE indicated all individuals most likely belonged to one cluster in the historic dataset, although the two cluster model was only slightly less supported (Ln likelihood$_{(K=1)}$ = -1192, sd = 0.4; Ln likelihood$_{(K=2)}$ = -1207, sd = 11.6) and Q values were noticeably different in northern and southern individuals (Q values for K = 2 shown in Fig. 1-2). The mean individual

proportion of ancestry from the assigned cluster was greater for GENELAND assignments than STRUCTURE assignments (58.6% and 56.4%, respectively). GENELAND indicated the presence of two subpopulations in contemporary NH, a northern and a southern deme, but with the border between them farther south than it had been historically (Fig. 1-2). STRUCTURE clearly indicated only one distinct genetic cluster in contemporary NH. The mean individual proportion of ancestry from the assigned GENELAND clusters in contemporary NH was 61.2%.

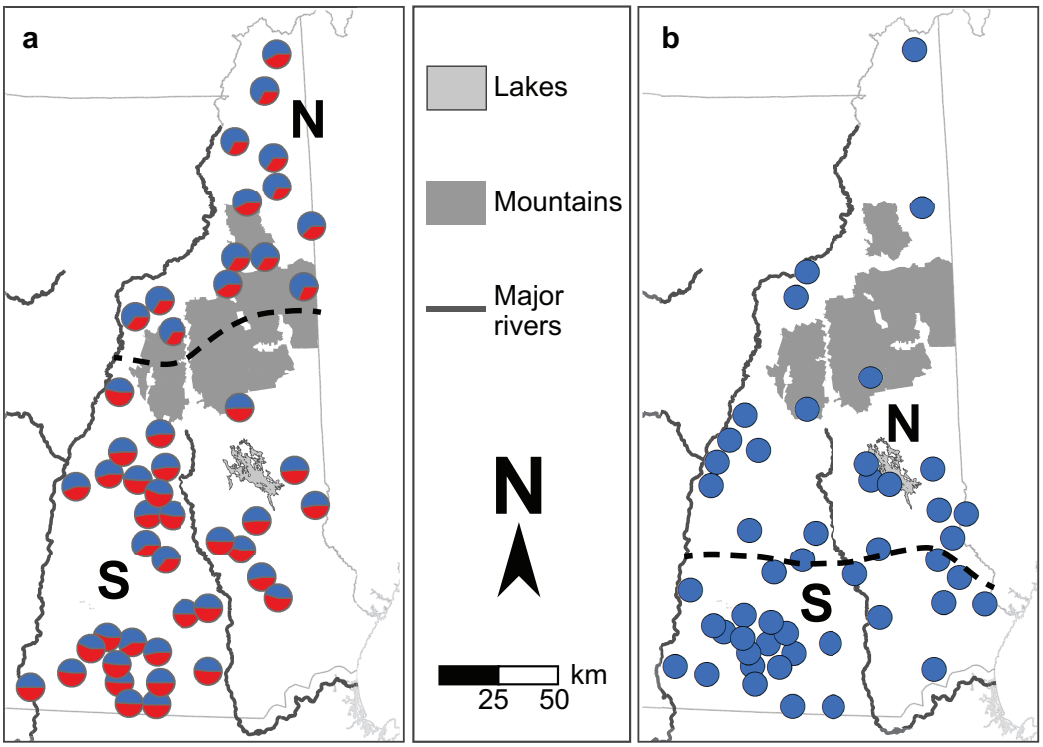


Figure 1-2. Population structure for (a) historic samples and (b) contemporary New Hampshire samples. Dashed lines represent approximate borders between subpopulations as determined by the modal probability of cluster membership for each 4.5 km pixel in GENELAND. Pie charts represent the proportion of ancestry in individuals from each of the clusters identified in STRUCTURE.

Contemporary genetic structure in the New England region: Contemporary analysis for the NER in GENELAND showed five subpopulations (Fig. 1-3) with a mean individual proportion of

ancestry from the assigned cluster of 66.0%. Hierarchical analysis in STRUCTURE discovered two clusters each having two secondary clusters when analyzed individually, for a total of four distinct clusters. The mean individual proportion of ancestry from the assigned STRUCTURE clusters was 60.0%. STRUCTURE results aligned well with GENELAND results with the exception of insufficient evidence for a unique Eastern subpopulation. Even though STRUCTURE did not estimate the differences as large enough to warrant a unique cluster, GENELAND identified differences in ancestry for individuals from the Eastern subpopulation (Fig. 1-3). The incorporation of spatial data allows GENELAND to discern population structure where STRUCTURE may not (Safner et al. 2011). Hence, modal individual subpopulation assignments from GENELAND (designated by dashed lines in Figs. 1-2 and 1-3) were used for all subsequent analyses.

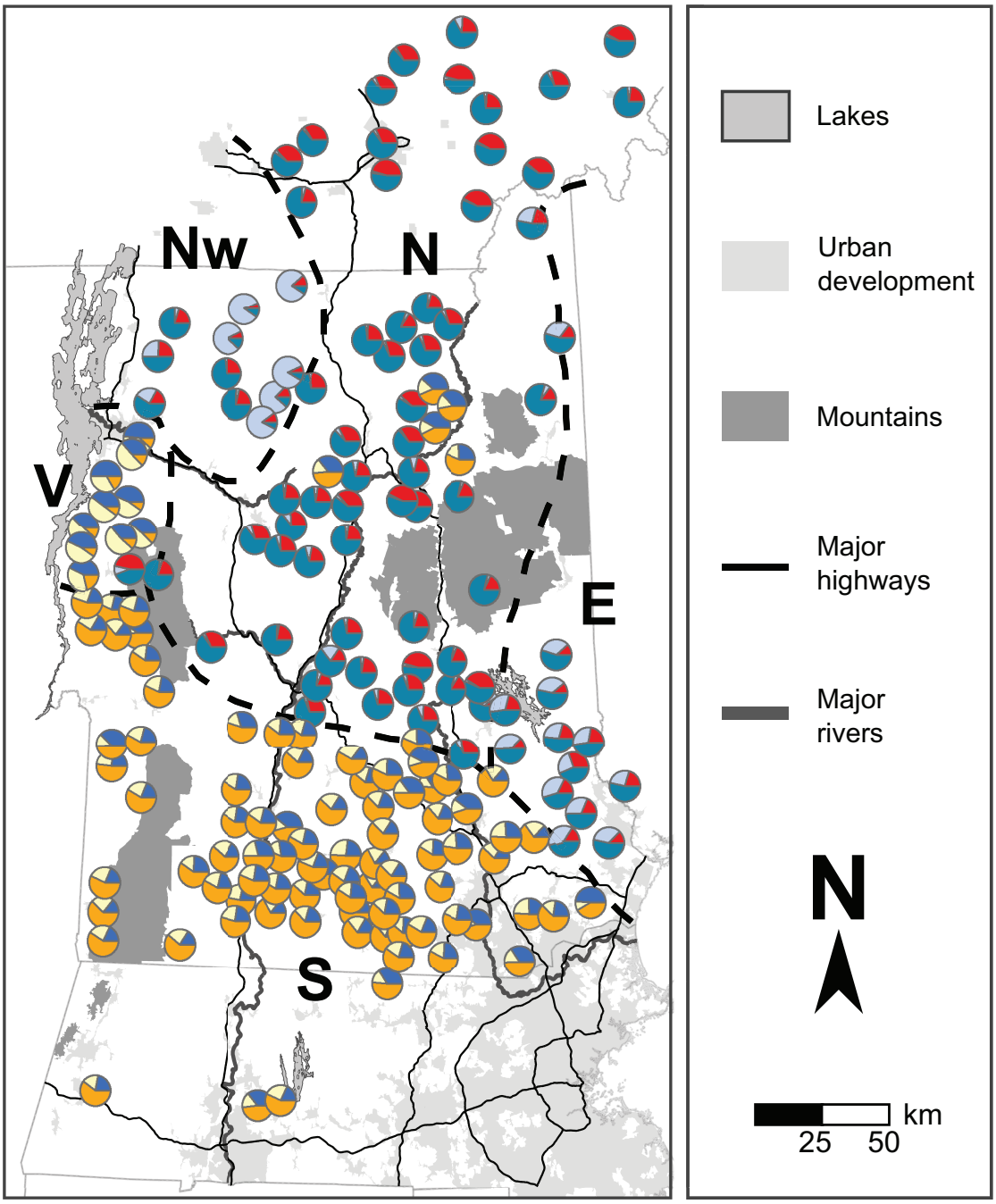


Figure 1-3. Contemporary population structure of bobcats in the New England region. Eastern (E), North Central (N), Southern (S), Vermont lowlands (V), and Northwest (Nw) subpopulations are labeled. Dashed lines represent approximate borders between subpopulations as determined by the modal probability of cluster membership for each 4.5 km pixel in GENELAND. Pie charts represent the proportion of ancestry in individuals from each of the clusters identified in STRUCTURE. The upper level of hierarchical structure is denoted by warm colors (Southern and VT Lowlands) and cool colors (Northwest, North Central, and Eastern), and different shades of warm or cool colors represent secondary structure.

Spatial principal component analysis: Clustering analysis based on spatial PCA resulted in three clusters in historic and one cluster in contemporary NH. Across the entire contemporary NER, sPCA found four clusters. The results of the GENELAND and sPCA clustering methods were significantly correlated for the historic and contemporary datasets (Table 1-2). sPCA detected one additional historic cluster and one fewer contemporary NH cluster, however IBD was non-significant in both these groups and sPCA may not perform as well in such situations. Analysis in the contemporary NER resulted in four clusters, as it failed to differentiate between the Northwest and North Central populations discovered by both GENELAND and STRUCTURE. To visualize the similarity of results between the genetic and non-genetic methods, we plotted the mean of the first two principal components (PC1 and PC2) grouped by GENELAND assignments (Fig. 1-4). PC1 mainly distinguished between the VT Lowlands subpopulation and the remaining groups, whereas PC2 generally represented a north-south gradient.

Table 1-2. Bobcat population structure over historic (1952-1964) and contemporary (2010-2017) time periods, and for a more direct comparison, contemporary New Hampshire only. Correlations between genetic and geographic distance (IBD r) and significance (IBD *p)* were based on 100,000 permutations. Genetic clusters were estimated using a spatially explicit genetic models (GENELAND and STRUCTURE) and a multivariate model (sPCA). Agreement between the GENELAND and sPCA models (R^2) was calculated using contingency analysis; significance was determined with a chi-square test.

Time period	N	N Loci	IBD r	IBD *P*	GENELAND K	STRUCTURE K	sPCA K	R^2
Historic	59	8	0.07	0.10	2	1	3	0.74
Contemporary NH	59	8	0.04	0.27	2	1	1	-
Contemporary NER	236	17	0.05	0.02	5	4	4	0.56

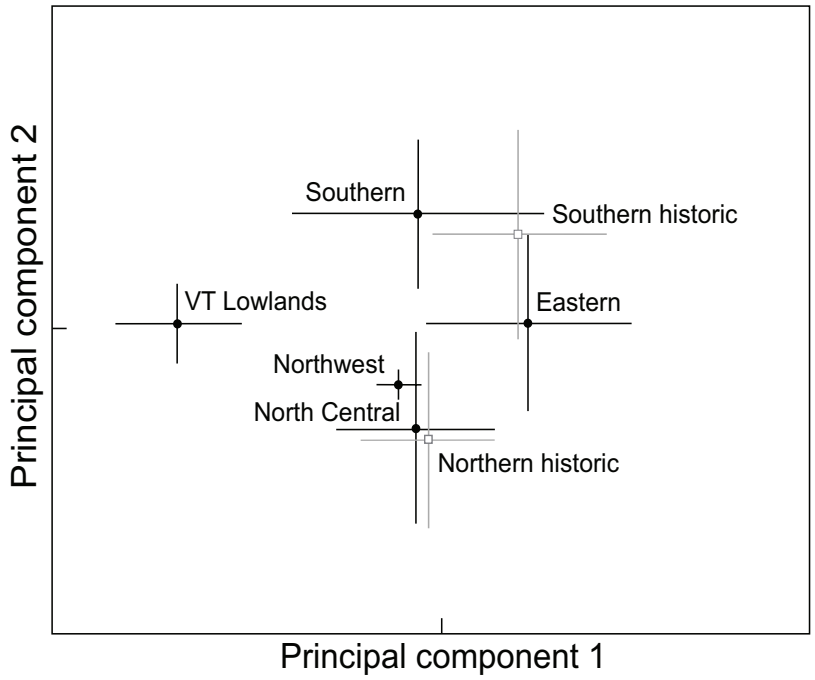


Figure 1-4. Mean (± 1 standard deviation) of the first two sPCA principal components plotted by GENELAND subpopulation. Black circles – contemporary subpopulations, open squares – historic subpopulations.

Gene flow: MIGRATE results identified a disproportionate gene flow in the historic population with higher rates from the Southern to the Northern population (Fig. 1-5a). For contemporary NH, this trend was reversed, with greater migration from the north to the south (Fig. 1-5b). Larger asymmetries could be distinguished in the contemporary NER population, with the North Central and Eastern subpopulations disproportionately contributing migrants to the other subpopulations (Fig. 1-5c). These two subpopulations may be source areas for a general pattern of east to west gene flow across the NER. Migration was much stronger from the North Central to the Southern subpopulation than in the opposite direction, again marking a stark shift from the more northward flow in historic times. There was a reciprocal relationship between pairwise F_{ST} and relative migration rates between subpopulations ($R^2 = 0.526$, $P = 0.018$).

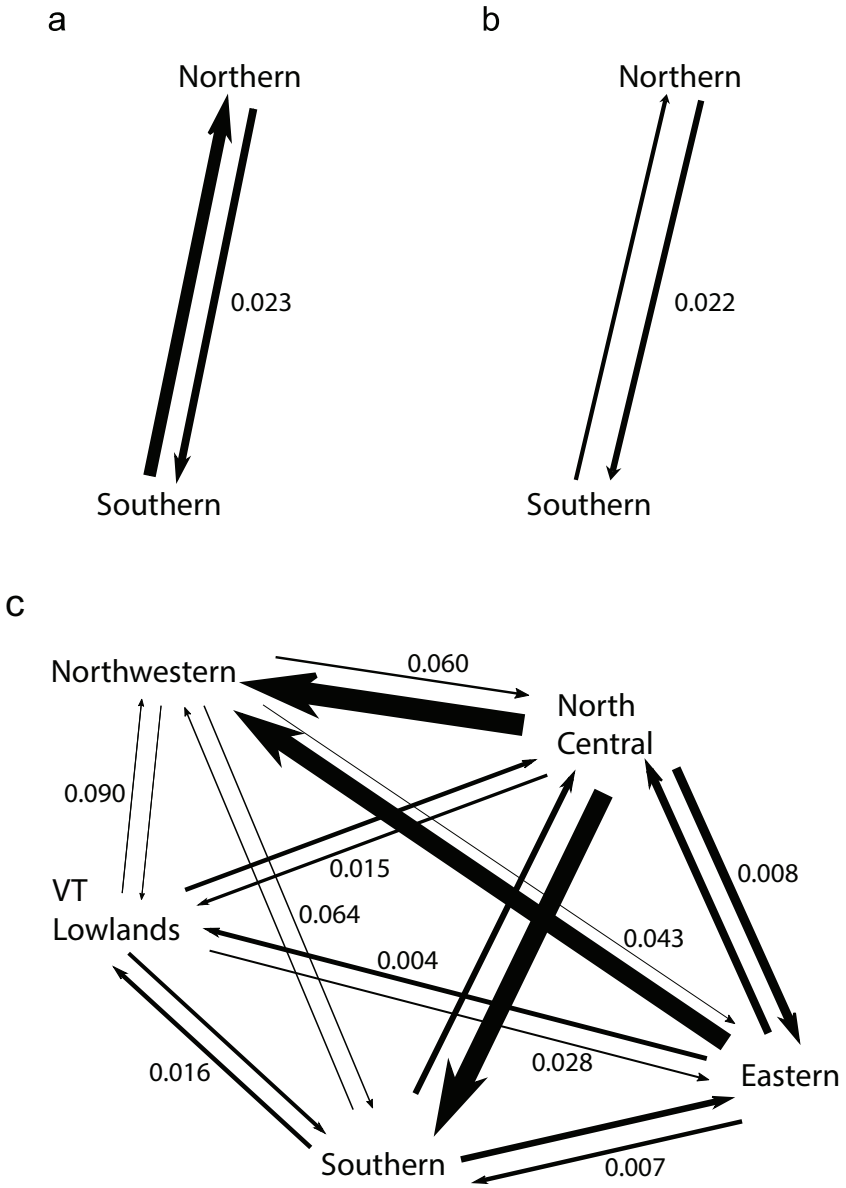


Figure 1-5. Relative migration rates among (a) historic, (b) contemporary New Hampshire, and (c) contemporary New England region subpopulations as calculated in MIGRATE. Arrow thickness is proportional to extent of gene flow, and numbers represent F_{ST} values calculated in GENALEX.

Genetic diversity, effective population size, and bottlenecks

We determined genetic diversity during the 1952-1964 and 2010-2017 sampling periods using the 6 loci that were shared by both periods. We found deviations from HWE for both the contemporary (P <0.001) and historic populations (P < 0.002). This was expected, as

subpopulation structure was found in both datasets (Table 1-2). The historic population exhibited greater diversity in number of alleles and allelic and private allelic richness (Table 1-3), whereas contemporary bobcats had a greater heterozygosity than the historic population. Both populations showed a heterozygote deficiency and the deficiency was greater in the contemporary population (Table 1-3), but none of these differed at the 0.05 level. F_{IS} estimates indicated a greater inbreeding coefficient in the historic population ($P = 0.007$).

Table 1-3. Genetic diversity metrics for bobcats sampled from two time periods, historic (1952-1964) and contemporary (2010-2017). Data for a random subsample of contemporary bobcats from NH are also shown. All comparisons are based on the 6 loci common to both sampling times. N indicates number of individuals in the analyses. Means and standard errors were calculated over loci for number of alleles (A), allelic richness (A_R), private allelic richness (A_P), observed heterozygosity (H_O), expected heterozygosity (H_E), and inbreeding coefficient (F_{IS}).

Time period	N	N Loci		A	A_R	A_P	H_O	H_E	F_{IS}
Historic	59	6	Mean	6.667	6.595	1.134	0.579	0.584	0.081
			SE	0.328	0.793	0.320	0.103	0.087	0.027
Contemporary NH	59	6	Mean	4.583	5.742	0.344	0.521	0.529	0.013
			SE	0.313	0.597	0.202	0.070	0.065	0.034
Contemporary NER	236	6	Mean	6.500	5.799	0.338	0.584	0.613	0.025
			SE	0.405	0.680	0.189	0.079	0.076	0.029

We also analyzed diversity trends among subpopulations within each time period using all available loci for the specific time period: 17 contemporary NER, 8 historic NH, and for more equitable comparison, 8 contemporary NH loci (Table 1-4). We found that the historic population was composed of two subpopulations that showed small but significant differences in genetic diversity; one north and the other south of the White Mountains (Fig. 1-2). The Southern population was geographically larger and showed greater allelic diversity ($P = 0.049$). The

Northern population had a greater expected heterozygosity ($P = 0.017$) and inbreeding coefficient ($P < 0.001$). In contemporary NH, the Northern subpopulation was geographically larger showed greater allelic richness, private allelic richness, and heterozygosity, though these were not significant at the 0.05 level.

Table 1-4. Estimates of genetic diversity for subpopulations within each time period using 8 historic, 8 contemporary New Hampshire, and 17 contemporary New England region loci. N indicates number of individuals in the analyses. Means and standard errors were calculated over loci for number of alleles (A), allelic richness (A_R), private allelic richness (A_P), observed heterozygosity (H_O), expected heterozygosity (H_E), and inbreeding coefficient (F_{IS}). See Figs. 2 and 3 for geographical location of subpopulations.

Time period	Subpopulation	N		A	A_R	A_P	H_O	H_E	F_{IS}
Historic	Northern	18	Mean	5.250	5.181	0.728	0.631	0.676	0.065
			SE	0.198	0.197	0.071	0.042	0.053	0.002
Historic	Southern	41	Mean	6.25	5.218	0.764	0.599	0.620	0.033
			SE	0.258	0.178	0.067	0.042	0.034	0.002
Contemporary NH	Northern	26	Mean	4.500	5.096	0.722	0.534	0.553	0.014
			SE	0.500	0.550	0.270	0.117	0.102	0.037
Contemporary NH	Southern	33	Mean	4.667	4.826	0.452	0.507	0.524	0.009
			SE	0.422	0.378	0.167	0.088	0.092	0.049
Contemporary NER	Eastern	24	Mean	5.235	4.086	0.207	0.618	0.666	0.056
			SE	0.098	0.060	0.016	0.049	0.035	0.034
Contemporary NER	North Central	80	Mean	6.176	4.110	0.203	0.686	0.717	-0.033
			SE	0.111	0.058	0.010	0.070	0.052	0.011
Contemporary NER	Southern	111	Mean	6.235	3.963	0.227	0.647	0.677	0.018
			SE	0.101	0.060	0.014	0.057	0.052	0.016
Contemporary NER	VT Lowlands	15	Mean	4.294	3.571	0.127	0.696	0.636	-0.072
			SE	0.074	0.061	0.009	0.054	0.048	0.032
Contemporary NER	Northwest	6	Mean	3.412	3.412	0.128	0.676	0.578	-0.19
			SE	0.050	0.072	0.012	0.072	0.049	0.080

The contemporary NER population was composed of five subpopulations, with the greatest diversity found along the NH-VT border in the Southern and North Central subpopulations. Differences existed in allelic diversity ($P < 0.001$), observed heterozygosity ($P = 0.020$), and expected heterozygosity ($P < 0.001$). Post-hoc Tukey tests indicated that these trends are driven largely by a lack of diversity in the VT Lowlands and Northwest subpopulations, which were significantly different from the other three. Additionally, the North Central subpopulation had greater allelic diversity and observed heterozygosity than others. Inbreeding coefficients varied among subpopulations ($P < 0.001$) with the greatest values in the Southern and Eastern subpopulations and the most negative value in the VT Lowlands.

Estimates of effective population size were much larger for the contemporary NH bobcat population than the historical one (Table 1-5). A 77% decline in N_E was observed after 1959 in the historic samples, which coincides with a steep drop in the number of bobcats harvested in New Hampshire (Litvaitis et al. 2006). N_E of the Southern historic subpopulation was far lower than for the Northern subpopulation. Despite the decrease in N_E within the time period, no evidence for a significant genetic bottleneck was found in either subpopulation or in the state as a whole.

When estimating N_E for contemporary NER samples, the largest effective population size was found in the North Central subpopulation, closely followed by the Southern subpopulation (Table 1-5). The lowest N_E occurred in the VT Lowlands subpopulation. A temporal comparison between 2009-2012 and 2013-2016 for the NER showed that N_E increased by 46%. Evidence for a bottleneck was found in the Eastern subpopulation (Table 1-5; 6 out of 8 parameter combinations).

Table 1-5 Effective population size and evidence of bottlenecks for historic (1952-1964) and contemporary (2010-2017) bobcat populations using 8 historic and 17 contemporary loci. N_E was calculated in LDN_E (Waples and Do 2008), excluding rare alleles (< 0.05) and jackknifing loci to obtain minimum and maximum values. Negative values indicate insufficient sample size for accurate estimate. Bottleneck tests were considered significant if any of 8 parameter combinations resulted in $P < 0.05$

Period	Subgroup	N_E	Min N_E	Max N_E	Significant bottleneck?
Historic	All years	52	31	109	No
Historic	1952-1959	124	42	∞	No
Historic	1960-1964	29	12	3920	No
Contemporary NH	All years	222	152	381	Yes
Contemporary NH	2009-2012	167	100	417	No
Contemporary NH	2013-2016	243	128	1355	Yes
Historic	Northern	78	19	∞	No
Historic	Southern	43	23	129	No
Contemporary NER	All subpopulations	479	334	793	No
Contemporary NER	Eastern	71	39	258	Yes
Contemporary NER	North Central	459	218	∞	No
Contemporary NER	Southern	424	231	1732	No
Contemporary NER	VT Lowlands	29	16	85	No
Contemporary NER	Northwest	-186	9	∞	No

Discussion

We assessed the population genetic structure and patterns, direction, and magnitude of gene flow as well as the genetic diversity and effective population sizes of bobcats in the NER during two time periods. The historic period (1952-1964) reflects a time of record high harvests and a drastic population decline, whereas the recent period (2010-2017) corresponds to a time of intense anthropogenic development. Overall, an across-time period comparison indicated a shift in population genetic structure along with a decrease in genetic diversity.

Population genetic structure and gene flow

Historic population structure in NH consisted of a Northern and a Southern subpopulation (pairwise F_{ST} = 0.023) whose border corresponded precisely with the White Mountains. Analysis of a comparable contemporary NH dataset (59 individuals at 8 loci) revealed a similar north-south division and F_{ST} value (0.022), but structure was less evident and the divide between the subpopulations shifted about 80 km south. Theoretically, this pattern is expected at the leading edge of a range expansion. Founder events promote greater structure and inbreeding coefficients, both of which we found in the historic data. This pattern is subsequently reduced as gene flow reverses and the population homogenizes (Excoffier et al. 2009; Hagen et al. 2015). At a large scale, bobcats have been undergoing a northward range expansion during the last 200 years which is associated with reduced genetic diversity at the leading edge independent of population size (Hewitt 2000; Cobben et al. 2011; Koen et al. 2014). We found bobcats in the NER had lower heterozygosity and allelic richness when compared to populations in the core of their range, such as in the southeastern United States (Reid 2006), Oregon (Reding et al. 2013a), Ohio (Anderson et al. 2015), Illinois (Croteau et al. 2010), and Iowa (Reding et al. 2013b). At a smaller scale, the spatial extent of the historic Southern subpopulation aligned closely with the hypothesized pre-Columbian range (Seton 1925), and we found asymmetrical gene flow biased toward northward movement in these subpopulations. Furthermore, we found a greater number of alleles, higher allelic richness, and more private alleles in the Southern subpopulation than north of the White Mountains. This uneven pattern of diversity largely dissolved in contemporary NH, and gene flow estimates suggest the leading edge population has begun to equilibrate. Because the trend of reduced diversity in more northern populations is less evident in the contemporary NER and migration rates between northern and southern subpopulations are

currently southward biased, it is likely that local dynamics (e.g., management- or habitat-dependent differences in bobcat abundance) are currently more important than range-wide dynamics in explaining population genetic patterns.

Community dynamics in the face of climate change may play a role in the population genetics of bobcats in the NER. Bobcats and Canada lynx are sympatric in northern NH. Lynx have had a competitive advantage in the north due their ability to thrive in areas of greater elevation and snow cover. Furthermore, Peers et al. (2013) found that lynx rely more heavily on this specialization in areas of sympatry with bobcats. However, in the last half century the NER has seen steadily increasing temperatures along with a decrease in snowfall (Huntington et al. 2004; Burakowski et al. 2008), effectively reducing the advantageous conditions for lynx. We found a shift toward southerly gene flow in contemporary NH bobcats, as well a dramatic increase in N_E, even in the northern parts of the study area. Historically, northern NH may have been acting as a sink for bobcats because it supplied less quality habitat and greater competition. An increase of available suitable habitat and a reduction in competition may have increased the reproductive success for bobcats in northern NH. Habitat availability and quality has been found to play an important role in population growth for other mesocarnivores species (Kosterman et al. 2018; Green et al. 2018). Coupled with high harvest pressure in southern NH, this climate-induced shift may have allowed for rapid population expansion and for the northern region to become a source area for bobcats in NH.

Based on our estimates of gene flow (Fig. 1-5), movement patterns in contemporary NER populations were mainly northeast to southwest across the region. The Eastern and North Central subpopulations exhibited a highly asymmetrical westward gene flow. Due to the different management regimes between New Hampshire (no harvest) and Vermont (regulated harvest),

New Hampshire bobcats may be serving as a source for harvested populations in the west. As home ranges are vacated due to harvesting, males in surrounding areas can expand their ranges into emptied areas (Lynch et al. 2008). A comparison of sex ratios across the NH-VT border from 2013 to 2015 provides evidence for New Hampshire males expanding into neighboring Vermont. Within 20 km of the New Hampshire border, the ratio of harvested males:females is 1.50, but drops to 0.93 further west. No similar data are available for comparisons across borders with other neighboring states or southern Canada. Hence, we cannot determine if New Hampshire bobcats represent a source population for neighboring states, or if westward gene flow is a general trend across New England and Quebec.

Bobcats in the VT Lowlands are isolated, revealing little gene exchange with other subpopulations as evidenced by high F_{ST} values (Fig. 1-5). Potential barriers include the Green Mountains to the east, I-89 in the north, and in the west, the lower portions of Lake Champlain, which at its narrowest point is about 200 m across. However, the southern boundary of this subpopulation does not correspond to any obvious physical barrier to gene flow (Farrell et al. 2018). The observed isolation may be a result of habitat-induced behavioral change. The VT Lowlands are one of the most fragmented areas in the NER; local land cover consists of large tracts of agriculture interspersed with small forest patches. This creates an abundance of prey and highly suitable edge habitat (Reed et al. 2016). Tucker et al. (2018) found that species occupying human-modified habitats move significantly less than their conspecifics in more natural areas, particularly in the presence of enhanced food resources (Prange et al. 2004). Additionally, the VT Lowlands region (e.g., the Split Rock Wildway) is part of the 'Two Countries, One Forest' (2C1Forest) initiative, a Canadian-U.S. collaborative of conservation efforts. The initiative seeks to maintain a network of wildlands in the Northern Appalachian region, extending from New

York to Nova Scotia. Thus, it is possible that the VT Lowlands subpopulation contains alleles introduced by bobcats from New York.

Genetic diversity, effective population size, and bottlenecks

We found consistent evidence for a modest decrease in genetic diversity between the historic and contemporary time periods. We found lower allelic richness and private allelic richness along with greater heterozygosity deficit through time. This pattern could result from a loss of rare alleles in the NER and is consistent with a recent bottleneck and an increasingly fragmented population (Nagylaki 1985). Multivariate analysis of genetic structure suggested the appearance of novel barriers to gene flow at some point between the time periods sampled, particularly in the southern portion of the NER. A plot of the first two sPCA variables revealed high similarity between the historic Southern population and contemporary NER Southern and Eastern subpopulations (Fig. 1-4). However, we found evidence that the two contemporary populations have diverged and are spatially separated along a highly developed landscape. Likewise, the historic Northern subpopulation clustered with the contemporary NER's Northwest and North Central subpopulations. Anthropogenic disturbance is less prevalent in the northern NER, and current subpopulations are not as distinct from one another.

Starting in the 1950s, New Hampshire bobcat populations supported harvests of over 300 animals per year, culminating in 421 individuals in 1959, followed by a steep decline in harvested animals in the 1960s (Litvaitis et al. 2006). From the mid 1960s until 1989, when hunting and trapping seasons were permanently closed, no more than 40 bobcats per year were harvested (exception, 1973: 55 animals). Although harvests are not an estimate of abundance, they can indicate large shifts in population size. Using our historic DNA samples, we were able to detect a sharp drop corresponding to the time period after record high harvests. Our estimates

of effective population sizes reveal a decrease of N_E from 124 (1952-1959) to a low of 29 (1960-1964). Furthermore, when comparing historic subpopulations, we found N_E was lower in the Southern subpopulation where harvest pressure was greater. Because harvests continued for more than 20 years, it is likely that bobcat abundance continued to decline.

Stricter harvest regulations (including a closed season in New Hampshire beginning in 1989) likely contributed to a rebound in bobcat populations as evidenced by a four-fold increase in N_E in New Hampshire and generally robust N_E across the NER. We found a bottleneck in the contemporary NER's Eastern subpopulation. Bobcats are relatively new arrivals in the Seacoast area of New Hampshire (Litvaitis et al. 2006), which corresponds to the location of the Eastern subpopulation. Additionally, by 2010 this area had received most of the human population influx in the state (U.S. Census Bureau 2018), is highly developed, and contains the state's highest road densities (Litvaitis et al. 2015). Human-modified landscapes represent novel habitats that are exploited by bobcats (Tigas et al. 2002; Riley et al. 2003, 2010; Ordeñana et al. 2010), hence it is likely that the observed bottleneck in this subpopulation is due to a founder effect.

Our study showed that bobcats in the NER have experienced a reduction in genetic diversity when comparing historic and contemporary time periods, likely due to range expansion dynamic and a recent population bottleneck. We also found evidence that population structure has changed in the past 60 years. Both natural (habitat and community dynamics) and anthropogenic (fragmentation and land use) factors seem to contribute to subpopulation structure. However, some of the structure of the contemporary landscape remains cryptic. Specifically, there are divisions among subpopulations that do not correspond to obvious natural barriers. Likewise, some major highways seem to be effective barriers whereas others are not. A more detailed, fine-scale analysis of bobcat behavior and habitat use, including the differences

between home range versus dispersal habitat, may help resolve these questions and aid in identifying where specific actions (e.g., a wildlife underpass) may ameliorate the effects of anthropogenic barriers (Baigas et al. 2017). Although there are likely species-specific differences in what is a barrier to daily movements or juvenile dispersal, bobcats may be a useful model organism to investigate how wide-ranging species are affected by landscape fragmentation (Litvaitis et al. 2015). Finally, our study highlights the benefits of a historical perspective in interpreting contemporary population genetic data. Our conclusions from contemporary data may have been very different without knowledge of patterns in recent history. The historical dataset allowed for greater inference into present population genetic patterns and the trajectory of bobcats in New England.

CHAPTER II

TEMPORAL PATTERNS OF DIET SPECIALIZATION IN BOBCATS (*Lynx rufus*)

Introduction

Bobcats (*Lynx rufus*) in the New England region (NER) present a unique system to study anthropogenic impacts on trophic dynamics. In the last 70 years, they have experienced drastic changes in abundance and land use patterns. The population was subjected to intense harvest pressure and habitat loss in the early and mid 20th century which nearly led to their extirpation in New Hampshire (Litvaitis et al. 2006). Despite a sharp increase in human population (Johnson 2012) and developed landscapes (Martinuzzi et al. 2015), there is evidence that conservation efforts have led to increasing bobcat abundance (Roberts and Crimmins 2010; Broman 2012; Mahard et al. 2016). Harvest numbers have risen steadily across the NER in the last decade (Vermont Fish and Wildlife Department, unpublished harvest data; Quebec Ministry of Forests, Wildlife and Parks, unpublished harvest data). Currently, New Hampshire does not have a bobcat harvest but the number of bobcat sightings in the state has risen even in highly developed areas.

A diet shift driven by land use changes may play a role in the resurgence of bobcats in the NER (Prange et al. 2003; Nelson et al. 2007). Bobcats are considered a generalist species because their geographic range spans many different ecoregions and they can occupy many different habitats (Hansen 2007). Theoretically, the diet of a habitat generalist reflects the prey community in their home range. Analysis of historic bobcat stomach contents in the NER suggests they were heavily dependent on lagomorphs, but other sources of prey significantly

contributed to the diet (Hamilton and Hunter 1939, Litvaitis et al. 1984, 2006, Dibello et al. 1990).

Prey availability can be a substantial factor in habitat selection (Godbois et al. 2003), and land cover can influence both the available prey community and habitat (Reed et al. 2017; Parsons et al. 2018). A historic legacy of farm abandonment and forest regrowth was evident during much of the 20th century in the NER (Litvaitis et al. 2006). An abundance of early successional habitat in the early and middle parts of the century followed by forest growth and maturation in the late 1900s likely influenced the bobcat diet. Additionally, the latter time period coincided with extensive mid- to low-intensity development. Bobcats may preferentially select for developed landscapes if the benefits of human-subsidized prey outweigh the risks associated with an increased human footprint in their territory (i.e., synurbization; Luniak 2004). For example, turkeys (*Meleagris gallopavo*) can flourish in agricultural areas due to increased availability of food (e.g., corn; Pollentier et al 2017) and in some areas of New England may be a significant and novel resource for contemporary bobcats. They were absent from the NER in the 1960s but are now widespread and abundant throughout the region (Walski 2015). Availability and use of such subsidies can have significant impacts on behavioral and population traits (Newsome et al. 2015b).

Stable isotope analysis (SIA) can effectively provide a record of an animal's diet (Ben-David and Flaherty 2012). The ratio of heavy to light isotopes (e.g., ^{13}C:^{12}C, or when in relation to a standard, $\delta^{13}C$) naturally varies in plant and animal tissues. This isotopic ratio is predictably incorporated into metabolically active tissues of consumers, including hair and bone. Knowledge of isotopic ratios in a predator and its prey allows for the estimation of diet breadth (Svanbäck et al. 2015), composition (McFadden et al. 2006; Schwartz et al. 2014), and origin (Newsome et al.

2015a). Human influences on the landscape, especially supplemental feeding of wildlife species, can lead to significant changes in carbon and nitrogen isotopic ratios of animals. Generally, human activities increase the availability of C_4 plant-based foods for wildlife. C_4 plants are non-native to the NER and have a significantly higher $\delta^{13}C$ value (Cerling et al. 1997; Newsome et al. 2015a). Similarly, $\delta^{15}N$ changes by the proportion of animal protein consumed (Kelly and Martínez del Rio 2010).

To understand how human land use influences bobcat foraging ecology in the NER, I used SIA to explore the bobcat diet during historic (1952-1964) and a contemporary (2009-2017) time periods. I calculated trophic and tissue discrimination factors for bobcats based on bone and hair samples. While both represent relatively long-term averages of diet, turnover rates in hair range from days to months (Ayliffe et al. 2004), whereas bone integrates dietary signals from months to years (Chisholm et al. 1983; Rucklidge et al. 1992). I compared diet composition and isotopic niche breadth across a period of land use change in the region to test whether the bobcat diet has changed between time periods and if those changes are driven by land use or prey choice in a generalist predator. If land use changes are the primary driver of diet, yearly variation would be negligible compared to changes between time periods. However, if bobcats respond more to smaller-scale changes in the prey community, the diet will exhibit high variability within time periods. I speculated that annual variation would be minimal compared to the difference in diet between time periods.

Materials and Methods

Study area

I explored bobcat diets across New Hampshire and Vermont from 1952-1964 and a 2009-2017. Between those periods, the region underwent a drastic change in land use and land cover.

There was an abundance of forest clearing for agricultural and pastoral use in the 1800s, followed by forest regrowth as those lands were abandoned from 1880-1930 (Litvaitis 1993). Hence, the historic NER had an abundance of mid-successional woodlands interspersed with wetland and scrub/shrub habitat. The historic period predates interstate highways and major urban development. By the contemporary sampling period, four interstates had been built across the study area, and the human population had increased more than twofold. Land cover is still dominated by second-growth forests with widespread low intensity development. The Champlain Valley in western Vermont represents a heavily used agricultural area. Urban development is greatest in southeastern New Hampshire, but low-intensity exurban development is widespread. An average of 38% of the land area and 75% of the human population lies within the wildland-urban interface, both of which are much higher than national averages (10% and 32%, respectively; Martinuzzi et al. 2015).

Sample collection and preparation

My source for bobcat samples varied by state and time period. I collected contemporary hair and bone samples (N = 97) in Vermont from legally harvested bobcats in collaboration with the Vermont Fish and Wildlife Department. Contemporary New Hampshire hair and bone samples (N = 54) were collected from vehicle mortalities, incidental traps, and nuisance animals in collaboration with New Hampshire Fish and Game. The male:female ratio of contemporary samples was 1.17. Historic samples are exclusively bone from New Hampshire and come from a skull collection housed at the University of New Hampshire (N = 120, male:female ratio = 0.94). Skulls were collected between 1952 and 1964 from bobcats turned in for bounty payment (C. Stevens, unpublished data). Prey hairs from across New Hampshire and Vermont (Table 2-1) were sampled from collections at the University of New Hampshire and University of

Massachusetts, vehicle mortalities, animals harvested by hunters and trappers, or as part of separate studies on rodents (Stephens 2018) and lagomorphs (Bauer 2018).

I compared the weight of adult (age 2 or older) bobcats in New Hampshire between 1952 and 1964 to those from 2009-2017. Hunter-harvested bobcats (i.e., those with the pelt removed) were not included in this analysis. Because weight may fluctuate throughout the year, I controlled for the time of year by ensuring that the proportion of the total number of samples from each month of the year was equal in each time period. Furthermore, to ensure that location was not confounding my analyses, I calculated the mean latitude and longitude of the samples used for each time period. In total, 126 females (101 historic and 25 contemporary) and 124 males (80 historic and 44 contemporary) were included in weight analysis.

I prepared bobcat and prey hairs or feathers for stable isotope analysis following a protocol adapted from O'Connell et al. (2001). I removed vanes from the rachis of each feather and treated them the same as hairs. I cut both into approximately 1 cm segments and washed them to remove any potential lipid contamination from the keratinous hair matrix. All samples were washed for 48h in isopropanol, followed by a second wash in fresh isopropanol for 20 minutes. I dried the samples, then washed them twice in 100% ethanol. Finally, I washed each sample twice in distilled water and dried them in an oven at 55 °C. Bobcat bone collagen was prepared following Crowley et al. (2010). I crushed 50 mg of skull bone into 1-10mm pieces and placed them in 5ml of 0.5M HCl on a shaker for 72 hours. HCl was replaced after 36 hours of incubation. I rinsed each sample five times with distilled water to remove any residue. Lipids were removed by vortexing and soaking bone in a 2:2:1 mixture of chloroform, methanol, and distilled water. I rinsed bones five times with distilled water, dried them in a 55 °C oven, and ground them to a powder in a mortar and pestle.

Stable isotope analysis

Samples were analyzed at the University of New Hampshire Stable Isotope Laboratory (UNH, Durham, NH; www.isotope.unh.edu) using an Elementar Americas Pyrocube elemental analyzer coupled to a GeoVision isotope ratio mass spectrometer. More detailed analytical methods are available in Appendix A. Here I report isotope ratios ($\delta^{13}C$ and $\delta^{15}N$) as parts per thousand (‰) and expressed in delta notation where

$$\delta^{13}C = \left(\frac{\frac{^{13}C_{sample}}{^{12}C_{sample}}}{\frac{^{13}C_{standard}}{^{12}C_{standard}}} - 1 \right) \times 1000$$

To account for temporal and tissue differences in the dataset, I made a number of adjustments to the data. Environmental $\delta^{13}C$ has exhibited a significant and steady decline since the industrial revolution due to the influx of depleted carbon from the burning of fossil fuels (i.e., the Suess Effect; Dean et al. 2014; Keeling 1979). To prevent this global environmental signal from masking a trophic signal, animal diet studies should adjust $\delta^{13}C$ values based on year of sampling and known rates of environmental $\delta^{13}C$ depletion (Chamberlain et al. 2005; Misarti et al. 2009; Szteren et al. 2018). I normalized all $\delta^{13}C$ values to the most recent sampling year (2017) by adding a correction factor calculated from published atmospheric $\delta^{13}C$ data and linearly extrapolated to account for the most recent years (McCarroll and Loader 2004).

Because I sampled bone and hair from bobcats and isotope ratios can vary between tissue types in the same individual, I calculated a tissue discrimination factor using samples of both tissue types from the same individual (N = 4). To directly compare $\delta^{13}C$ from bone and hair, I

added this discrimination factor to bone samples. Because isotope ratios systematically vary between consumer tissues and their diet, I calculated a trophic discrimination factor for use in mixing models by using captive bobcats with known diets. The diet consisted of whole rodents and a commercial carnivore food (Toronto Feline Diet). I used hair samples from three bobcats housed at Squam Lake Natural Science Center (Holderness, NH) along with samples of their diet (N = 4) and relative proportions of each source in the diet. Lastly, because trophic discrimination was based on muscle of prey species relative to bobcat hair and wild prey samples were hair, I calculated a discrimination factor for prey muscle to prey hair using small mammal samples for which both tissue types were available (N = 5).

I tested for differences in isotope ratios by age class, sex, season, time period, and, for hair samples, the body location sampled using univariate t-tests in JMP (SAS Institute Inc., Cary, NC). Isotope ratios in hair represent average diet in the days and months leading up to hair formation and growth (Kelly 2000; Ayliffe et al. 2004). Bobcats molt twice per year, hence samples collected from December through March represent diet during the fall molting period, and those sampled in April through November represent diet in the spring molting period (see chapter 3 for more information on timing of molt). I also tested for an influence of individual weight and year (within time periods) using linear regression in JMP. Bobcats harvested in Vermont were weighed without the pelt, hence I added a correction factor to account for the weight of the pelt (10% of body weight; C. Stevens, unpublished necropsy data).

I used the R package SIBER to test for differences in niche breadth between time periods and sexes. SIBER calculates maximum likelihood ellipses around grouped data in isotope space using Markov Chain Monte Carlo simulation in a Bayesian framework that is robust to differences in sample size and variance between groups (Jackson et al. 2011). The standardized

ellipse area is an estimate of the niche breadth, in this case representative of the range of resources bobcats use. To calculate ellipses, I ran 1,000,000 iterations with a burnin of 100,000 and thinned by 90.

I used the R package MixSIAR (Stock et al. 2018) to estimate the proportion of prey items in bobcat diets. MixSIAR uses source (prey) and consumer (bobcat) isotopic data in a Bayesian framework to calculate the proportion of each source in the diet of a consumer. Bobcats routinely prey on a large number of species (Fritts and Sealander 1978; Litvaitis et al. 1984, 2006; Rose and Prange 2015; Newbury and Hodges 2018). I collected data from 22 potential prey species, however some prey species have a similar diet and are difficult to isotopically distinguish from one another. Beaver (*Castor canadensis*), muskrat (*Ondatra zibethicus*), and ruffed grouse (*Bonasa umbellus*), were excluded from subsequent analyses because they have been shown in stomach content analyses to be rare in the bobcat diet (Rose and Prange 2015) and had similar but not identical isotope ratios to more common bobcat prey. Thus, I included 19 potential prey species in my analyses and grouped them into eight guilds (Table 2-1) based on their location in isospace. Turkeys (*Meleagris gallopavo*) were extirpated from the study area prior to the historical period but a successful reintroduction program began in 1969 (Walski 2015). Hence turkeys were not represented in historical analyses but were included in the contemporary period. Turkey $\delta^{13}C$ values were bimodally distributed across a range of about 9 ‰ (see Appendix G). I divided contemporary turkeys into two guilds (turkeys and subsidized turkeys) using hierarchical clustering on $\delta^{13}C$ values in JMP. For MixSIAR analyses, I ran 3 chains of 1,000,000 iterations each with a burnin of 500,000 and thinned by 500. I used informative priors based on analyses of stomach contents for historic (Litvaitis et al. 2006) and contemporary (Rose and Prange 2015) bobcats. I report the posterior estimates (mean ± SD) for

the proportion of each prey guild in bobcat diet by sex for each time period. I also report the posterior estimates individually for each year in which at least 10 bobcats were sampled.

Table 2-1 Potential bobcat prey species analyzed in isotopic mixing models. Nineteen prey species were grouped into eight guilds based on isotopic similarity. Samples came from harvested animals, vehicle mortalities, and museum specimens housed at the University of New Hampshire and University of Massachusetts.

Common name	**Scientific name**	**N** Hist., Contemp.	**Isotopic Guild**	**N** Hist., Contemp.
Opossum	*Didelphis virginiana*	5, 4	Carnivores	17, 12
Raccoon	*Procyon lotor*	3, 6		
Striped skunk	*Mephitis mephitis*	3, 1		
Stoat	*Mustela erminea*	3, 1		
Mink	*Neovison vison*	3, 0		
Cottontail	*Sylvilagus* spp.	7, 4	Lagomorphs	12, 19
Snowshoe hare	*Lepus americanus*	5, 15		
White-tailed deer	*Odocoileus virginianus*	1, 16	Large mammals	11, 20
Woodchuck	*Marmota monax*	7, 0		
Porcupine	*Erethizon dorsatum*	3, 4		
Voles	*Myodes gapperi, Microtus* spp.	11, 0	Small mammals	31, 97
Shrews	*Blarina brevicauda, Sorex* spp.	7, 1		
White-footed mouse	*Peromyscus leucopus*	13, 96		
Eastern chipmunk	*Tamias striatus*	5, 22	Squirrels	16, 33
Gray squirrel	*Sciurus carolinensis*	6, 5		
Flying squirrel	*Glaucomys* spp.	5, 6		
Chicken	*Gallus gallus domesticus*	0, 19	Poultry	5, 19
Pheasant	*Phasianus colchicus*	5, 0		
Turkey	*Meleagris gallopavo*	0, 17	Turkeys	0, 17
Turkey	*Meleagris gallopavo*	0, 22	Subsidized turkeys	0, 22

Results

I found a significant increase in the adult weight of bobcats in New Hampshire. The increase was more pronounced in males than females, with individuals gaining an average of 2.11 kg and 1.14 kg, respectively (Fig. 2-1).

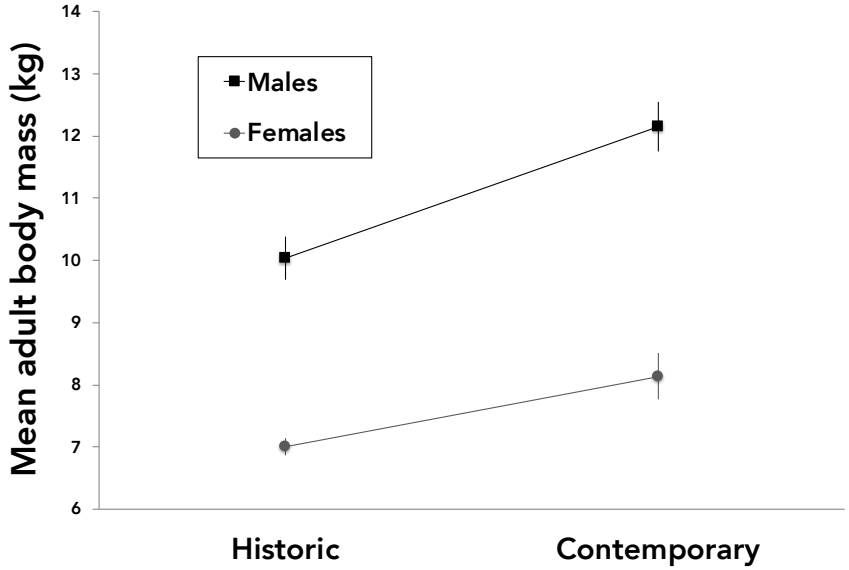


Figure 2-1 Mean weight of adult bobcats has increased between historic (1952-1964) and contemporary (2009-2017) sampling periods in New England. T-tests were significant for both males ($t = 3.98$, $P < 0.001$) and females ($t = 2.83$, $P = 0.008$). Error bars represent standard error.

I analyzed C and N isotope ratios in 154 contemporary bobcat samples (M:F ratio = 1.28) and in 122 historic samples (M:F ratio = 0.94; Fig. 2-2). Because I analyzed different tissues from each time period, I calculated a tissue discrimination factor between bobcat bone and hair (N = 4) and used it to adjust bone isotope ratios. I calculated trophic discrimination factors using consumer and source isotope ratios from captive bobcats (N = 3) with a known diet and applied them to the wild samples. Discrimination values applied in this study are shown in Table 2-2. Neither isotope ratio was affected by age class ($P = 0.432$ and 0.735, respectively), season ($P = 0.561$ and 0.345, respectively), or body location sampled ($P = 0.170$ and 0.158, respectively). There were differences between sexes and time periods. Males had greater $\delta^{13}C$ ($P = 0.048$) and $\delta^{15}N$ ($P < 0.001$) than females. Bobcats sampled from the contemporary period had greater $\delta^{13}C$ ($P < 0.001$) than they did historically, but no difference was found in $\delta^{15}N$ ($P = 0.757$). $\delta^{15}N$

increased with bobcat weight, but only for males in the fall (P = 0.018). There was no discernable trend across years within time periods. Data for categorical comparisons is shown in Appendix H.

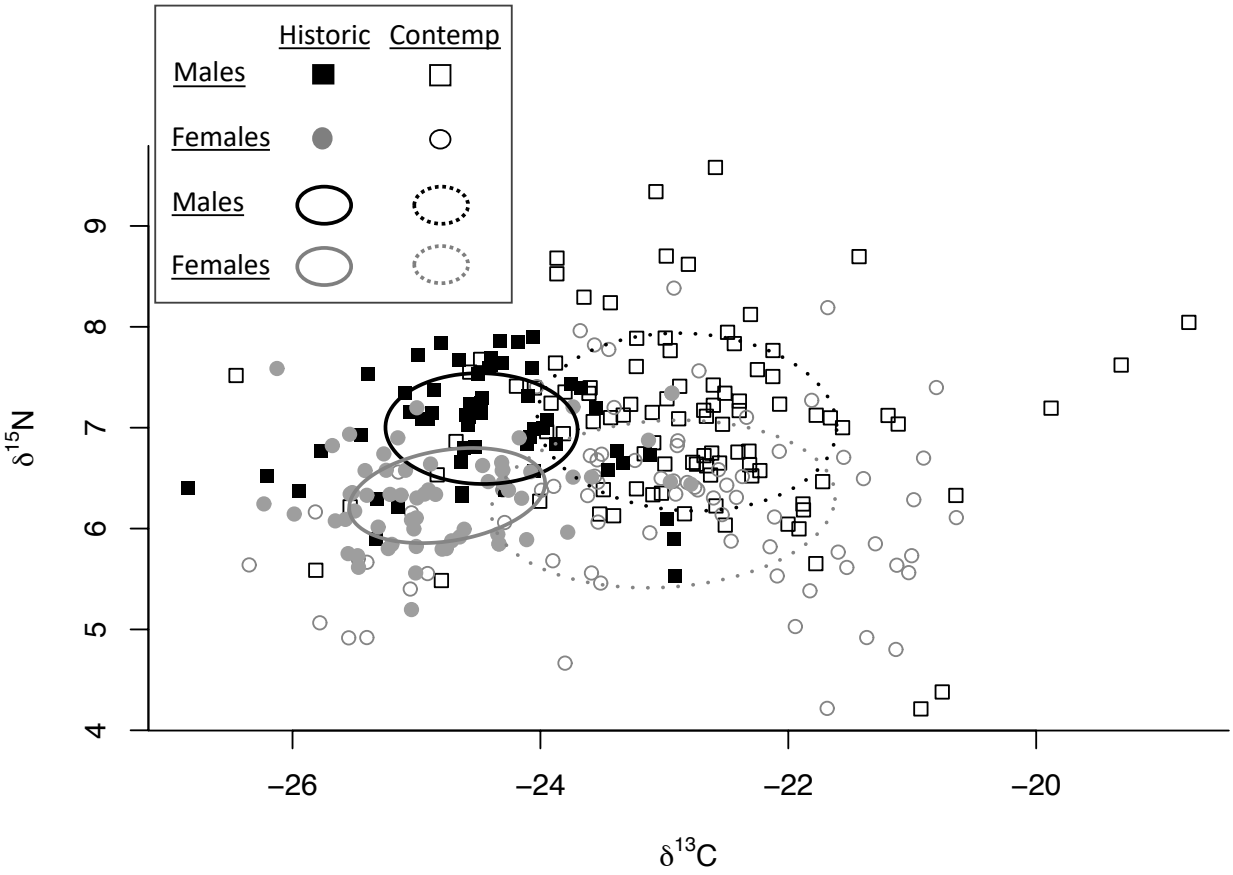


Figure 2-2 Bobcat isotope data from across New England grouped by time period (contemp = 2009-2017, historic = 1952-1964) and sex. Maximum likelihood ellipses were calculated in the R package SIBER. Units are in parts per thousand (‰). Mean values (± 1 SD) for each group are as follows: Historic males $\delta^{13}C$ = -24.482 ± 0.786, $\delta^{15}N$ = 6.987 ± 0.558; Historic females $\delta^{13}C$ = -24.769 ± 0.798, $\delta^{15}N$ = 6.326 ± 0.470; Contemporary males $\delta^{13}C$ = -22.791 ± 1.269, $\delta^{15}N$ = 7.039 ± 0.891; Contemporary females $\delta^{13}C$ = -22.954 ± 1.341, $\delta^{15}N$ = 6.274 ± 0.836;

Table 2-2 Discrimination factors calculated from bobcats in this study. Tissue discrimination (bone-hair and muscle-hair) was calculated using bobcats or diet items for which both tissue types were available. Bone values represent only the organic (collagen) portion of bone. Trophic discrimination (prey-bobcat) was calculated using captive bobcats with known diets.

	N	$\Delta^{13}C$	SD	$\Delta^{15}N$	SD
Bobcat bone - Bobcat hair	4	1.296	0.520	0.136	0.534
Prey muscle - Bobcat hair	7	-2.339	0.369	-3.596	0.466
Prey muscle - Prey hair	5	-1.218	1.826	0.237	0.686

SIBER analyses indicated variation in $\delta^{15}N$ between sexes in both time periods and an increase in $\delta^{13}C$ between periods for both sexes. Overlap between the sexes increased from 66.1% historically to 74.3% in the contemporary period. Standard ellipse area, an indicator of niche breadth, was roughly three times larger in contemporary bobcats than historic (Fig. 2-3).

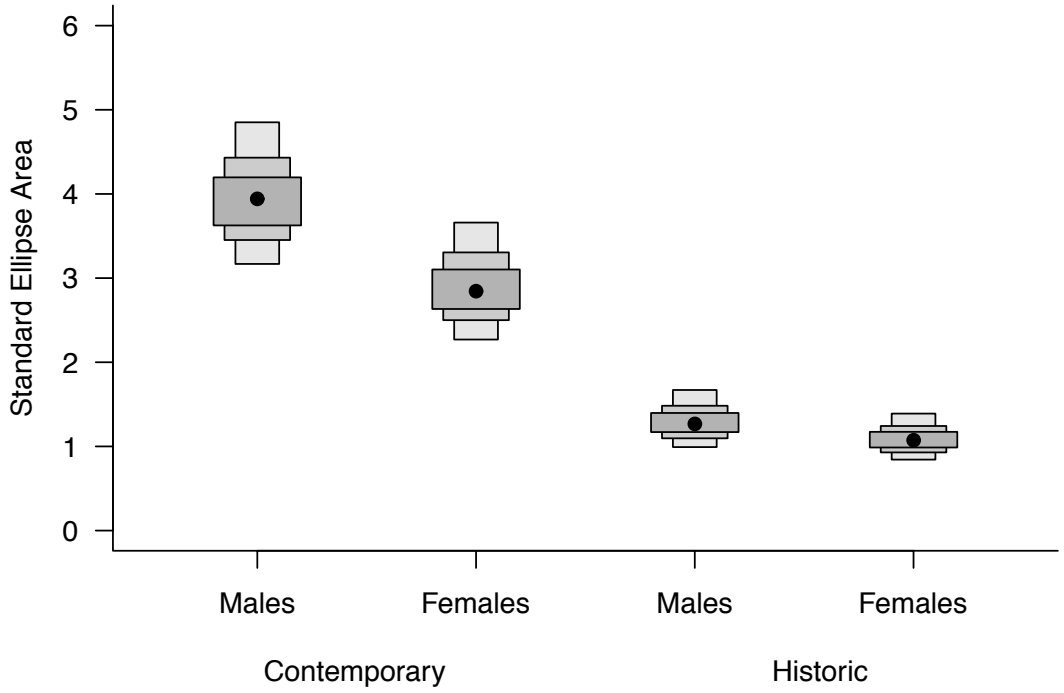


Figure 2-3 Standardized ellipse area as calculated in SIBER, a proxy for trophic niche, were larger in contemporary bobcats in New England. Male ellipses were slightly larger than females in both the contemporary and historic time periods. Units are in parts per thousand squared ($‰^2$).

Bobcat isotope data for each time period fell within a bounding polygon of prey guild mean values (± 1 SD) after correction for trophic discrimination (Fig. 2-4). Historical diet overwhelmingly consisted of lagomorphs, followed by large mammals, small mammals, and squirrels (Fig. 2-5). The carnivore and poultry guilds made up insignificant proportions of bobcat diets during both time periods, as did both turkey guilds in the contemporary period. As expected based on the area of SIBER ellipses, the contemporary diet was more varied and evenly distributed across squirrels, large and small mammals, and lagomorphs. Analysis between the sexes across years showed that females exploited lagomorphs significantly more than males. There was minimal yearly variation, and both sexes responded similarly to yearly fluctuations.

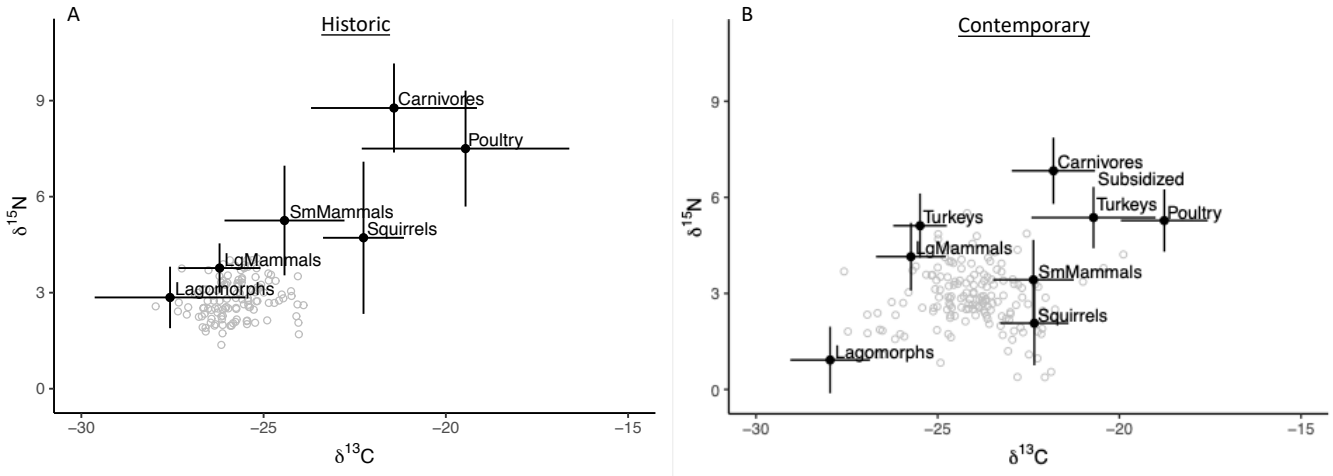


Figure 2-4 Bobcat (gray circles) and prey guild isotope values (black circles; mean ± 1 SD) used in mixing models to determine bobcat diet proportions in New England. Historic data are shown in panel A and contemporary data are in panel B. Units are in parts per thousand (‰).

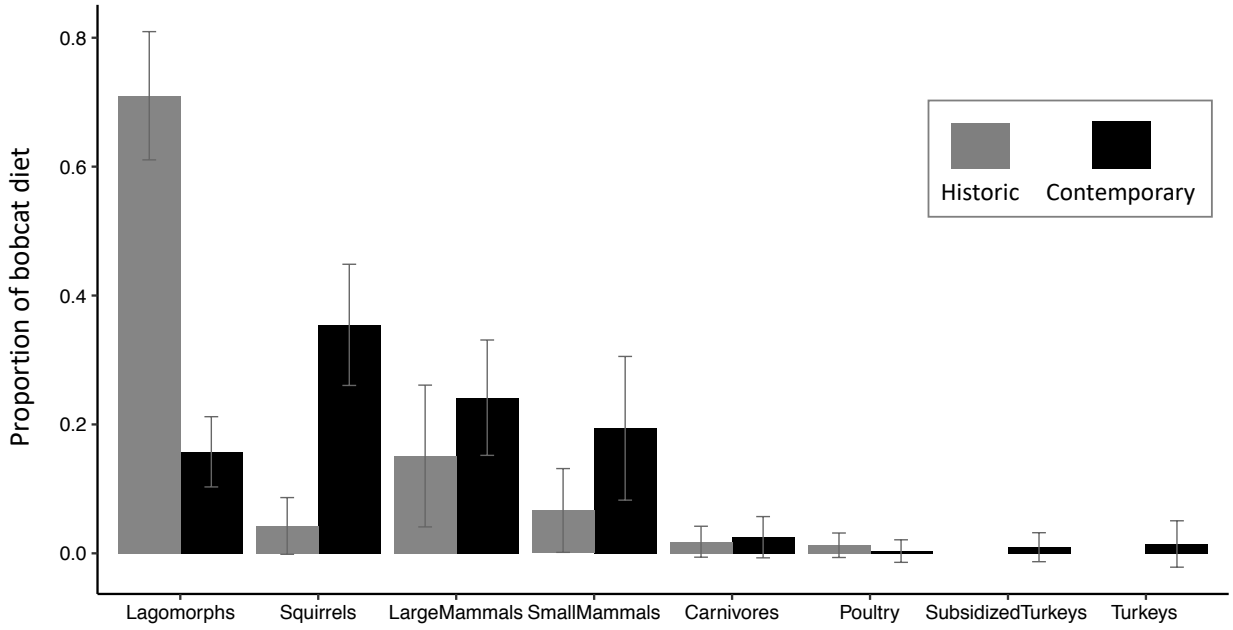


Figure 2-5 Results of mixing models show a shift in the major prey of bobcats between historic (gray bars) and contemporary (black bars) time periods in New England. Results also show a broader and more even diet in contemporary bobcats.

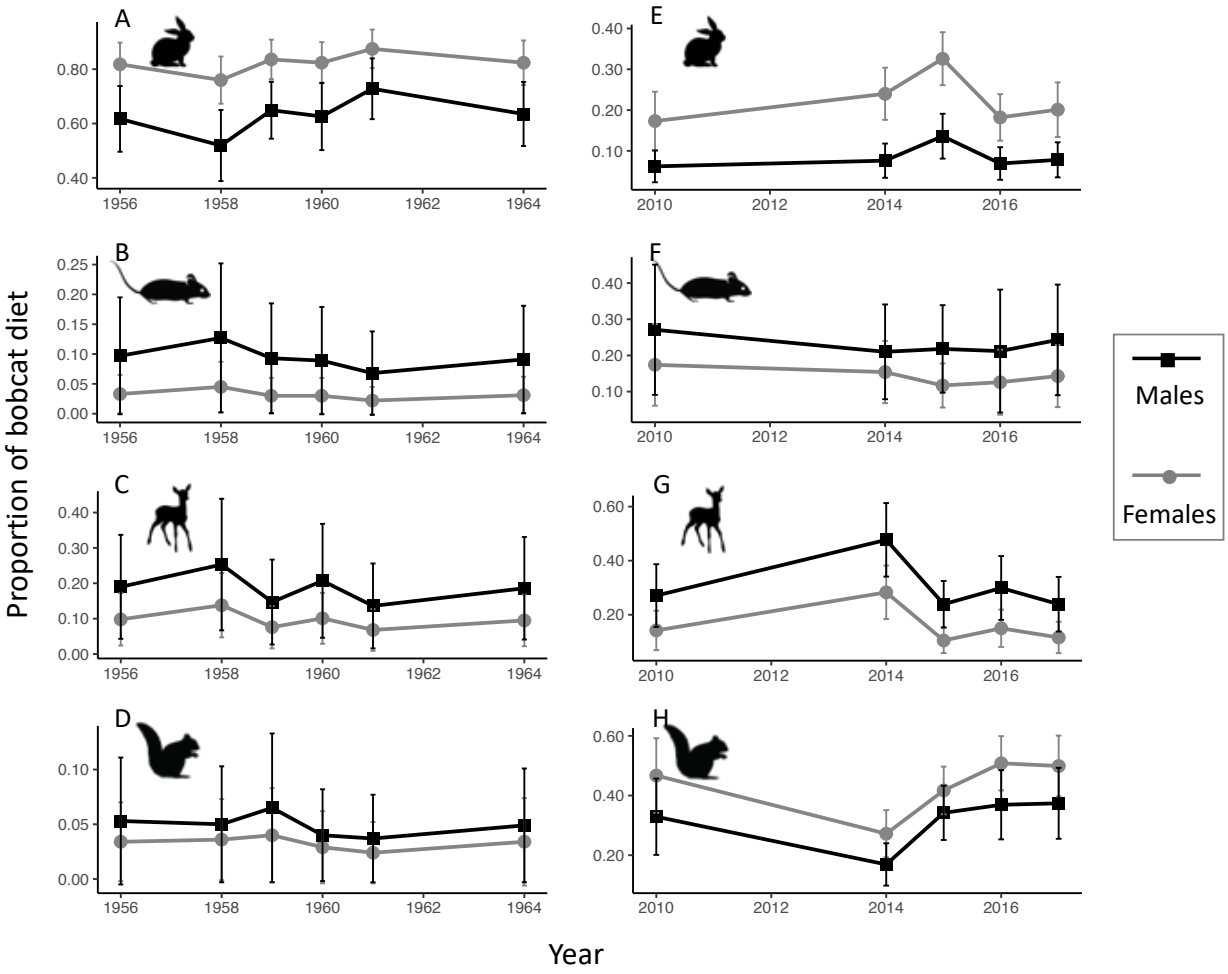


Figure 2-6 Yearly variation in proportion of bobcat diet for important prey guilds during the historical (A-D) and contemporary (E-H) time periods in New England. The scale of the Y-axis varies in each panel so as to show the data as clearly as possible.

Discussion

I found an increase in weight of bobcats in New Hampshire between the historic and contemporary time periods while controlling for sex, age class, location, and month of sampling. The mean historic sample location was 49 km NNE of the mean contemporary location. New Hampshire is home to two morphologically distinct subspecies of bobcat with *L. rufus rufus* inhabiting the southern portion of the state and *L. rufus gigas* in the north (Reding et al. 2012). *L. r. gigas* is the largest subspecies, hence the more northern center of sampling in the historic

population may skew individual weights upward. Nonetheless, results show an average increase in contemporary weight of 1.14 kg and 2.11 kg for females and males respectively (Fig. 2-1). Hence, a significant change in diet content or prey availability likely occurred in the population. I also found evidence that yearly variation in diets was negligible compared to differences between the historic and contemporary time period. This suggests the bobcat diet is more sensitive to long-term land use changes than fluctuations in prey availability.

The tissue discrimination factors calculated in this study aligned well with published values. A study in humans calculated $\Delta^{13}C_{(bone\text{-}hair)}$ to be 1.41 ± 0.45 and $\Delta^{15}N_{(bone\text{-}hair)}$ to be 0.86 ± 0.17 (O'Connell et al. 2001), both of which are similar to my calculated values for bobcats (Table 2-2). The C and N trophic discrimination factors I calculated are very similar to values reported for other carnivores (Roth and Hobson 2000; Newsome et al. 2010; Parng et al. 2014) with one exception. My $\Delta^{13}C_{(prey\ muscle\text{-}bobcat\ hair)}$ was nearly 3‰ lower than what Parng et al. (2014) calculated for bobcat hair. This discrepancy may be due to nutritional content in the diet of bobcats used in this study. The captive bobcat diet consisted of whole rodents (73.3%; C:N = 3.57 ± 0.34) and commercial carnivore feed (26.7%; C:N = 4.90 ± 0.15). The latter is fortified with vitamin and fatty acid supplements, and Newsome (2010) have shown that lipid content in prey items is negatively correlated with $\Delta^{13}C$ values. Hence a lower discrimination may be due to excess fat in the diet of bobcats sampled for this study. Because my values largely agree with those calculated in other studies of carnivores (Roth and Hobson 2000; Newsome et al. 2010; Parng et al. 2014) and favorably align wild bobcat data with prey data in isospace (Fig. 2-4), the use of my $\Delta^{13}C$ values is reasonable.

I found an increase in bobcat $\delta^{13}C$ between historic and contemporary time periods of 1.7 ‰. On average, $\delta^{13}C$ of prey guilds remained relatively constant, increasing by only 0.38 ‰. The

largest change was in the small mammal guild, which increased by 1.98 ‰. Mixing model estimates suggest small mammals were a minor component in the historical bobcat diet (consistent with Litvaitis et al. 1984), thus it is unlikely the trend I saw in bobcats is solely the result of the isotopic ratio change in small mammals. The increased $\delta^{13}C$ likely results from a shift away from lagomorphs as a primary food source (71% of historic diet) to a more evenly distributed diet with squirrels as the leading component (35%). This change may have been driven by differences in land use and bobcat habitat selection between time periods.

Bobcats are commonly viewed as generalist predators that exploit a broad range of resources relative to their availability on the landscape (Fritts and Sealander 1978; Litvaitis et al. 1984; Rose and Prange 2015; Newbury and Hodges 2018). However, some studies suggest bobcats do not always conform to a generalist foraging model, but instead act as pseudo-specialist foragers equally efficient as true specialists in exploiting a given resource (Godbois et al. 2003; Peers et al. 2012; López-Vidal et al. 2014). My data support the idea of bobcats as facultative generalists that have a broad fundamental dietary niche (range of all possible resources), but often exhibit a much narrower realized niche (i.e., the actual resources used; Shipley et al. 2009). The standard ellipse areas, a proxy for realized niche (Fig. 2-3), were about three times larger for contemporary than historic bobcats. The breadth of the realized niche may depend on prey abundance, habitat selection, nutritional and metabolic needs, or capture and handling costs associated with prey-specific traits (Potter et al. 2018).

My mixing model results indicate historic bobcats were lagomorph specialists, whereas contemporary bobcats have a much larger realized dietary niche (Fig 2-5). These data are supported by an analysis of bobcat stomach contents in New Hampshire in the 1950s, which also show lagomorphs as a dominant prey species (Litvaitis et al. 2008), though not nearly as

dominant as my results suggest. While robust data on long-term regional abundance of my prey guilds are sparse, their populations have likely remained more constant region-wide than the long-term change in bobcat's diet would suggest. Whereas New England cottontail populations have drastically declined between time periods, Eastern cottontail populations have increased to fill a similar niche, though not quite in equal abundance and distribution (Probert and Litvaitis 1996; Litvaitis et al. 2008). White-tailed deer populations can greatly fluctuate year to year, but of the five highest harvest years on record in New Hampshire, two of them occurred during the historic time period and two during the contemporary time period (New Hampshire Fish and Game Department 2017). Abundance of members of the squirrel guild is largely tied to the amount and configuration of forest patches (Williamson 1983; Fisher and Merriam 2000).

While the landscape in the NER has undergone major changes in the last two centuries (i.e., land clearing for agriculture and large-scale farm abandonment), those changes have been relatively minor since this study's historic time period. The major differences in land use are the maturation of young forests and the region-wide increase in development. The former may contribute to greater squirrel guild abundance in aging forest patches (Fisher and Merriam 2000) and a reduction in the cottontail's preferred early successional habitat (Litvaitis et al. 2008). The latter resulted from a 115% increase in the human population in the NER between time periods (U.S. Census Bureau 2018). Much of the development associated with this population increase was low-density suburban or exurban tracts that encroached on what had recently been continuous habitat (Martinuzzi et al. 2015). This type of land use can increase habitat diversity, concentrate potential prey species (Moss et al. 2016; Parsons et al. 2018), and reduce intra- and inter-species competition (Bateman and Fleming 2012; Smith et al. 2018). Additionally, low-density development provides species in the squirrel guild with abundant food, shelter, and

protection from predators who may be more wary of humans (Benson 2013). Consequently, the change in land use between time periods likely increased resource availability and decreased competition which allowed bobcats to inhabit a larger fundamental niche.

If prey abundance alone was responsible for bobcat diet shifts, I would expect variation in the bobcat diet between years within a time period. Fluctuations in prey species abundance such as snowshoe hare cycles (Elton and Nicholson 1942) or increases in small mammals during tree masting years (Jensen et al. 2012; Stephens 2018) are common at scales that would fit within time periods, yet bobcat diet was relatively stable. The change in diet between time periods combined with the lack of significant yearly variation in bobcat diet within time periods (Fig. 2-6) suggests other processes are more influential than natural fluctuations in prey abundance. Other studies have shown similar changes in the carnivore diet in relation to human land use. Cancio et al. (2017) found diet diversity of red fox was greatest at intermediate levels of human land use. Similarly, anthropogenic land use has been shown to significantly alter carnivore diet by changing the prey community (Farias and Kittlein 2008).

Nutrient content of prey can be a strong driver of prey choice in generalist predators (Erlenbach et al. 2014; Kohl et al. 2015). Carnivores, especially obligate carnivores, typically select for prey that optimize the intake of protein (Hewson-Hughes et al. 2011). Lagomorphs have the highest protein composition of any common bobcat prey item; however, they also have the lowest fat content, total energy, and digestibility (Powers et al. 1989). Despite a preference for protein-rich diets, lipids and carbohydrates are also important in carnivore diet and individuals will compensate for deficiencies when given the opportunity (Jensen et al. 2014). Hence, it is not likely that bobcats would consistently select a lipid-poor food such as

lagomorphs in the presence of more diverse prey unless encounter rates with that prey were disproportionately high (Scheel 1993).

δ^{15}N values were nearly identical between time periods, but in both periods, males were 0.71 ‰ enriched compared to female bobcats. It is likely the result of females being more heavily dependent on lagomorphs than males. When averaged across prey species, the data showed a decrease in δ^{15}N of 1.53 ± 1.19 ‰ between time periods (Fig. 2-7). Several studies have noted a depletion in environmental δ^{15}N values during the 20th century, attributable to the burning of fossil fuels and the application of synthetic fertilizers (Hastings et al. 2009; Holtgrieve et al. 2011; Felix and Elliott 2013; Dean et al. 2014). Hence the depletion I observed in prey species could be reflective of a change in the environmental baseline rather than a true trophic change. Although many studies apply a correction to δ^{13}C values to account for an environmental depletion (Chamberlain et al. 2005; Misarti et al. 2009; Szteren et al. 2018), to my knowledge no isotopic study of animal diets has corrected for the "noise" caused by environmental δ^{15}N depletion despite the possibility of an altered trophic "signal". I employed a *post hoc* correction to prey δ^{15}N data similar to the Suess correction I used for δ^{13}C values (see Methods). I adjusted all historic prey samples to 2017 baseline δ^{15}N values using the equation derived by Holtgrieve et al. (2011) to describe the 20th century δ^{15}N depletion in sediments across 25 North American lakes:

$$\delta^{15}\mathrm{N}(T_i) = C_0 - C_0^{kT_i} + 1$$

where C_0 is the pre-industrial δ^{15}N, k is a rate constant, and T_i is the number of years between the sample year and 1895. After correction, the difference between historical and contemporary prey

$\delta^{15}N$ was 0.34 ± 1.12 (Fig. 2-7). Interestingly, there was very little difference between unadjusted $\delta^{15}N$ of bobcats between time periods but applying the correction would result in an approximately 1.87 ‰ trophic enrichment in contemporary bobcats.

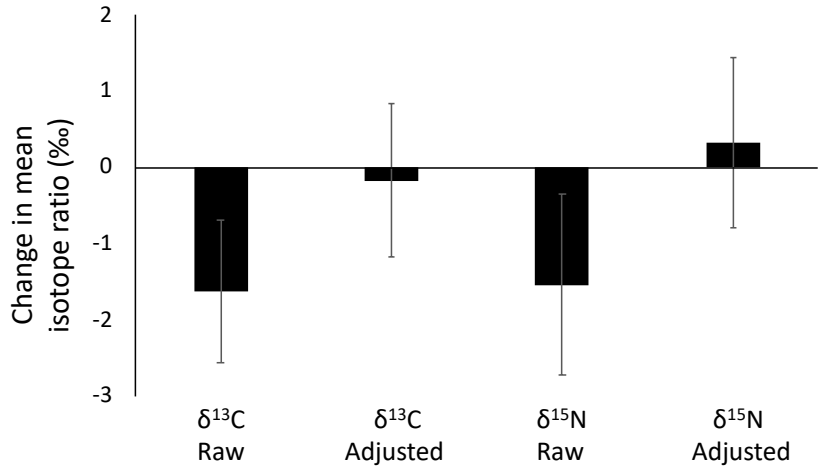


Figure 2-7 Difference in mean hair isotope values between historic and contemporary time periods, averaged across the 9 prey species with multiple samples in each period. Raw values include no correction. Adjusted $\delta^{13}C$ values are corrected for the Suess effect using atmospheric $\delta^{13}C$ data (McCarroll and Loader 2004). Adjusted $\delta^{15}N$ values are corrected for atmospheric changes using a temporal model of $\delta^{15}N$ depletion from sediment cores (Holtgrieve et al. 2011).

I found a bimodal distribution of $\delta^{13}C$ values for turkeys in which 56.4% of individuals clustered in the higher subsidized group (mean = -20.711, SD = 1.708) and 43.6% clustered in the lower group (mean = -25.486, SD = 0.736). This may be the result of some flocks specializing on agricultural subsidies (e.g., livestock feed corn). The geographic mean location for the two turkey groups were separated by only 62 km which is well within the standard deviation of both X and Y coordinates. This suggests that in total, turkeys are distributed relatively equally across all of the study area and across a gradient of anthropogenic to natural landscapes. Turkey reintroduction efforts that began in the late 20th century have been very

successful and turkey habitat preferences overlap with those of bobcats (Walski 2015; Reed et al. 2016). Furthermore, the resurgence in bobcat populations (Litvaitis et al. 2006; Broman 2012) largely coincided with that of turkeys (Walski 2015). Nonetheless, contemporary bobcats had a very low proportion of both turkey groups in their diet. This may be a result of interference competition in which coyotes exclude bobcats from preying on turkeys, especially if other potential prey are abundant (Wilson et al. 2010). Nielsen et al. (2018) found that in areas where both carnivore species were sympatric with turkeys – which is true throughout the NER – coyote presence was correlated with greater nest success and survival. Additionally, turkeys exhibit substantial anti-predator behaviors such as flocking and mobbing (Spears et al. 2003). The costs associated with capture and handling of turkeys may deter bobcats from regular predation attempts. Because we used isotopes in hair to determine diet in the contemporary period, our study is limited to the diet during active hair growth in the fall and spring molting periods (November and March, respectively; see chapter 3). Thus we cannot rule out turkeys as a seasonally important food source for bobcats, particularly in winter when other prey are scarcer. Bobcats have a large degree of plasticity in their diet and have been found to prefer larger prey in winter months (Hamilton and Hunter 1939; Marston 1942; Newbury and Hodges 2018).

Intraguild predation, also known as superpredation, can be a common occurrence in felids (Palomares and Caro 1999; de Oliveira and Pereira 2014). Individual size is typically the deciding factor in intraguild interactions (Wilson et al. 2010; Allen et al. 2016). My carnivore guild included the opossum and members of the placental order Carnivora that are on average smaller than bobcats. Nonetheless, that guild represented an insignificant proportion of the bobcat diet in both time periods. Predation on other members of the carnivore guild may represent an unnecessary risk for bobcats, which likely explains the low diet proportion. Capture

costs associated with intraguild predation for bobcats are often much higher than those associated with smaller prey such as squirrels or small mammals and can include the risk of serious injury or death (Mukherjee and Heithaus 2013). Availability of alternative prey is one of the main drivers of superpredation, hence the lack of predation on other carnivores may be an additional indication of a robust prey base for bobcats in the contemporary NER (Lourenço et al. 2018)

Results of this study suggest that landscape scale changes in land use had a larger impact on the diet of a generalist predator through time than individual or population level processes. I suggest forest maturation and an increase in anthropogenic development led to a subsequent change in habitat selection by bobcats from a historic preference for lagomorph-heavy early-successional habitat to a contemporary preference for suburban/exurban land use. A preference for moderately developed landscapes can benefit mesocarnivores, primarily by increasing the diversity and abundance of prey (Cancio et al. 2017; Lombardi et al. 2017; Parsons et al. 2018). However, living in proximity to humans can also indirectly reduce individual fitness (Riley et al. 2007; Lee et al. 2012; Birnie-Gauvin et al. 2016; Smith et al. 2018). Finding approaches that benefit human-mesopredator coexistence and minimize costs, are critical for long-term conservation efforts in the face of increasing landscape development.

CHAPTER III

RESPONSE OF BOBCAT (*Lynx rufus*) HAIR CORTISOL LEVELS TO LAND USE CHANGE AND CLIMATE

Introduction

Although bobcats are sensitive to development and landscape fragmentation (Crooks 2002; Riley et al. 2003; Ruell et al. 2012), their abundance across their range has increased (Roberts and Crimmins 2010) resulting in more frequent human-bobcat interactions (Ordeñana et al. 2010; Riley et al. 2010; Broman et al. 2014; Mahard et al. 2016). The ecological processes driving increased contact may be informative to species conservation and sustainability efforts by increasing our understanding of habitat preferences across a range of land use. For example, high population densities may force dispersing individuals into suboptimal habitat which may include developed areas. Alternatively, resource supplies in such areas may lead to active selection of developed areas by wildlife. However, if the benefits of anthropogenic resources such as food subsidies and heat island effects are greater than the risks associated with human contact, individuals may select for developed habitat and habituate to human-induced disturbances (i.e., synurbization; Luniak 2004).

Inhabiting anthropogenic landscapes likely impacts the stress physiology of bobcats. Stress is an adaptive response to environmental challenges that can lead to increased fitness but can also have negative physiological effects (Wingfield and Romero 2011). In mammals, perceived stressors activate the hypothalamic-pituitary-adrenal (HPA) axis by increasing systemic concentrations of cortisol, a steroid hormone whose primary function is energy

regulation. Cortisol aids in relieving the stressor (e.g., fight or flight response) and promotes a subsequent return to homeostasis via negative feedback within the HPA axis. Stressors of high intensity or long duration dampen the feedback, resulting in chronically elevated levels of cortisol. Such elevation leads to allostatic overload (McEwen 2005), a state in which individuals show decreased immune function, slowed growth and tissue repair, reduced reproductive capacity, and nutritional deficiencies (Busch and Hayward 2009). These effects can have negative impacts at the individual and population level (Busch and Hayward 2009; Rebolo-Ifrán et al. 2015; Lafferty et al. 2015).

Landscape changes associated with human activities are a major stressor of wildlife populations (Ellis et al. 2012). A measure of physiological indicators across spatial scales can potentially provide insights into the effects of anthropogenic disturbances on the health of individuals and populations. Hair cortisol has been recognized as an indicator of the stress response, including its elevation during prolonged or repeated exposure to stressors. Despite the adaptive nature of the stress response (Boonstra 2013), exposure to chronic stress can (among other effects) result in a decreased immune response, increasing disease susceptibility (Martin 2009) and a reduction in reproductive success, which ultimately will affect population dynamics directly (Romero 2004).

An individual's abiotic environment can also impact physiological parameters. Abnormal temperatures or precipitation patterns can disrupt the adaptive nature of behaviors and traits in consumers and their prey (Millspaugh et al 2001; Lenarz et al. 2009; Mills et al. 2013). Bobcats in New England are at the northern edge of their range, thus are living at the extremes of the species tolerance levels (Hansen 2007). The metabolic demands on bobcats during winter in New England are greater than in other parts of their range (Newbury and Hodges 2019) and may result

in dietary and physiological changes (Hamilton and Hunter 1939; Litvaitis et al. 1986; Newbury and Hodges 2018).

Cortisol is incorporated into growing hair proportionately to systemic levels, providing a temporal record of the hormone level in mammals (Davenport et al. 2006; Macbeth et al. 2010; Terwissen et al. 2014; Mastromonaco et al. 2014; Lafferty et al. 2015). Hair cortisol concentration (HCC) is increasingly used in studies of stress in wildlife species because it has several benefits relative to other methods (e.g., blood, feces, saliva). Hair is relatively easy to collect, can be collected non-invasively, and the cortisol bound in hair is stable for long periods of time (Webb et al. 2010; Dantzer et al. 2014). HCC is less sensitive to acute stressors and natural cortisol fluctuations, such as diel rhythms. Furthermore, it represents a long-term average through the growing phase of the hair. Consequently, high HCC indicates chronic exposure to perceived stressors (Russell et al. 2012). Home ranges of wide-ranging species like the bobcat can encompass many different types of habitat, thus individuals are exposed to a variety of land uses on a regular basis. As such, HCC is a good metric to study landscape-scale stressors at the population level (Mastromonaco et al. 2014).

Cortisol concentrations have been found to vary by age (Cattet et al. 2018) and sex (Lafferty et al. 2015) in some mammalian carnivores, but not in others (Terwissen et al. 2013). Metabolic demands (Harlow et al. 1990) or reproductive cycles (Handa et al. 1994) influence levels seasonally, and body condition (Lyons et al. 2017; Wolf et al. 2018) and food availability (Jenni-Eiermann et al. 2008) correlate negatively with stress hormone concentrations. Furthermore, human land use can affect cortisol levels through animal-human interactions (Ellenberg et al. 2007), habitat alteration via urbanization (Fokidis et al. 2009; Russ et al. 2015) or fragmentation (Millspaugh et al. 2001; Brearley et al. 2012). Developed landscapes tend to be

more heterogeneous and have smaller patch sizes than undeveloped areas (Luck and Wu 2002). They also create ecological communities distinct from those that evolved in natural areas (Kowarik 2011). These novel landscape patterns and persistent unfamiliar stimuli can act as chronic stressors in human-dominated systems. However the response to such stressors is often species and context dependent (Birnie-Gauvin et al. 2016).

Cortisol is integrated into hair only during active hair growth (Russell et al. 2012). Bobcats molt in spring and fall, however details on the timing of the molt are largely unknown. Furbearing species in northern latitudes typically experience a spring molt between January and April and a fall molt between September and December, and each molt may last several weeks (Maurel et al. 1986). HCC in bobcats represents an average of systemic cortisol levels only during the molting period prior to sample collection. Thus, it is a measure of stress during a small portion of time and may not be representative of stress levels throughout an annual cycle. Nonetheless, the molting periods coincide with critical times of the annual cycle – mating season around the spring molt, onset of winter and resource scarcity around the fall molt – hence an understanding of stress levels during the molt has important conservation value.

Understanding how biotic and abiotic habitat factors influence the stress levels of bobcats may aid species conservation and management efforts. I explored organismal and landscape variables that may be associated with molting period hair cortisol concentration in New Hampshire (NH) and Vermont (VT) bobcats. The bobcat population in this study area is recovering from recent lows in abundance during the 1980s and is currently robust across the region (Litvaitis et al. 2006; Broman 2012; Vermont Fish and Wildlife, unpublished harvest data). I explored relationships between HCC and several types of anthropogenic land use, land cover categories preferred by bobcats in their home ranges (third-order habitat selection; Reed et

al 2017), and climatic variables. I predicted that anthropogenic land cover categories would be a better predictor of HCC than undeveloped habitat because of frequent exposure to novel environmental stressors (e.g., contact with humans, pets, roads, noise, etc.). I also predicted a positive correlation between HCC and anthropogenic land use and increased HCC associated with more severe environmental conditions.

Materials and Methods

Study area

My study area encompassed New Hampshire (NH) and Vermont (VT). The major land cover types in both states are deciduous, coniferous, or mixed forests interspersed with early successional habitats and wetlands. The most developed areas are the Seacoast region in southeast NH and to a lesser extent the Lake Champlain coast in northwestern VT. Agriculture is most intensive in the Champlain valley of western VT. Approximately 38% of the land area and 75% of the human population are within the wildland urban interface (WUI; Martinuzzi et al. 2015), defined as areas of development that lie within or near large natural habitat blocks. These percentages are much higher than the national averages of 10% and 32%, respectively.

Sample collection

In collaboration with the Vermont Fish and Wildlife and New Hampshire Fish and Game Departments, hair samples were obtained from 124 bobcats between 2010 and 2017. In VT, I sampled bobcats that were legally harvested by hunters or trappers, whereas NH samples were obtained from vehicle mortalities, incidental captures, and nuisance animals handled by state biologists. I used a clean razor to shave the hair from approximately 3 cm^2 on the rear upper leg of each individual. For harvested individuals where pelts had been removed, samples were taken

from a rear foot. Because hair cortisol concentrations (HCC) can vary by body location (Terwissen et al. 2013), I tested for differences in a subset of 21 individuals for which leg and foot samples were available. Sex, weight, estimated age, harvest date, and town of capture were recorded for each individual. Samples were stored in paper envelopes at -20ºC.

Cortisol extraction and enzyme immunoassay

Hair samples can carry exogenous cortisol from fecal, salivary, or environmental sources, hence they are typically washed in methanol prior to cortisol assays. However, washing can leach endogenous cortisol from hair (Hamel et al. 2011). To examine this, I used a subset of 8 hair samples to test whether methanol washing prior to the assay altered HCC. Each hair sample was visually inspected to ensure that no debris was present. Half of each sample was placed in a glass vial and rinsed with methanol for 60 s then left to dry in a fume hood, while the other half was not washed. I quantified cortisol in each sample and compared results using a matched pairs t-test. Although six of eight unwashed samples had higher HCC, the difference was not significant at the 0.05 level ($t = 1.599$, $P = 0.0769$), suggesting a fairly low probability of external contamination for my samples. Thus, the unlikelihood of contamination, the high specificity of the cortisol assay, and the ability to detect outliers are sufficient to produce quality data without risking loss of endogenous cortisol through washing. Consequently, I visually inspected each sample but did not pre-wash them with methanol.

Approximately 30 mg of each hair sample was ground in a BeadBug homogenizer (Sigma-Aldridge, St. Loius, MO, USA) for one minute. Ground hair was incubated in a shaker at room temperature for 24 hours in HPLC grade methanol (50 µl/mg hair) to extract cortisol (Terwissen et al. 2014). Next, 450 µl of the supernatant was transferred to a clean tube and

evaporated under a nitrogen gas stream. Dried cortisol extract was resuspended in 150 µl phosphate buffered saline and quantified using a commercially available expanded range high sensitivity cortisol enzyme immunoassay kit (Salimetrics, State College, PA). I calculated HCC (ng cortisol per g hair) by dividing the amount of cortisol quantified in the assay by the mass of the hair sample and log transformed the data so it conformed to a normal distribution.

Assay validation

I validated the cortisol assay using several methods. To ensure the sample analyte responded similarly to that in assay standards and was independent of cortisol concentration, I tested for parallelism between the standard curve and serial dilutions of pooled extracts. Extracts were concentrated to 1x, 2x, 4x, and 10x concentrations, assayed, and plotted against the standard curve. Pooled extracts ranged from 6.4-64 ng cortisol per sample, a range encompassing 89% of the experimental data. Data for each group was fitted to a three-parameter logistic model and parallelism was assessed using an F-test in JMP (SAS Institute Inc., Cary, NC).

I determined assay precision by examining intra-assay (same extraction and 96-well assay plate), inter-assay (same extraction, different plate), and inter-extraction variation (same plate, different extraction). For each level, I calculated the coefficient of variation (CV) between samples from the same individual. Assay accuracy was determined by recovery of known quantities of cortisol. I diluted a commercial cortisol solution (Sigma-Aldrich, St. Louis, MO, USA) in methanol to a concentration of either 1 or 2 µg/dl (250 or 500 ng cortisol per well) and subjected the spiked samples to the same drying, resuspension, and assay protocol as hair samples. Accuracy was calculated as the measured cortisol/known cortisol x 100%. Because the duration of time from sampling to assay varied widely between my samples, I used a linear

regression to test for a relationship between HCC and duration from sampling date to assay date to ensure cortisol did not degrade during storage of hair samples. Similarly, because the amount of hair used for extractions varied from 8 to 59 mg, I tested for a relationship between HCC and sample weight.

Organismal analyses

Resource availability and reproductive cycles likely produce seasonal differences in bobcat HCC, which would allow me to determine a more precise timing of the bobcat molting period in the study area. If a baseline seasonal difference in cortisol levels exists, I expected to see a difference in HCC from before to after a molting period. To determine molt timing, I used the hair samples collected from wild bobcats as well as samples from captive bobcats kept in relatively constant environmental conditions at Squam Lakes Natural Science Center (Holderness, NH) and Buttonwood Zoo, (New Bedford, MA). Hair samples were collected from the flank of 5 captive bobcats throughout the course of a year. To determine when hair HCC most differed between summer and winter months, I used a t-test to compare average HCC from 6, 7, 8, or 9 month moving windows beginning in February, March, April, or May and ending in September, October, November, or December. I also used t-tests to examine relationships between HCC and season, body sample location, age class (juvenile = 0-1; adult = 2+), and sex, and linear regression to test for a relationship between HCC and bobcat weight.

Landscape analyses

I used a nonparametric multiplicative regression (NPMR) modeling framework as implemented in HYPERNICHE (McCune 2006) to model landscape influences on HCC. NPMR is

especially useful in ecology because it uses multiplicative rather than additive parameter estimates, mimicking an organism's simultaneous response to multiple predictor variables. Furthermore, it does not require *a priori* knowledge to assign model forms. HYPERNICHE uses cross-validation to prevent overfitting while maximizing model parsimony and allows for comparisons of the relative contribution of multiple predictors to a response variable, as well as how those predictors interact.

In HYPERNICHE, I conducted a free search of multivariate models using a local mean Gaussian form with HCC as the response variable. I evaluated predictor variables at the scale of towns (mean area = 92.9 km^2) and wildlife management units (WMU; mean area = 1256.1 km^2). Male bobcat home ranges in New Hampshire average 64.1 km^2 (about 70% of mean town area; Reed 2013), thus the proportion of land cover types in a town represents an approximation of the available habitat in a male home range. I included analyses at the WMU scale to see whether HCC could provide useful information to managers working at that scale. WMUs are used in the management of common game species (e.g., white-tailed deer in the NER) and are delineated based on land cover types, anthropogenic factors such as human population density and land ownership, and recognizable features such as major roads or water features. Within each unit (town or WMU), I used the National Land Cover Dataset (U.S. Geological Survey 2011) to calculate the percentage of land cover types that are significant predictors of optimal bobcat habitat (Reed et al. 2017): development (high, medium, and low intensity), open development, agriculture (pasture or cultivated crops), wetlands (woody and emergent wetlands), and shrub/scrub. I also calculated road density, percent WUI, and mean elevation in each unit. Weather patterns, especially unusually severe temperatures and precipitation, may impact foraging or finding mates, thus potentially impacting HCC over time scales relevant to hair

growth. Using CLIMOD 2 data (Northeast Regional Climate Center, www.nrcc.cornell.edu), the mean monthly temperature and precipitation were calculated for each unit in the study area during the molting month immediately preceding sampling. All predictor variables were scaled from 0 to 1 to ensure parameter estimates were comparable between predictors. Prior to modeling, I ensured predictor variables were not highly correlated. For two variables with a correlation coefficient > 0.7 or < -0.7, the variable that was the best univariate predictor of HCC was retained. Variables retained for NPMR modeling were WUI, development, open development, agriculture, wetlands, shrublands, elevation, mean monthly temperature, and mean monthly precipitation. I found the optimal model for each of *n* predictors and chose the final model based on a 3% improvement criterion over the model with one less predictor. Here I report xR^2 (cross-validated R^2), sensitivity, and tolerance for the best-fit models. Sensitivity is a measure of each predictor's importance to the model and ranges from 0 to 1. Tolerance represents the range of data points that affects the estimate at a target point. Biologically, low tolerance indicates a strong response over a small range of a given predictor, whereas high tolerance indicates greater resilience across a wider range of the predictor variable (McCune 2006).

Results

Assay validation

To assess parallelism, I fit three-parameter logistic models to a series of cortisol standards and pooled extracts (standard $R^2 = 0.998$; extract $R^2 = 0.999$). A parallelism test indicated strong similarity between standard and pooled extract curves ($F = 0.044$, $P = 0.958$). Intra-assay variation, measured as the CV between hair samples from the same extraction and assayed on the

same plate, was 1.9% ± 0.1 ($\bar{x}$ ± SE). Inter-assay variation, or the CV between samples from the same extraction but run on a different plate, was 6.1% ± 1.0, and inter-extraction variation, in which a sample was extracted two different times and assayed on the same plate, was 15.5% ± 1.8. Accuracy of the assay, as determined by recovery from samples spiked with known amounts of cortisol, was 86.9% ± 5.2 ($\bar{x}$ ± SE). No relationships were found between HCC and length of time from sampling to assay (P = 0.574), or between HCC and the amount of hair used in the extraction (P = 0.198).

Organismal analyses

I found that HCC was not affected by body location sampled (foot or hip; t = 0.276, P = 0.784) or age class (adult or juvenile; t = 0.928, P = 0.358). However, HCC differed by sex (t = 2.020, P = 0.0457), with females exhibiting higher HCC. A moving window analysis showed the largest difference was between wild bobcat hair samples collected December through March and those collected April through November (Fig. 3-1). Therefore, I determined the spring and fall molt to take place in March and November, respectively. Hair samples collected December through March represent mean cortisol levels in November and those collected from April through November represent mean cortisol levels in March. Fall HCC was greater in wild bobcats (t = -3.773, P = 0.002), but no seasonal difference was evident in captive bobcats (t = 0.942, P = 0.382). Linear regression showed an inverse relationship between HCC and bobcat weight (P = 0.006). This trend was likely due to the higher HCC in females and a noted sexual dimorphism in body size (Hansen 2007). No similar trend was evident when analyzing males (P = 0.097) or females (P = 0.278) separately. To avoid compounding organismal and landscape contributions to HCC, landscape analyses were conducted separately for males and females. Furthermore,

spring samples (N = 10) were omitted from landscape analyses so as not to compound landscape analyses with the seasonal effect I found in wild bobcats.

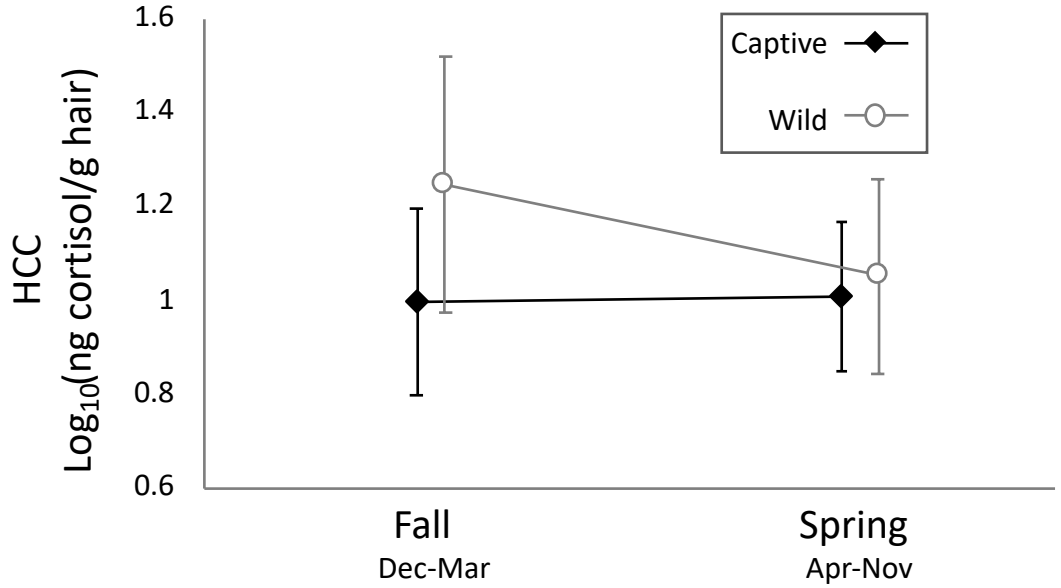


Figure 3-1 Mean seasonal hair cortisol concentrations (± 1 SD) in wild (open circles) and captive (closed diamonds) bobcats. A moving window mean analysis showed HCC values differed only between the December-March and April-November windows ($t = 3.142$, $P = 0.005$) for wild bobcats. No two windows were significantly different at the 0.05 level in captive bobcats (April-November window $t = 0.777$, $P = 0.449$).

Landscape analyses

Landscape predictors of HCC were modeled separately for males and females at the town and WMU scale using HYPERNICHE (Table 3-1). I found that female HCC responded to the amount of wildland urban interface (WUI) and open development at the town scale (Fig. 3-2a). WUI was the most important predictor of female HCC with cortisol highest at intermediate percentages of WUI. Open development (anthropogenic landscapes that are < 20% impervious surface; golf courses, parks, cemeteries, etc.) was also significant at the town scale and showed a positive linear relationship to HCC. However, there was a synergistic interaction between WUI

and open development (Fig. 3-2b). There was little effect of open development at low levels of WUI, but when WUI was high an increase in the amount of open development could drastically increase HCC (Fig. 3-2).

For males, agriculture was the most important predictor of HCC, but WUI was also significant (Fig. 3-2c). HCC was highest at intermediate levels of agriculture and dropped only slightly at high levels. A greater amount of WUI correlated with lower cortisol levels. Synergistic effects were also evident between agriculture and WUI (Fig. 3-2d). HCC was lowest when one variable was high and the other was low. An inflection point was evident at a scaled predictor value of 0.7, which corresponds to approximately 45% of a town dedicated to agricultural land use.

Table 3-1 Top nonparametric multiplicative regression models of hair cortisol concentration for each sex at the town and WMU scale. The best model was chosen based on at least a 3% increase in cross-validated R^2 over the model with one fewer predictor variable. Sensitivity represents the relative importance of that predictor to the model and tolerance represents a relative degree of resilience by the response variable across a range of values in the predictor variable.

Scale	Sex	Response	N Predictors	xR^2	Predictors	Sensitivity	Tolerance
Town	Female	HCC	2	0.060	WUI	0.259	0.234
					Open development	0.203	0.734
	Male	HCC	2	0.071	Agriculture	0.400	0.196
					WUI	0.269	0.766
WMU	Female	HCC	4	0.044	Agriculture	0.213	0.284
					Development	0.394	0.534
					Temperature	0.286	0.758
					Precipitation	0.441	0.762
	Male	HCC	3	0.080	Precipitation	0.283	0.216
					Temperature	0.169	0.766

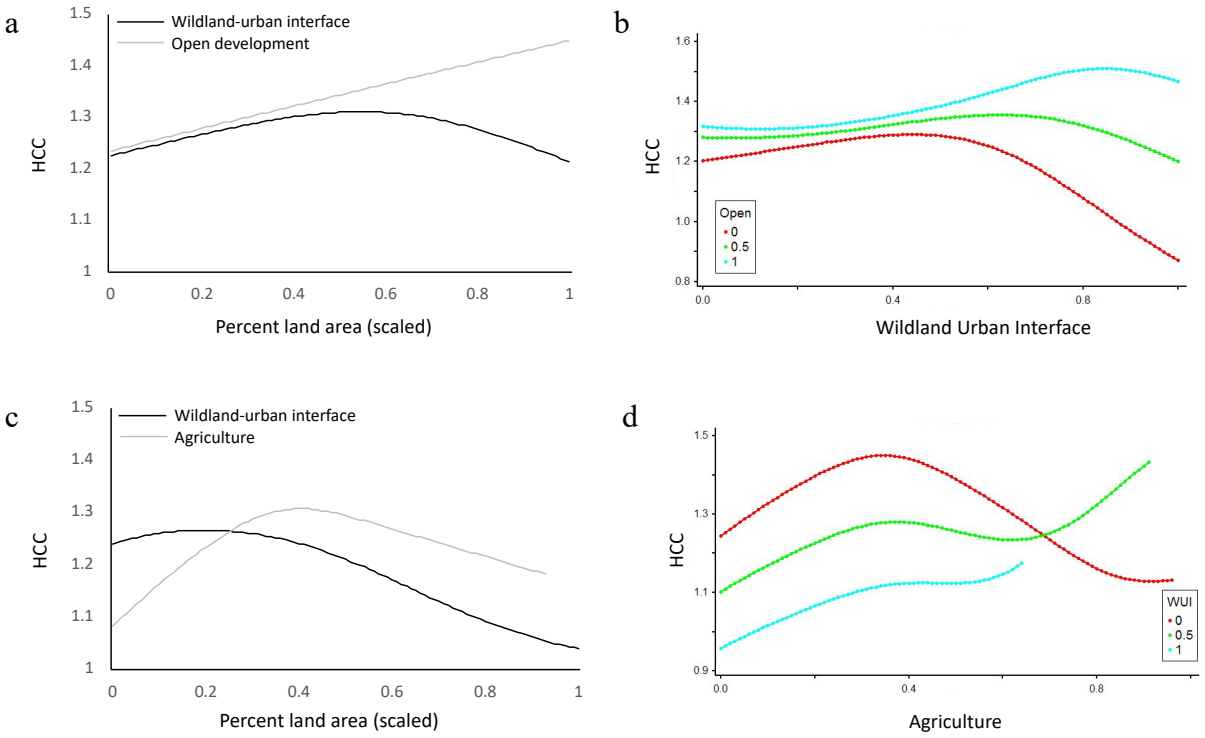


Figure 3-2 HYPERNICHE model results for female (a and b) and male (c and d) bobcats at the town scale. Values on the horizontal axis represent proportion of town comprised of a land use type, scaled 0 to 1. Y-axis is hair cortisol concentration in units of Log_{10}(ng cortisol/g hair). (a) Wildland urban interface (WUI) was the most important predictor of hair cortisol concentration (HCC) for females, with areas of intermediate amounts of WUI inducing the highest HCC. Open development was positively correlated with HCC. (b) Interactive effects between the two significant female predictor variables. (c) Agriculture was the most important predictor variable for males with intermediate levels of agriculture inducing the highest HCC. The wildland urban interface (WUI) was also important. More area in the WUI was associated with lower cortisol. (d) Interactive effects between significant predictors for male bobcats.

At the WMU level, variables associated with climate and weather patterns were the most influential predictors of HCC (Fig. 3-3). Mean monthly precipitation and temperature were important for both sexes, while agriculture and development also affected female HCC. The HCC response to predictor variables was much more moderate in females than males at this larger scale.

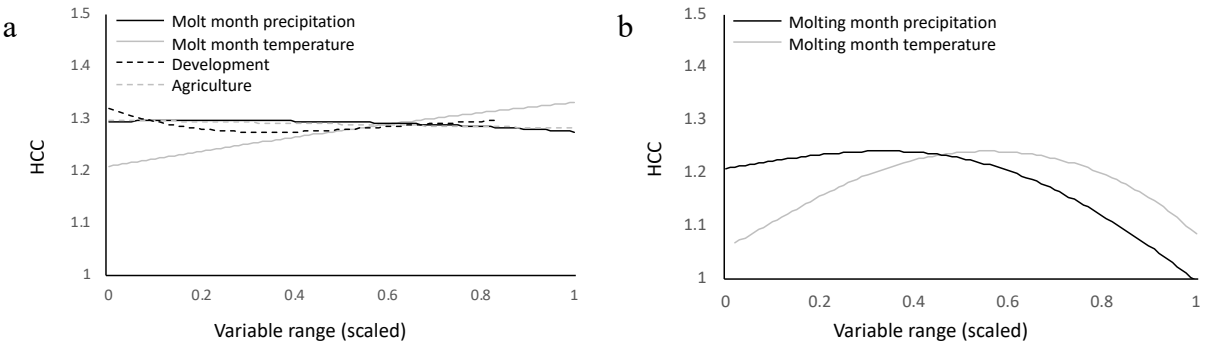


Figure 3-3 HYPERNICHE model results for female (a) and male (b) bobcats at the wildlife management unit scale. Values on the horizontal axis represent proportion of town comprised of a land use type, scaled 0 to 1. Y-axis is hair cortisol concentration in units of Log_{10}(ng cortisol/g hair). Climatic variables were the most important drivers of hair cortisol concentration for both sexes, but females also showed minor responses to development and agriculture.

Discussion

In this study, I quantified how stress in bobcats, as measured via HCC, relates to both natural and anthropogenic habitat characteristics. At the organismal level, I found higher HCC in females than males. This may be due to a higher baseline cortisol level in females. Physiological differences in stress hormones between sexes are well known in mammals (Handa et al. 1994; Lafferty et al. 2015; Costantini et al. 2019). As sole providers for offspring during the first year of life, female bobcats must secure resources within their home range and are more territorial with conspecifics than males (Hansen 2007). Stevenson *et al*. (2018) found male coyotes, who typically defend the territory of a pack, had elevated cortisol levels relative to females and attributed the difference to the intrusion by researchers during study. Greater territoriality may also make females more susceptible to stress as a result of encounters with other species, including humans, in their home range (Creel et al.2013, Eggermann et al. 2013). A female's smaller home range and smaller body size may also make securing resources more difficult,

especially when resources begin to get scarce in the late fall. Lastly, differences in HCC between males and females may be a result of differential habitat selection. Third-order habitat selection (within home ranges) can vary between male and female bobcats (Litvaitis et al. 1986b). Modified landscapes create ecological traps, areas that appear to provide higher quality habitat than they actually do, and reduce the ability of animals to accurately assess habitat quality (Lamb et al. 2017). Selecting sub-optimal habitat may result in fewer resources, which can ultimately trigger the stress response (Bryan et al. 2013).

I estimated the timing of the seasonal molts in bobcats to be March and November. To my knowledge, no previous study has estimated timing of bobcat molt in New England. Maurel *et al*. (1986) found similar timing in the molts of red foxes (*Vulpes vulpes*) and mink (*Mustela vison*) in France at locations similar in latitude to New England. HCC in samples collected from wild bobcats after the fall molt was greater than in those collected after the spring molt. However, this does not appear to be a species-wide pattern in baseline cortisol levels. Captive and wild bobcats have similar HCC in the spring, but HCC rises in wild bobcats in the fall while there was no change for captive bobcats (Fig. 3-1). Wild bobcats may be responding to changes in prey availability in the fall versus the spring to which captive bobcats on constant diets are not subjected. Stress hormones respond to nutritional and energetic demands (Busch and Hayward 2009). Many potential bobcat prey species have litters early in the year, hence prey density and naivety likely decrease in the fall, which can lead to higher cortisol levels (Kitaysky et al. 2007; Jenni-Eiermann et al. 2008; Bryan et al. 2013). This pattern of resource availability may be especially difficult for females who share a home range with her most recent offspring through their first winter. When the sexes were analyzed separately, I found a strong seasonal effect in females (i.e., greater HCC in fall; $t = -4.682$, $P = 0.001$), and a much weaker one in males ($t =$ -

2.101, $P = 0.068$). Captive bobcat HCC, an estimate of baseline levels, did not reveal a seasonal signal and was similar to wild bobcat HCC in spring for both sexes. Hence, the discrepancy in patterns among the sexes is most likely due to a larger autumnal HCC increase in females. Male home ranges are several times larger than that of females (Litvaitis et al. 1986b). Having access to more resources may alleviate the nutritional stress which females experience in fall. However, I cannot rule out a male-specific vernal increase in HCC accounting for the lack of a significant difference between fall and spring HCC. Social dynamics, specifically a polygynous mating system, may increase male HCC in wild bobcats. Mating has been shown to increase cortisol levels in wild mammals of both sexes, but especially males (Lidgard et al. 2008; Eggermann et al. 2013; Edwards et al. 2016; Boonstra et al. 2017). The spring molt partially overlaps with breeding season, which in New England takes place between February and April (Anderson and Lovallo 2003).

My hypothesis that anthropogenic land use would be better predictors of HCC in bobcats was supported at the town scale. Despite including preferential bobcat habitat variables as predictors in my models, all top models included only anthropogenic land use as predictors. My hypothesis that bobcat HCC would increase with anthropogenic land use was only partially supported. Individuals living in areas of high agricultural use and open development have higher cortisol levels. However, development associated with human housing (WUI) corresponded with lower HCC. Lower HCC values at very high proportions of WUI in towns suggest that bobcats can habituate to human presence and may select for it when availability of anthropogenic resources is above a threshold level. This is especially true for males, whose HCC was much more responsive (i.e., decreased faster) than females with increasing WUI. Some degree of selection for human-modified habitat has been noted in bobcats (Lombardi et al. 2017),

especially males (Riley et al. 2003). Occupancy probability for mesocarnivores is greater in suburban and exurban areas than rural or wild areas (Parsons et al. 2018). Additionally, Kays *et al.* (2017) found bobcats were likely to frequent sites associated with human housing and recreational trail use. While habituation to human presence may allow bobcats to access resources that otherwise might be unavailable, there are risks associated with synurbization including increased mortality (Tigas et al. 2002), disease transmission (Serieys et al. 2014), and an enhanced response to other environmental stressors (Romero 2004).

There are important similarities between open development and agriculture that contrast the WUI and may explain the opposite responses in HCC. Agricultural areas and open development are both defined by a low vegetative diversity. Bobcats prefer natural habitat with high structural diversity such as shrublands, woody wetlands, and forest edges (Reed et al. 2017). Open and agricultural land use provide bobcats with synanthropic prey attracted by supplemental food, but prey diversity and abundance are greater only in edge areas and are reduced in core areas (Ratcliffe and Crowe 2001; Braga et al. 2015; Gallé et al. 2019). Hence, edge resources may attract bobcats to farms or open development. But as the amount of agricultural area increases the disadvantages associated with core areas increase faster than the benefits of edge habitats, limiting bobcat success in those areas (Reding et al. 2012). Because resources in the WUI are more evenly distributed throughout the entire area (Bateman and Fleming 2012; Moss et al. 2016), availability of synanthropic prey (e.g., gray squirrels) likely rises linearly with amount of WUI. Furthermore, frequent successional disturbance, landscaping practices, and availability of shelter associated with built infrastructure (especially in suburban and exurban development) provide structural diversity that can support more abundant and diverse fauna (Goddard et al. 2010; Parsons et al. 2018).

Drivers of HCC at the WMU scale were dominated by weather variables, which have been shown to influence mammalian cortisol levels (Milas et al. 2018). Precipitation during the fall molting period corresponded with lower HCC and was the leading predictor for both male and female bobcats, though the magnitude of the response was far more substantial for males (Fig. 3-3). I estimated the fall molt takes place primarily in November, when precipitation in the study area includes a significant proportion of snow (Huntington et al. 2004). Historically, lagomorphs (*Sylvilagus floridanus*, *S. transitionalis*, and *Lepus americanus*) and white-tailed deer (*Odocoileus virginianus*) have been the main winter prey items of bobcats in New Hampshire (Litvaitis et al. 1984; but see chapter 2). Snow allows bobcats to exploit weather-driven advantages over these prey. For example, snow cover reduces movement behavior in deer (Moen 1976) and disrupts crypsis in many potential prey species, including lagomorphs (Mills et al. 2013). I found a positive relationship between HCC and temperature for females, whereas male HCC increased until temperatures reached a scaled predictor value of 0.6, corresponding to approximately 8°C, at which point HCC decreased (Fig. 3-3b). Abnormal temperatures that fluctuate from seasonal norms can have significant impacts on wildlife species. Seasonally low temperatures can contribute to the impacts of snow mentioned above. Higher than expected temperatures, even in winter months, can induce thermal stress in mammals (Lenarz et al. 2009) and correlate to higher cortisol levels (Millspaugh et al. 2001).

Our analyses highlighted a mismatch in scale between manageable environmental drivers of HCC and actual wildlife management units in NH and VT. WMUs are often delineated using political designations or anthropogenic boundaries (e.g., highways) that are ecologically and biologically not meaningful. This can limit efficacy of species management practices (Linnell et al. 2001; Meisingset et al. 2018). Because bobcats exist in large home ranges at low densities

(Clare et al. 2015), can greatly fluctuate in abundance (Litvaitis et al. 2006), and are subject to harvest throughout much of their range (although currently protected in NH; Woolf and Hubert 1998; Hansen 2007; Roberts and Crimmins 2010), it is especially important that management occurs at ecologically relevant scales. I found limited evidence that land-use relates to cortisol levels in bobcats at the WMU scale. However, towns with more area dedicated to open development or agriculture correspond to higher cortisol levels, which in turn may reduce reproductive rates and disease resistance. Consequently, habitat conservation and development practices at the town level may be more effective for long-term conservation efforts.

CHAPTER IV

AN INTEGRATED FRAMEWORK FOR UNDERSTANDING BOBCAT ECOLOGY IN THE NEW ENGLAND REGION

Introduction

In 1869, the naturalist John Muir penned one of the most iconic passages in ecological literature. During a summer immersed in the Sierra Nevada wilderness and observing the natural world, he wrote "when we try to pick out anything by itself, we find it hitched to everything else in the universe" (Muir 1911). Despite a broad recognition of the interconnectedness of ecological processes in natural systems, study and management of those systems is often narrow and focused on a single issue (Reagan 2006). Taking a multidisciplinary approach toward wildlife ecology and management will enable more effective long-term conservation outcomes (Jacobson et al. 2010). This involves a more holistic understanding of factors that influence ecological patterns including their interactions with human systems (Riley et al. 2002). Population genetic studies are much more meaningful in a conservation context when they can be linked to broader ecological, environmental, and biological data (Manel et al. 2003; Habel et al. 2015). Studying the physiology of wildlife species can give early warnings of potential conservation issues (Madliger et al. 2017). Furthermore, integrating ecological data in human social contexts is necessary for the field to remain relevant and maximize positive impacts (Frank et al. 2015; Decker et al. 2016, 2019).

Bobcats in New England represent an ideal system in which to explore links between human land use and ecological processes in an integrated framework. They are reclusive, typically avoiding human contact, but are also highly adaptable to varied habitats including human-dominated areas (Tigas et al. 2002; Riley et al. 2003; Janecka et al. 2016). As facultative generalists, their diet can widely vary based on local conditions and biological factors (Litvaitis et al. 1984; Shipley et al. 2009; Newbury and Hodges 2018). In the New England region (NER), the population is experiencing a resurgence after nearly being extirpated in parts of this area in the 1980s (Litvaitis et al. 2006), thus region-wide demographic parameters are dynamic. Harvest seasons in the NER (except in NH) provide an opportunity for extensive sampling and collaboration with agencies and hunters. Additionally, there is great public interest in these charismatic felids, which provides ample opportunity for engagement with public stakeholders.

To explore the interrelatedness of genetic population structure, diet, and stress levels of bobcats, I conducted new integrative analyses on data from the first three chapters of this dissertation. Diet proportions of major prey guilds and hair cortisol concentration were examined in light of contemporary population structure. I also explored whether diet had an effect on cortisol levels. I expected diet proportions and cortisol levels to vary among subpopulations due to habitat, bobcat demographic, and prey community characteristics. Finally, I review the overarching goals of this entire work as an example of integrated wildlife ecology.

Materials and Methods

To explore the relationships between genetic population structure, diet, and cortisol concentration, I used a subset of bobcat data consisting of individuals for whom I had stable isotope and hair cortisol data (N = 115). Only 21 of these individuals were included in genetic

analyses, so I assigned the remaining 94 individuals to one of the 5 contemporary genetic subpopulations based on the modal cluster prediction for their town of origin as calculated in GENELAND.

Diet – subpopulation interaction

I used MixSIAR to determine proportions of each of the four dominant prey guilds (lagomorphs, large mammals, small mammals, squirrels) in the diet of bobcats from each of the five contemporary subpopulations (northwestern, northern, Vermont lowlands, eastern, southern; see chapter 1). I used $\delta^{13}C$ and $\delta^{15}N$ as the response variables and subpopulation as a categorial predictor. I ran 3 chains of 1,000,000 iterations each with a burnin of 500,000 and thinned by 500. I used informative priors based on global posterior estimates from analyses conducted in chapter 2. Here I report the posterior estimates (mean ± SD), as well as correlations of diet proportions within each subpopulation.

To test for landscape differences that may be driving prey proportions between subpopulations, I performed a nominal logistic regression in JMP. The dependent variable was the preferred diet within the subpopulation (squirrel or lagomorph), and predictor variables were percentages of the 13 land cover types present in the study area (U.S. Geological Survey 2011) and wildland urban interface (WUI; Martinuzzi et al. 2015) in towns within each subpopulation. Predictor variables with a pairwise correlation > 0.7 or < -0.7 were not included in the final model. Of all potential predictors, only the levels of development (open, low, medium, and high) and wetland types (herbaceous and woody) were correlated. I grouped all levels of development and both types of wetlands into their own comprehensive categories. I log transformed the following land cover variables so they conformed to a normal distribution: development,

shrub/scrub, grassland, agriculture, and wetlands. Lastly, I scaled all land cover variables from 0 to 1 to ensure parameter estimates were comparable between predictors. The ten land cover variables included in the model were WUI, development, deciduous forest, coniferous forest, mixed forest, shrub/scrub, grassland, cropland, wetland, and pasture/hay.

Diet – hair cortisol interaction

To investigate the relationship between cortisol and diet, I used hair cortisol concentration (HCC) as a continuous factor in a $\delta^{13}C$ and $\delta^{15}N$ isotopic mixing model using the 115 individual bobcats for which both isotopic and HCC data were available. MixSIAR regresses proportions of each diet source across the entirety of a continuous variable to assess how dietary sources change with values of the factor. I ran 3 chains of 1,000,000 iterations each with a burnin of 500,000 and thinned by 500 and used informative priors based on global posterior estimates from previous analyses (see chapter 2). Because both diet and HCC can significantly differ between sexes, I analyzed the females and males separately. To visualize the results, I plotted the predicted proportions of each prey guild (middle 50% of posterior estimates) in bobcat diets across the range of log-transformed HCC values for each sex.

Subpopulation – hair cortisol interaction

I used a two-way ANOVA in JMP (SAS Institute Inc., Cary, NC) to test for an effect of subpopulation on cortisol levels. I used HCC as the response variable and subpopulation as the main factor. Because HCC can also vary between males and females, I also used sex as a cofactor. I report the R^2 and P values for the whole model as well as P values for each factor and the interaction between subpopulation and sex. Using the lm function in R, I also fit linear

models for each subpopulation. In each model, HCC was the response variable and the proportion of squirrels and lagomorphs in an individual's diet was the predictor variable. Models were evaluated using beta estimates, R^2, and P values.

Results

Diet – subpopulation interaction

Mixing model results for subpopulations indicated two characteristic diet groups, specifically a squirrel-heavy and a lagomorph-heavy group (Fig. 4-1). There was a significant negative correlation between the proportion of lagomorphs and squirrels in the bobcat diet (Fig. 4-2). Bobcat diet in the northern subpopulation, and to a slightly lesser extent the northwestern subpopulation, consisted primarily of lagomorphs. In the southern and VT lowlands subpopulations, squirrels were the dominant prey item. The eastern subpopulation was a relatively even mix across all four prey guilds.

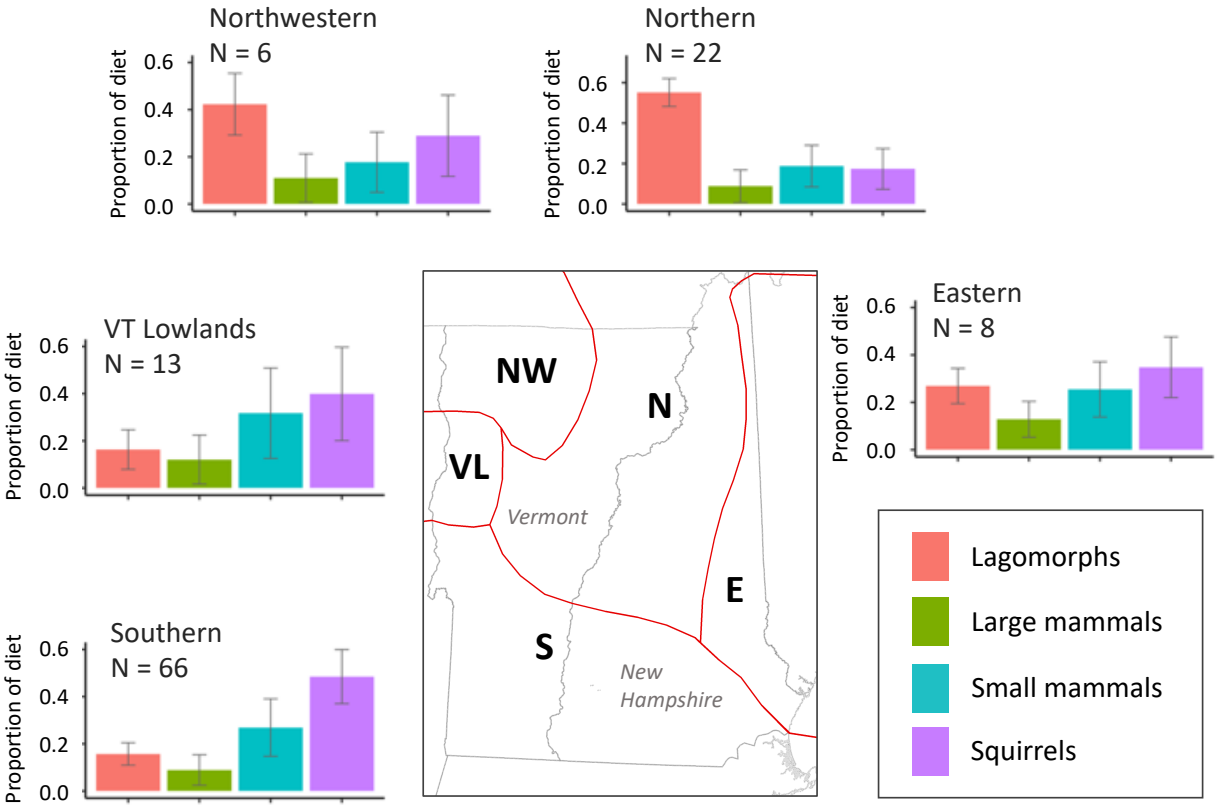


Figure 4-1 Mixing model results for bobcats in each of the 5 genetic subpopulations: southern (S), Vermont lowlands (VL), northwestern (NW), northern (N), and eastern (E). Each bar represents the mean (±1 SD) posterior estimate of the proportion of each prey guild in the diet of bobcats within a given subpopulation. Middle panel represents the location of subpopulations, separated by red lines.

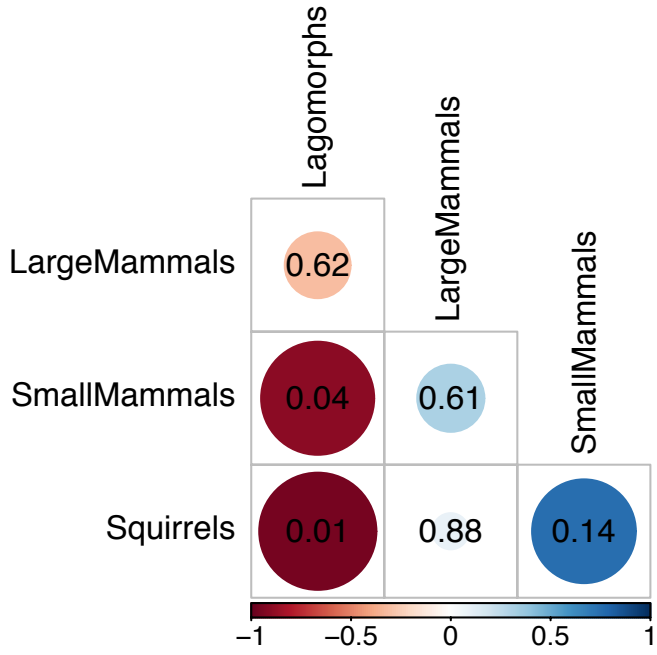


Figure 4-2 Correlations between prey guild proportions within genetic subpopulations. Significant negative correlations were found between lagomorphs and squirrels (r = -0.956) and lagomorphs and small mammals (r = -0.891). P values for correlation coefficients are written in their respective squares.

Nominal regression of land cover variables on subpopulation areas with different diet proportions produced a model with an R^2 = 0.874. Only 4 of the 10 land cover variables significantly differed in abundance between areas with squirrel-heavy diets and those with lagomorph-heavy diets (Fig. 4-3). Lagomorph-heavy diets were more prevalent in the northern and northwest subpopulations, and those areas had more cropland and shrubland. Diets of bobcats in the southern and VT lowland subpopulations consisted primarily of squirrels, and those areas had more land in pasture and wetland. None of the forest types nor development differed from the null hypothesis of equal proportions in all subpopulations.

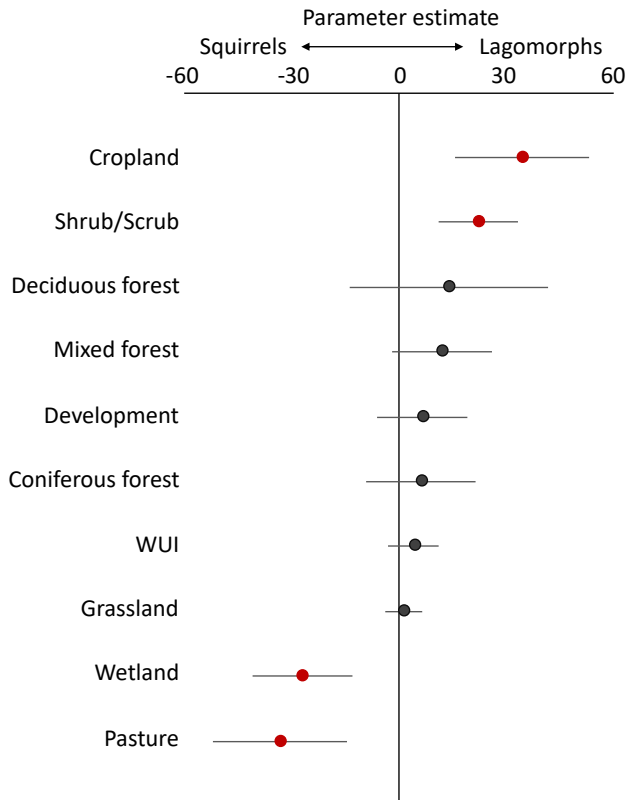


Figure 4-3 Results of a nominal logistic regression for landscape differences between areas where bobcats have squirrel-heavy diets versus areas where they have lagomorph-heavy diets. Points represent model parameter estimates (± SE) for each land cover variable. Parameters with red points differed from zero ($P < 0.07$). The overall model $R^2 = 0.874$.

Diet – hair cortisol interaction

A regression of the proportion of each prey guild over the range of HCC values indicated that the proportion of large mammals had the largest impact on cortisol (Fig. 4-4). While the range of posterior parameter estimates for lagomorphs, squirrels, and small mammals overlapped across much of the range of cortisol values, two trends were identified for both sexes. First, the proportion of large mammals was negatively correlated with HCC. For females with higher HCC values, proportion of the large mammal guild in their diet was lower than other guilds. Similarly, males with lower HCC had a greater proportion of large mammals in their diet than any other

prey guild. Second, the proportion of squirrels in the diet was positively correlated with HCC. This trend was stronger for females, whose median squirrel guild proportion increased from 25.6% of diet at minimum HCC values to 51.8% at maximum HCC values.

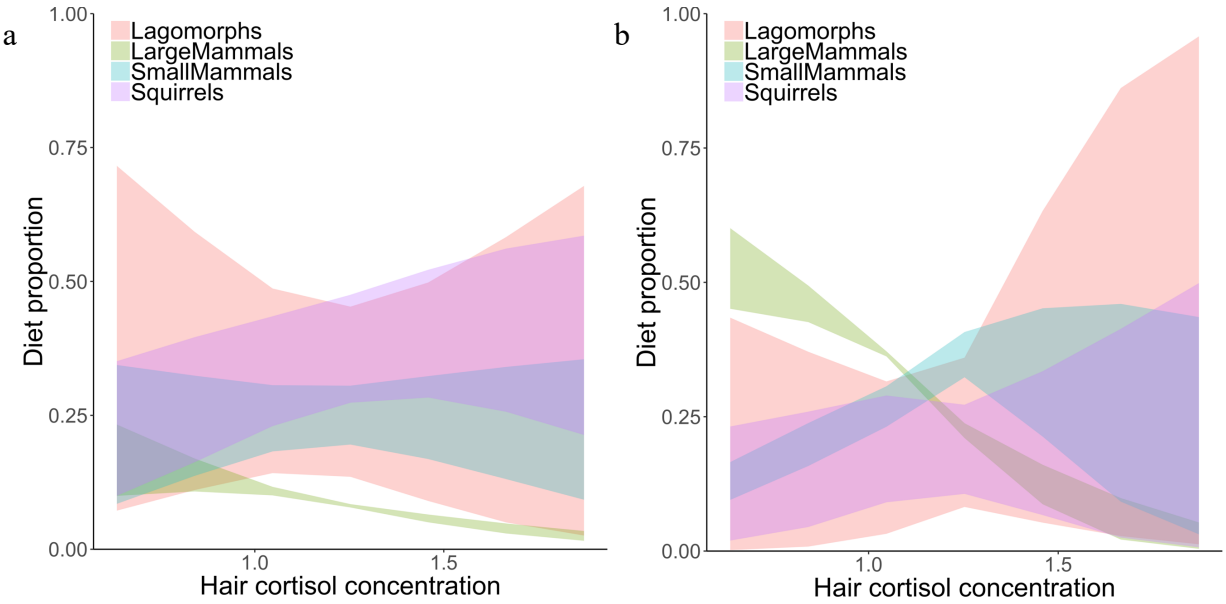


Figure 4-4 Ribbon plots of the middle 50% of posterior draws of bobcat diet proportions across the range of cortisol values for females (a) and males (b). Hair cortisol concentration is in units of Log_{10}(ng cortisol/g hair).

Subpopulation – hair cortisol interaction

Results of a two-way ANOVA suggested that HCC was independent of genetic subpopulations (Fig. 4-5). I found no difference in mean cortisol levels among subpopulations, however there were some trends worth noting. The VT lowlands subpopulation had the highest mean HCC for both sexes. Mean HCC was greater for females except in the northwestern subpopulation, where male HCC was slightly higher.

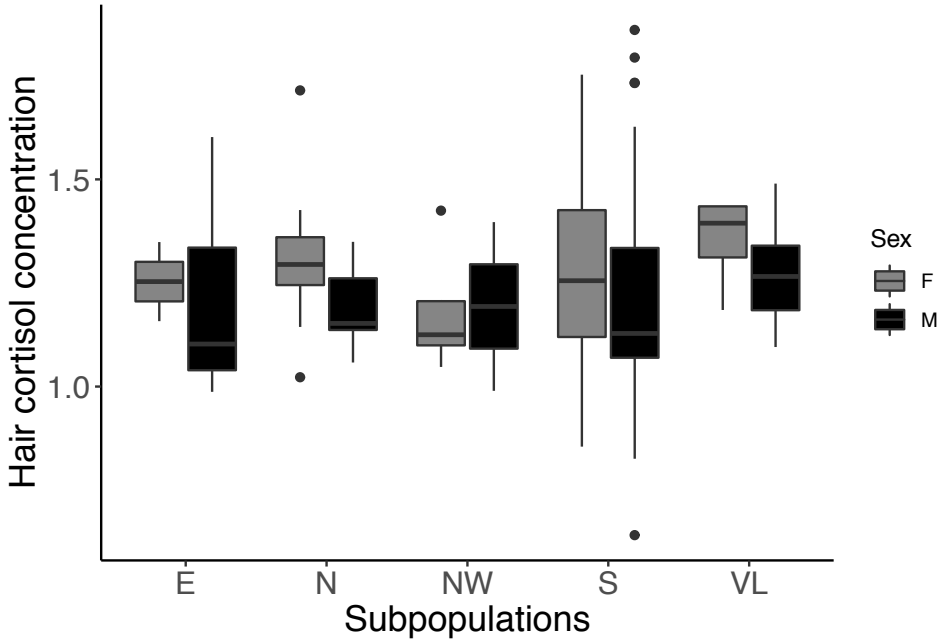


Figure 4-5 Average hair cortisol concentration (ng cortisol per g hair) in each subpopulation for males and females. Y-axis is hair cortisol concentration in units of Log_{10}(ng cortisol/g hair). Dots indicate outliers in each subpopulation. Two-way ANOVA indicated neither subpopulation nor sex were significant factors (P = 0.848 and 0.358, respectively), nor was their interaction term (P = 0.977). Model R^2 = 0.039. Sample sizes were as follows: E = 8, N = 22, NW = 6, S = 66, VL = 13.

The most significant regression estimates were for HCC with lagomorph proportion in the VT lowlands, HCC with squirrel diet proportion in the southern subpopulation, and HCC with lagomorph proportion in the northwestern subpopulation (Table 4-1). All were positive correlations. The only negative correlations, indicating lower cortisol with higher prey guild proportion, were for squirrels in the northwestern subpopulation and lagomorphs in the southern subpopulation, although neither was significant. It is interesting to note that in the northwest and southern subpopulations, the dominant prey guild was positively correlated with HCC and the non-dominant prey guild was negatively correlated.

Table 4-1 Results of linear regression of major prey source of HCC (Log_{10}(ng cortisol/g hair)) for each subpopulation. Positive estimates indicate higher cortisol levels in hair with increasing proportion of that prey guild in the diet. * indicates significance or near significance at the 0.05 level.

	Subpopulation	Estimate	SE	*t*	*P*	Model R^2
HCC ~ pSquirrel	Eastern	0.776	0.544	1.428	0.203	0.253
HCC ~ pSquirrel	Northern	0.068	0.317	0.215	0.832	0.002
HCC ~ pSquirrel	Northwestern	-0.951	0.868	-1.096	0.335	0.231
HCC ~ pSquirrel	Southern	0.475	0.242	1.961	0.054*	0.057
HCC ~ pSquirrel	VT lowlands	0.025	0.308	0.081	0.937	0.001
HCC ~ pLagomorphs	Eastern	1.042	1.255	0.830	0.438	0.103
HCC ~ pLagomorphs	Northern	0.025	0.170	0.148	0.884	0.001
HCC ~ pLagomorphs	Northwestern	1.009	0.422	2.392	0.075*	0.589
HCC ~ pLagomorphs	Southern	-0.677	0.636	-1.065	0.291	0.017
HCC ~ pLagomorphs	VT lowlands	1.146	0.501	2.288	0.043*	0.322

Discussion

I was able to identify links between human land use, population structure, diet, and stress hormone levels by studying them in a wild population through time. I found evidence that land use can directly impact the genetic structure, diet, and stress levels of bobcats and evidence of interactions between those three aspects of bobcat ecology independent of land use (Fig. 4-6). Because I designed this study to holistically examine the potential for direct and indirect interactions, I often did not have the power to explicitly test the mechanisms behind those connections. However now that a comprehensive framework is established, additional tests can be designed using more rigorous sampling to identify the underlying mechanisms and to quantify their impacts.

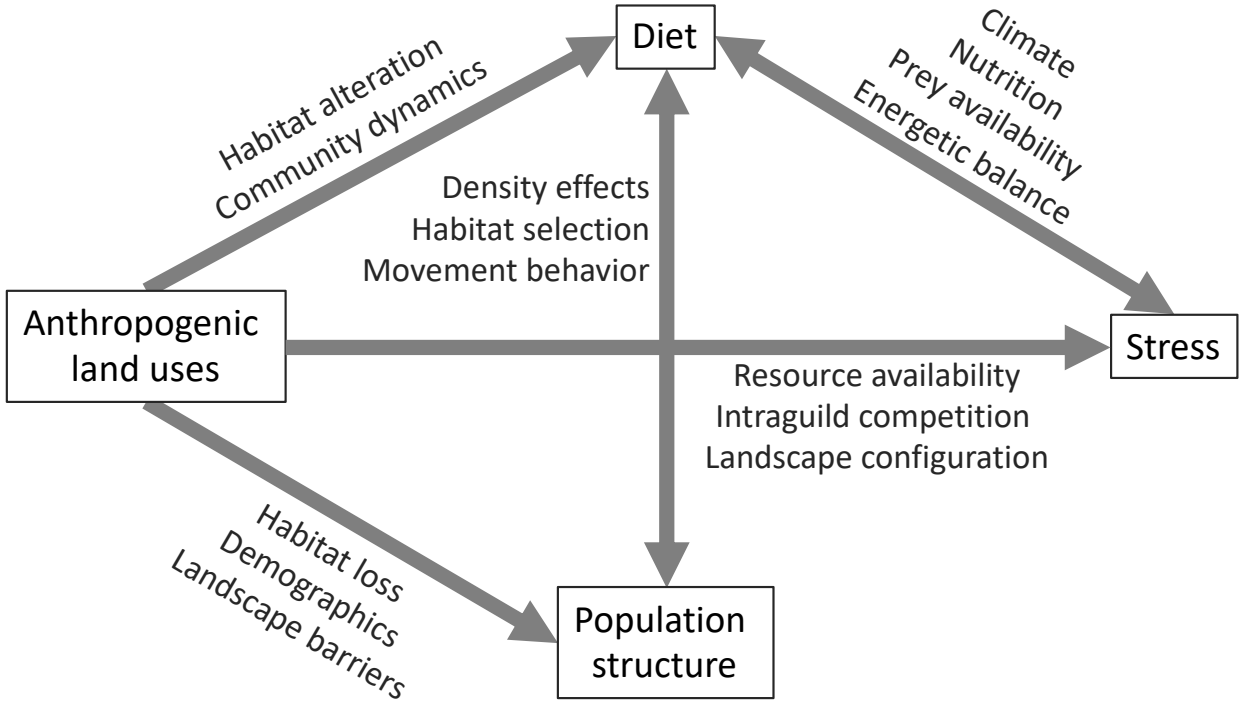


Figure 4-6 Framework for linking land use patterns in the New England region with genetic, trophic, and stress patterns in bobcats.

Direct links between land use and population structure or diet are well established. Landscape barriers to gene flow and habitat loss due to landscape development are known drivers of population structure in wide-ranging species (Tigas et al. 2002; Riley et al. 2003; Ruell et al. 2012; Hornseth et al. 2014; Poessel et al. 2014). Likewise, many studies have explored how human-induced habitat alteration leads to changes in wildlife communities. Those changes may positively impact trophic patterns of predators by increasing prey abundance (McKinney 2002; Prange et al. 2004) and diversity (Resasco et al. 2018; Parsons et al. 2018). Conversely, they may negatively impact predators through increased competition (Smith et al. 2018) or exclusion from optimal habitat (Warsen et al. 2014).

I found that bobcat diets differed among genetic subpopulations, a reflection of significant differences in the landscape. At a small scale, differences in prey selection may primarily be a function of availability; but prey availability has causes and consequences rooted in other ecological phenomena. Processes linking isotopic diet data to population structure have been explored mainly in birds (Clegg et al. 2003; Rundel et al. 2013; Ruegg et al. 2017; Gadek et al. 2018), and similar studies are rarer for carnivores. Pilot et al. (2012) found strong correlations between genetic dissimilarity and dietary distance in isotopic space for European wolves, which they attributed to habitat selection based on cues that signal the availability of preferred prey. Often those cues are impressed on individuals in their natal home ranges, thus they have important implications for dispersal behaviors (Davis and Stamps 2004). Other studies have noted that ecological dissimilarity correlates with genetic subdivision of carnivore populations (Rueness et al. 2003; Sacks et al. 2005). Stark differences in conspecific density (Young et al. 2019) or movement behaviors within-home ranges (Prange et al. 2003; Tucker et al. 2018) may also contribute to the relationship between diet and population structure, especially near human-dominated landscapes.

Trophic dynamics can have direct impacts on stress hormone levels in wild populations by altering ease of access to resources for consumers (Kitaysky et al. 2007; Pokharel et al. 2018) or indirectly by mediating competitive interactions (Bryan et al. 2013; Lafferty et al. 2015). Results of this study indicate there is a relationship between hair cortisol concentration and bobcat consumption of two prey guilds. Greater diet proportions of the large mammal prey guild, primarily white-tail deer and porcupines, was associated with lower HCC. HCC increased with higher proportions of squirrels in the diet. Bobcats are well-adapted to exploit prey of a wide variety of sizes (Meachen-Samuels and Van Valkenburgh 2009). The profitability of each of

these prey items is subject to costs associated with capture and processing, encounter rate, prey behavior, and nutritional value. However, some studies suggest that larger prey are more profitable for felids (Hart et al. 1996; Ray and Sunquist 2001). Further, Litvaitis et al. (1986a) found that larger bobcats (especially males) were more likely to prey on deer and those that did were in better physical condition. They also found that even moderately sized bobcats were able to take advantage of large mammals as prey. This suggests large mammals may be a more profitable prey species for bobcats than smaller-bodied prey such as squirrels. Thus, the link between more profitable prey species and body condition may explain both the negative association between HCC and large mammals and the positive association between squirrels and HCC.

I did not find strong evidence of a direct relationship between subpopulation structure and HCC. However, intervening processes that connect land use and genetic structure to diet may indirectly affect levels of stress hormones. For example, variation in human influence on the landscape within subpopulations can drastically alter population density of bobcats (Lewis et al. 2015; Young et al. 2019) and their prey (Resasco et al. 2018; Parsons et al. 2018). This in turn, influences competitive dynamics and resource selection by individuals. Socially subordinate individuals can exhibit increased cortisol levels (Bryan et al. 2013; Bourbonnais et al. 2013, 2014; Lafferty et al. 2015). My data suggest interference competition may affect the relationship between HCC and diet. I found evidence of a negative association between HCC and consumption of the non-dominant diet source within the southern and northwestern subpopulations (Table 4-1). For example, squirrels were the dominant prey item across the southern subpopulation. Bobcats in that subpopulation that had a greater proportion of lagomorphs in their diet had a lower HCC. In both areas, there was also a positive relationship

between HCC and the dominant diet source. If the diet-subpopulation association reflects an optimal strategy based on habitat or behavioral characteristics for individuals in an area, an alternate strategy such as specializing on another prey source may provide a distinct energetic benefit that becomes evident in hair cortisol data.

Conclusion

The overarching theme of this dissertation was to employ an integrated approach to wildlife management by using a multidisciplinary, community-engaged endeavor to promote species conservation (Allen et al. 2014; Frank et al. 2015). There were three main objectives. First, I wanted to understand the genetics, diet, and stress physiology of bobcats in New England. Furthermore, I wanted to gain a more holistic understanding of the biological and ecological processes at play for individuals and populations of a highly adaptable species surviving in human-dominated environments. Because bobcats are a wide-ranging carnivore and exist at a low density on the landscape, it is difficult to design a study with a robust enough sample population to explicitly test responses across a broadly multidisciplinary suite of characteristics such as genetics, diet, and stress. Additionally, while we know species respond to their landscapes, those responses can be tempered in a highly vagile species that experiences a wide range of habitat types within a home range. This work has shown that connections do exist between anthropogenic land use, population genetics, diet, and stress hormone levels. However, further study is needed to explain the underlying processes.

A second objective was to promote opportunistic sampling (e.g., harvested animals, vehicle mortalities, museum and captive specimens) as an effective and efficient method to learn about the ecology of a species. This type of sampling strategy provides a rich data source that is

currently underutilized in wildlife research (Jessup 2003). The main benefit of opportunistic sampling is its cost effectiveness and high return per unit effort. It can be equally effective as other more common non-invasive sampling methods for estimating population parameters (De Barba et al. 2010) It can also substantially increase sample size and spatial resolution of analyses (Rehnus and Bollmann 2016), and in some circumstances can be preferable to systematic sampling (Lewandowski and Specht 2015). It frequently enables greater collaboration between researchers, agencies (wildlife-focused and otherwise), and the public, thus increasing the stakeholder base in wildlife science. Involving a broader community in conservation leads to more meaningful and effective outcomes (Newig and Fritsch 2009; Ballard et al. 2017) and is a critical aspect of integrated wildlife management (Reagan 2006).

The third and perhaps most impactful goal was to provide the broader community with knowledge and tools to help navigate toward greater coexistence with wildlife. The resurgence of the bobcat population in New Hampshire and a legislative attempt to reopen a harvest season in the state led to an abrupt and highly politicized spike of interest in bobcats and in wildlife management during the course of this study. I was able to leverage this interest into a suite of unique outreach experiences for a broad range of audiences. Bridging the gap between the public, wildlife agencies, and researchers is a critical component of effective management (Riley et al. 2018). Aside from being a source of information about a publicly managed resource at a critical time for management of that resource, I sought to engage citizens in critical discussion about motivations of stakeholders in conservation science (Kellert 1985; Austin et al. 2010), dispel stereotypes about scientists (Losh 2010; McClain and Neeley 2015), and promote enthusiasm and competency for ecological study.

As expected, this work provides fertile ground for future explorations into the relationships between human land use and the ecology of wildlife species. Studies should include experiments designed to test the precise mechanisms underlying those relationships. For example, quantifying the abundance and nutritional value of major bobcat prey items within subpopulations would help elucidate the drivers of diet patterns. Exploring whether or not a greater bobcat population density leads to occupation of less suitable habitat and different prey choice would help determine competitive effects on diet and stress patterns. A larger scale spatial and temporal comparison of cortisol levels in bobcat hair (e.g., using museum specimens) would help clarify the links between stress and habitat. Because bobcats have generalist and specialist characteristics, are adaptable but sensitive to habitat change, and have large geographic ranges, they are a good model system for many carnivore species (Litvaitis et al. 2015). A greater understanding of bobcat ecology will lead to more sustainable wildlife populations.

LIST OF REFERENCES

Allen ML, Wilmers CC, Elbroch LM, et al (2016) The importance of motivation, weapons, and foul odors in driving encounter competition in carnivores. Ecology 97:1905–1912. doi: 10.1002/ecy.1462

Allen W, Ogilvie S, Blackie H, et al (2014) Bridging disciplines, knowledge systems and cultures in pest management. Environ Manage 53:429–440. doi: 10.1007/s00267-013-0180-z

Anderson CS, Prange S, Gibbs HL (2015) Origin and genetic structure of a recovering bobcat (*Lynx rufus*) population. Can J Zool 93:889–899. doi: 10.1139/cjz-2015-0038

Anderson EM, Lovallo MJ (2003) Bobcat and Lynx. In: Feldhamer GA, Thompson BC, Chapman JA (eds) Wild Mammals of North America: Biology, management, and conservation, 2nd edn. Johns Hopkins University Press, Baltimore, MD, pp 758–786

Austin Z, Smart JCR, Yearley S, et al (2010) Identifying conflicts and opportunities for collaboration in the management of a wildlife resource: a mixed-methods approach. Wildl Res 37:647. doi: 10.1071/WR10057

Ayliffe LK, Cerling TE, Robinson T, et al (2004) Turnover of carbon isotopes in tail hair and breath CO^2 of horses fed an isotopically varied diet. Oecologia 139:11–22. doi: 10.1007/s00442-003-1479-x

Baigas PE, Squires JR, Olson LE, et al (2017) Using environmental features to model highway crossing behavior of Canada lynx in the Southern Rocky Mountains. Landsc Urban Plan 157:200–213. doi: 10.1016/j.landurbplan.2016.06.007

Ballard HL, Robinson LD, Young AN, et al (2017) Contributions to conservation outcomes by natural history museum-led citizen science: Examining evidence and next steps. Biol Conserv 208:87–97. doi: 10.1016/j.biocon.2016.08.040

Bateman PW, Fleming PA (2012) Big city life: carnivores in urban environments. J Zool 287:1–23. doi: 10.1111/j.1469-7998.2011.00887.x

Bauer M (2018) Assessing the effects of habitat restoration on shrubland specialists: case study on the New England cottontail and shrubland birds. M.S. thesis, University of New Hampshire

Beerli P (2013) MIGRATE documentation. Florida State University. http://popgen.sc.fsu.edu/migratedoc.pdf. Accessed 3 March 2018

Beerli P, Felsenstein J (2001) Maximum likelihood estimation of a migration matrix and effective population sizes in n subpopulations by using a coalescent approach. Proc Natl Acad Sci 98:4563–4568. doi: 10.1073/pnas.081068098

Ben-David M, Flaherty EA (2012) Stable isotopes in mammalian research: a beginner's guide. J Mammal 93:312–328

Birnie-Gauvin K, Peiman KS, Gallagher AJ, et al (2016) Sublethal consequences of urban life for wild vertebrates. Environ Rev 24:416–425. doi: 10.1139/er-2016-0029

Boonstra R (2013) Reality as the leading cause of stress: rethinking the impact of chronic stress in nature. Funct Ecol 27:11–23. doi: 10.1111/1365-2435.12008

Boonstra R, Dušek A, Lane JE, Boutin S (2017) When the ball is in the female's court: How the scramble-competition mating system of the North American red squirrel has shaped male physiology and testosterone dynamics. Gen Comp Endocrinol 252:162–172. doi: 10.1016/j.ygcen.2017.06.016

Bourbonnais ML, Nelson TA, Cattet MRL, et al (2014) Environmental factors and habitat use influence body condition of individuals in a species at risk, the grizzly bear. Conserv Physiol 2:cou43. doi: 10.1093/conphys/cou043

Bourbonnais ML, Nelson TA, Cattet MRL, et al (2013) Spatial analysis of factors influencing long-term stress in the grizzly bear (*Ursus arctos*) population of Alberta, Canada. PLoS ONE 8:e83768. doi: 10.1371/journal.pone.0083768

Braga CA de C, Prevedello JA, Pires MRS (2015) Effects of cornfields on small mammal communities: a test in the Atlantic Forest hotspot. J Mammal 96:938–945. doi: 10.1093/jmammal/gyv094

Brearley G, McAlpine C, Bell S, Bradley A (2012) Influence of urban edges on stress in an arboreal mammal: a case study of squirrel gliders in southeast Queensland, Australia. Landsc Ecol 27:1407–1419. doi: 10.1007/s10980-012-9790-8

Broman DJA (2012) A comparison of bobcat (*Lynx rufus*) habitat suitability models derived from radio telemetry and incidental observations. Master's Thesis, University of New Hampshire

Broman DJA, Litvaitis JA, Ellingwood M, et al (2014) Modeling bobcat *Lynx rufus* habitat associations using telemetry locations and citizen-scientist observations: are the results comparable? Wildl Biol 20:229–237

Bryan HM, Darimont CT, Paquet PC, et al (2013) Stress and reproductive hormones in grizzly bears reflect nutritional benefits and social consequences of a salmon foraging niche. PLoS ONE 8:e80537. doi: 10.1371/journal.pone.0080537

Burakowski EA, Wake CP, Braswell B, Brown DP (2008) Trends in wintertime climate in the northeastern United States: 1965–2005. J Geophys Res 113. doi: 10.1029/2008JD009870

Busch DS, Hayward LS (2009) Stress in a conservation context: A discussion of glucocorticoid actions and how levels change with conservation-relevant variables. Biol Conserv 142:2844–2853. doi: 10.1016/j.biocon.2009.08.013

Cambridge Systematics, Inc. (1994) New England Transportation Initiative. States of CT, ME, MA, NH, RI, VT, and the New England Governor's Conference

Cancio I, González-Robles A, Bastida JM, et al (2017) Landscape degradation affects red fox (*Vulpes vulpes*) diet and its ecosystem services in the threatened Ziziphus lotus scrubland habitats of semiarid Spain. J Arid Environ 145:24–34. doi: 10.1016/j.jaridenv.2017.05.004

Carmichael LE, Clark W, Strobeck, C. (2000) Development and characterization of microsatellite loci from lynx (*Lynx canadensis*), and their use in other felids. Mol Ecol 9:2155–2234

Cattet M, Stenhouse GB, Boulanger J, et al (2018) Can concentrations of steroid hormones in brown bear hair reveal age class? Conserv Physiol 6:coy001. doi: 10.1093/conphys/coy001

Cerling TE, Harris JM, MacFadden BJ, et al (1997) Global vegetation change through the Miocene/Pliocene boundary. Nature 389:153–158

Chamberlain CP, Waldbauer JR, Fox-Dobbs K, et al (2005) Pleistocene to recent dietary shifts in California condors. Proc Natl Acad Sci 102:16707–16711. doi: 10.1073/pnas.0508529102

Chisholm BS, Nelson DE, Hobson KA, et al (1983) Carbon isotope measurement techniques for bone collagen: Notes for the archaeologist. J Archaeol Sci 10:355–360

Clare JDJ, Anderson EM, MacFarland DM (2015) Predicting bobcat abundance at a landscape scale and evaluating occupancy as a density index in central Wisconsin. J Wildl Manag 79:469–480. doi: 10.1002/jwmg.844

Clegg SM, Kelly JF, Kimura M, Smith TB (2003) Combining genetic markers and stable isotopes to reveal population connectivity and migration patterns in a Neotropical migrant, Wilson's Warbler (*Wilsonia pusilla*). Mol Ecol 12:819–830

Cobben MMP, Verboom J, Opdam PFM, et al (2011) Projected climate change causes loss and redistribution of genetic diversity in a model metapopulation of a medium-good disperser. Ecography 34:920–932. doi: 10.1111/j.1600-0587.2011.06713.x

Costantini D, Czirják GÁ, Melzheimer J, et al (2019) Sex and species differences of stress markers in sympatric cheetahs and leopards in Namibia. Comp Biochem Physiol A Mol Integr Physiol 227:8–13. doi: 10.1016/j.cbpa.2018.09.002

Coulon A, Fitzpatrick JW, Bowman R, et al (2008) Congruent population structure inferred from dispersal behaviour and intensive genetic surveys of the threatened Florida scrub-jay

(*Aphelocoma cœrulescens*). Mol Ecol 17:1685–1701. doi: 10.1111/j.1365-294X.2008.03705.x

Creel S, Christianson D, Schuette P (2013) Glucocorticoid stress responses of lions in relationship to group composition, human land use, and proximity to people. Conserv Physiol 1:cot021. doi:10.1093/conphys/cot021

Crooks KR (2002) Relative sensitivities of mammalian carnivores to habitat fragmentation. Conserv Biol 16:488–502

Croteau EK, Heist EJ, Nielsen CK (2010) Fine-scale population structure and sex-biased dispersal in bobcats (*Lynx rufus*) from southern Illinois. Can J Zool 88:536–545. doi: 10.1139/Z10-024

Crowley BE, Carter ML, Karpanty SM, et al (2010) Stable carbon and nitrogen isotope enrichment in primate tissues. Oecologia 164:611–626. doi: 10.1007/s00442-010-1701-6

Dantzer B, Fletcher QE, Boonstra R, Sheriff MJ (2014) Measures of physiological stress: a transparent or opaque window into the status, management and conservation of species? Conserv Physiol 2:cou023. doi: 10.1093/conphys/cou023

Davenport MD, Tiefenbacher S, Lutz CK, et al (2006) Analysis of endogenous cortisol concentrations in the hair of rhesus macaques. Gen Comp Endocrinol 147:255–261. doi: 10.1016/j.ygcen.2006.01.005

Davis JM, Stamps JA (2004) The effect of natal experience on habitat preferences. Trends Ecol Evol 19:411–416. doi: 10.1016/j.tree.2004.04.006

De Barba M, Waits LP, Genovesi P, et al (2010) Comparing opportunistic and systematic sampling methods for non-invasive genetic monitoring of a small translocated brown bear population. J Appl Ecol 47:172–181. doi: 10.1111/j.1365-2664.2009.01752.x

De Meeûs T (2018) Revisiting F_{IS}, F_{ST}, Wahlund effects, and null alleles. J Hered 109:446–456. doi: 10.1093/jhered/esx106

de Oliveira TG, Pereira JA (2014) Intraguild predation and interspecific killing as structuring forces of carnivoran communities in South America. J Mamm Evol 21:427–436. doi: 10.1007/s10914-013-9251-4

Dean JR, Leng MJ, Mackay AW (2014) Is there an isotopic signature of the Anthropocene? Anthr Rev 1:276–287. doi: 10.1177/2053019614541631

Decker D, Smith C, Forstchen A, et al (2016) Governance principles for wildlife conservation in the 21st Century. Conserv Lett 9:290–295. doi: 10.1111/conl.12211

Decker DJ, Forstchen AB, Siemer WF, et al (2019) Moving the paradigm from stakeholders to beneficiaries in wildlife management. J Wildl Manag. doi: 10.1002/jwmg.21625

Dibello FJ, Arthur SM, Krohn WB (1990) Food Habits of Sympatric Coyotes *Canis latrans*, Red Foxes *Vulpes vulpes*, and Bobcats *Lynx rufus* in Maine. Can Field-Nat 104:403-408.

Dray S, Dufour A-B (2007) The ade4 package: implementing the duality diagram for ecologists. J Stat Softw 22:. doi: 10.18637/jss.v022.i04

Earl DA, vonHoldt BM (2012) STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. Conserv Genet Resour 4:359–361. doi: 10.1007/s12686-011-9548-7

Edwards PD, Palme R, Boonstra R (2016) Seasonal programming, not competition or testosterone, drives stress-axis changes in a partially-semelparous mammal. Horm Behav 85:96–101. doi: 10.1016/j.yhbeh.2016.08.007

Eggermann J, Theuerkauf J, Pirga B, et al (2013) Stress-hormone levels of wolves in relation to breeding season, pack size, human activity, and prey density. Ann Zool Fenn 50:170–175. doi: 10.5735/086.050.0304

Ellenberg U, Setiawan AN, Cree A, et al (2007) Elevated hormonal stress response and reduced reproductive output in yellow-eyed penguins exposed to unregulated tourism. Gen Comp Endocrinol 152:54–63. doi: 10.1016/j.ygcen.2007.02.022

Ellis RD, McWhorter TJ, Maron M (2012) Integrating landscape ecology and conservation physiology. Landsc Ecol 27:1–12. doi: 10.1007/s10980-011-9671-6

Elton C, Nicholson M (1942) The ten-year cycle in numbers of the Lynx in Canada. J Anim Ecol 11:215. doi: 10.2307/1358

Erlenbach JA, Rode KD, Raubenheimer D, Robbins CT (2014) Macronutrient optimization and energy maximization determine diets of brown bears. J Mammal 95:160–168. doi: 10.1644/13-MAMM-A-161

Evanno G, Regnaut S, Goudet J (2005) Detecting the number of clusters of individuals using the software structure: a simulation study. Mol Ecol 14:2611–2620. doi: 10.1111/j.1365-294X.2005.02553.x

Excoffier L, Foll M, Petit RJ (2009) Genetic consequences of range expansions. Annu Rev Ecol Evol Syst 40:481–501. doi: 10.1146/annurev.ecolsys.39.110707.173414

Faircloth BC, Reid A, Valentine T, et al (2005) Tetranucleotide, trinucleotide, and dinucleotide loci from the bobcat (*Lynx rufus*). Mol Ecol Notes 5:387–389. doi: 10.1111/j.1471-8286.2005.00936.x

Farias AA, Kittlein MJ (2008) Small-scale spatial variability in the diet of pampas foxes (*Pseudalopex gymnocercus*) and human-induced changes in prey base. Ecol Res 23:543–550. doi: 10.1007/s11284-007-0407-7

Farrell LE, Levy DM, Donovan T, et al (2018) Landscape connectivity for bobcat (*Lynx rufus*) and lynx (*Lynx canadensis*) in the northeastern United States. PLoS ONE 13:e0194243. doi: 10.1371/journal.pone.0194243

Felix JD, Elliott EM (2013) The agricultural history of human-nitrogen interactions as recorded in ice core $\delta^{15}N\text{-}NO_3^-$. Geophys Res Lett 40:1642–1646. doi: 10.1002/grl.50209

Fisher JT, Merriam G (2000) Resource patch array use by two squirrel species in an agricultural landscape. Landsc Ecol 15:333-338

Fokidis HB, Orchinik M, Deviche P (2009) Corticosterone and corticosteroid binding globulin in birds: Relation to urbanization in a desert city. Gen Comp Endocrinol 160:259–270. doi: 10.1016/j.ygcen.2008.12.005

Foster DR, Motzkin G, Bernardos D, Cardoza J (2002) Wildlife dynamics in the changing New England landscape. J Biogeogr 29:1337–1357. doi: 10.1046/j.1365-2699.2002.00759.x

Frank B, Monaco A, Bath AJ (2015) Beyond standard wildlife management: a pathway to encompass human dimension findings in wild boar management. Eur J Wildl Res 61:723–730. doi: 10.1007/s10344-015-0948-y

Fritts SH, Sealander JA (1978) Diets of bobcats in Arkansas with special reference to age and sex differences. J Wildl Manag 42:533. doi: 10.2307/3800815

Gadek CR, Newsome SD, Beckman EJ, et al (2018) Why are tropical mountain passes "low" for some species? Genetic and stable-isotope tests for differentiation, migration and expansion in elevational generalist songbirds. J Anim Ecol 87:741–753. doi: 10.1111/1365-2656.12779

Gallé R, Happe A-K, Baillod AB, et al (2019) Landscape configuration, organic management, and within-field position drive functional diversity of spiders and carabids. J Appl Ecol 56:63–72. doi: 10.1111/1365-2664.13257

Godbois IA, Conner LM, Warren RJ (2003) Bobcat diet on an area managed for Northern Bobwhite. Proc Annu Conf Southeast Assoc Fish Wildl Agencies 57:222–227

Goddard MA, Dougill AJ, Benton TG (2010) Scaling up from gardens: biodiversity conservation in urban environments. Trends Ecol Evol 25:90–98. doi: 10.1016/j.tree.2009.07.016

Green RE, Purcell KL, Thompson CM, et al (2018) Reproductive parameters of the fisher (*Pekania pennanti*) in the southern Sierra Nevada, California. J Mammal 99:537–553. doi: 10.1093/jmammal/gyy040

Guillot G, Mortier F, Estoup A (2005) GENELAND: a computer package for landscape genetics. Mol Ecol Notes 5:712–715. doi: 10.1111/j.1471-8286.2005.01031.x

Habel JC, Zachos FE, Dapporto L, et al (2015) Population genetics revisited–towards a multidisciplinary research field. Biol J Linn Soc 115:1-12

Hagen SB, Kopatz A, Aspi J, et al (2015) Evidence of rapid change in genetic structure and diversity during range expansion in a recovering large terrestrial carnivore. Proc R Soc B Biol Sci 282:20150092. doi: 10.1098/rspb.2015.0092

Hamel AF, Meyer JS, Henchey E, et al (2011) Effects of shampoo and water washing on hair cortisol concentrations. Clin Chim Acta 412:382–385. doi: 10.1016/j.cca.2010.10.019

Hamilton WJ, Hunter RP (1939) Fall and winter food habits of Vermont bobcats. J Wild Manag 3:99-103.

Handa RJ, Burgess LH, Kerr JE, O'Keefe JA (1994) Gonadal steroid hormone receptors and sex differences in the hypothalamo-pituitary-adrenal axis. Horm Behav 28:464–476. doi: 10.1006/hbeh.1994.1044

Hansen K (2007) Bobcat: Master of Survival. Oxford University Press, Inc., New York, NY

Harlow HJ, Beck TDI, Walters LM, Greenhouse SS (1990) Seasonal serum glucose, progesterone, and cortisol levels of black bears (*Ursus americanus*). Can J Zool 68:183–187. doi: 10.1139/z90-025

Hart JA, Katembo M, Punga K (1996) Diet, prey selection, and ecological relations of leopard and golden cat in the Ituri Forest, Zaire. Afr J Ecol 34:364–379. doi: 10.1111/j.1365-2028.1996.tb00632.x

Hastings MG, Jarvis JC, Steig EJ (2009) Anthropogenic impacts on nitrogen isotopes of ice-core nitrate. Science 324:1288–1288. doi: 10.1126/science.1170510

Hewitt G (2000) The genetic legacy of the Quaternary ice ages. Nature 405:907

Hewson-Hughes AK, Hewson-Hughes VL, Miller AT, et al (2011) Geometric analysis of macronutrient selection in the adult domestic cat, *Felis catus*. J Exp Biol 214:1039–1051. doi: 10.1242/jeb.049429

Holtgrieve GW, Schindler DE, Hobbs WO, et al (2011) A coherent signature of anthropogenic nitrogen deposition to remote watersheds of the northern hemisphere. Science 334:1545–1548. doi: 10.1126/science.1212267

Hornseth ML, Walpole AA, Walton LR, et al (2014) Habitat loss, not fragmentation, drives occurrence patterns of Canada Lynx at the southern range periphery. PLoS ONE 9:e113511. doi: 10.1371/journal.pone.0113511

Huntington TG, Hodgkins GA, Keim BD, Dudley RW (2004) Changes in the proportion of precipitation occurring as snow in New England (1949-2000). J Clim 17:2626–2636

Jackson AL, Inger R, Parnell AC, Bearhop S (2011) Comparing isotopic niche widths among and within communities: SIBER - Stable Isotope Bayesian Ellipses in R. J Anim Ecol 80:595–602. doi: 10.1111/j.1365-2656.2011.01806.x

Jacobson CA, Organ JF, Decker DJ, et al (2010) A conservation institution for the 21st century: implications for state wildlife agencies. J Wildl Manag 74:203–209. doi: 10.2193/2008-485

Jakobsson M, Rosenberg NA (2007) CLUMPP: a cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. Bioinformatics 23:1801–1806. doi: 10.1093/bioinformatics/btm233

Janecka JE, Tewes ME, Davis IA, et al (2016) Genetic differences in the response to landscape fragmentation by a habitat generalist, the bobcat, and a habitat specialist, the ocelot. Conserv Genet 17:1093–1108. doi: 10.1007/s10592-016-0846-1

Jenni-Eiermann S, Glaus E, Grüebler M, et al (2008) Glucocorticoid response to food availability in breeding barn swallows (*Hirundo rustica*). Gen Comp Endocrinol 155:558–565. doi: 10.1016/j.ygcen.2007.08.011

Jensen K, Simpson SJ, Nielsen VH, et al (2014) Nutrient-specific compensatory feeding in a mammalian carnivore, the mink, *Neovison vison*. Br J Nutr 112:1226–1233. doi: 10.1017/S0007114514001664

Jensen PG, Demers CL, Mcnulty SA, et al (2012) Marten and fisher responses to fluctuations in prey populations and mast crops in the northern hardwood forest. J Wildl Manag 76:489–502. doi: 10.1002/jwmg.322

Jessup DA (2003) Opportunistic research and sampling combined with fish and wildlife management actions or crisis response. ILAR J 44:277–285. doi: 10.1093/ilar.44.4.277

Johnson KM (2012) New Hampshire demographic trends in the twenty-first century. University of New Hampshire

Jombart T, Devillard S, Dufour AB, Pontier D (2008) Revealing cryptic spatial patterns in genetic variability by a new multivariate method. Heredity 101:92–103

Jorde PE, Ryman N (1995) Temporal allele frequency change and estimation of effective size in populations with overlapping generations. Genetics 139:1077–1090

Kalinowski ST (2005) HP-RARE 1.0: a computer program for performing rarefaction on measures of allelic richness. Mol Ecol Notes 5:187–189. doi: 10.1111/j.1471-8286.2004.00845.x

Kays R, Parsons AW, Baker MC, et al (2017) Does hunting or hiking affect wildlife communities in protected areas? J Appl Ecol 54:242–252. doi: 10.1111/1365-2664.12700

Keeling CD (1979) The Suess effect: ^{13}Carbon-^{14}Carbon interrelations. Environ Int 2:229–300. doi: 10.1016/0160-4120(79)90005-9

Kellert SR (1985) Public perceptions of predators, particularly the wolf and coyote. Biol Conserv 31:167–189. doi: 10.1016/0006-3207(85)90047-3

Kelly JF (2000) Stable isotopes of carbon and nitrogen in the study of avian and mammalian trophic ecology. Can J Zool 78:1–27

Kelly LJ, Martínez del Rio C (2010) The fate of carbon in growing fish: an experimental study of isotopic routing. Physiol Biochem Zool 83:473–480. doi: 10.1086/649628

Kitaysky A, Piatt J, Wingfield J (2007) Stress hormones link food availability and population processes in seabirds. Mar Ecol Prog Ser 352:245–258. doi: 10.3354/meps07074

Koen EL, Bowman J, Murray DL, Wilson PJ (2014) Climate change reduces genetic diversity of Canada lynx at the trailing range edge. Ecography 37:754–762. doi: 10.1111/j.1600-0587.2013.00629.x

Kohl KD, Coogan SCP, Raubenheimer D (2015) Do wild carnivores forage for prey or for nutrients?: Evidence for nutrient-specific foraging in vertebrate predators. BioEssays 37:701–709. doi: 10.1002/bies.201400171

Kosterman MK, Squires JR, Holbrook JD, et al (2018) Forest structure provides the income for reproductive success in a southern population of Canada lynx. Ecol Appl 28:1032–1043. doi: 10.1002/eap.1707

Kowarik I (2011) Novel urban ecosystems, biodiversity, and conservation. Environ Pollut 159:1974–1983. doi: 10.1016/j.envpol.2011.02.022

Lafferty DJR, Laudenslager ML, Mowat G, et al (2015) Sex, diet, and the social environment: factors influencing hair cortisol concentration in free-ranging black bears (*Ursus americanus*). PLoS ONE 10:e0141489. doi: 10.1371/journal.pone.0141489

Lamb CT, Mowat G, McLellan BN, et al (2017) Forbidden fruit: human settlement and abundant fruit create an ecological trap for an apex omnivore. J Anim Ecol 86:55–65. doi: 10.1111/1365-2656.12589

Lee EJ, Luedtke JG, Allison JL, et al (2010) The effects of different maceration techniques on nuclear DNA amplification using human bone. J Forensic Sci 55:1032–1038. doi: 10.1111/j.1556-4029.2010.01387.x

Lee JS, Ruell EW, Boydston EE, et al (2012) Gene flow and pathogen transmission among bobcats (*Lynx rufus*) in a fragmented urban landscape. Mol Ecol 21:1617–1631. doi: 10.1111/j.1365-294X.2012.05493.x

Lenarz MS, Nelson ME, Schrage MW, Edwards AJ (2009) Temperature mediated moose survival in northeastern Minnesota. J Wildl Manag 73:503–510. doi: 10.2193/2008-265

Lewandowski E, Specht H (2015) Influence of volunteer and project characteristics on data quality of biological surveys. Conserv Biol 29:713–723. doi: 10.1111/cobi.12481

Lewis JS, Logan KA, Alldredge MW, et al (2015) The effects of urbanization on population density, occupancy, and detection probability of wild felids. Ecol Appl 25:1880–1895

Li R, Chapman S, Thompson M, Schwartz M (2009) Developing a simple method to process bone samples prior to DNA isolation. Leg Med 11:76–79. doi: 10.1016/j.legalmed.2008.09.003

Li R, Liriano L (2011) A bone sample cleaning method using trypsin for the isolation of DNA. Leg Med 13:304–308. doi: 10.1016/j.legalmed.2011.07.001

Lidgard DC, Boness DJ, Bowen WD, McMillan JI (2008) The implications of stress on male mating behavior and success in a sexually dimorphic polygynous mammal, the grey seal. Horm Behav 53:241–248. doi: 10.1016/j.yhbeh.2007.10.003

Linnell JD, Andersen R, Kvam T, et al (2001) Home range size and choice of management strategy for lynx in Scandinavia. Environ Manage 27:869–879

Litvaitis JA (2001) Importance of early successional habitats to mammals in eastern forests. Wildl Soc Bull 29:466–473

Litvaitis JA (1993) Response of early successional vertebrates to historic changes in land use. Conserv Biol 7:866–873

Litvaitis JA, Barbour MS, Brown AL, et al (2008) Testing multiple hypotheses to identify causes of the decline of a lagomorph species: the New England cottontail as a case study. In: Alves PC, Ferrand N, Hackländer K (eds) Lagomorph Biology. Springer Berlin Heidelberg, pp 167–185

Litvaitis JA, Clark AG, Hunt JH (1986a) Prey selection and fat deposits of bobcats (*Felis rufus*) during autumn and winter in Maine. J Mammal 67:389–392

Litvaitis JA, Reed GC, Carroll RP, et al (2015) Bobcats (*Lynx rufus*) as a model organism to investigate the effects of roads on wide-ranging carnivores. Environ Manage 55:1366–1376. doi: 10.1007/s00267-015-0468-2

Litvaitis JA, Sherburne JA, Bissonette JA (1986b) Bobcat habitat use and home range size in relation to prey density. J Wildl Manag 50:110–117

Litvaitis JA, Stevens CL, Mautz WW (1984) Age, sex, and weight of bobcats in relation to winter diet. J Wildl Manag 48:632–635

Litvaitis JA, Tash JP (2008) An approach toward understanding wildlife-vehicle collisions. Environ Manage 42:688–697. doi: 10.1007/s00267-008-9108-4

Litvaitis JA, Tash JP, Stevens CL (2006) The rise and fall of bobcat populations in New Hampshire: Relevance of historical harvests to understanding current patterns of abundance and distribution. Biol Conserv 128:517–528. doi: 10.1016/j.biocon.2005.10.019

Lombardi JV, Comer CE, Scognamillo DG, Conway WC (2017a) Coyote, fox, and bobcat response to anthropogenic and natural landscape features in a small urban area. Urban Ecosyst 20:1239–1248. doi: 10.1007/s11252-017-0676-z

López-Vidal JC, Elizalde-Arellano C, Hernández L, et al (2014) Foraging of the bobcat (*Lynx rufus*) in the Chihuahuan Desert: generalist or specialist? Southwest Nat 59:157–166. doi: 10.1894/F01-CLG-59.1

Lorimer CG (2001) Historical and ecological roles of disturbance in eastern North American forests: 9,000 years of change. Wildl Soc Bull 29:425–439

Losh SC (2010) Stereotypes about scientists over time among US adults: 1983 and 2001. Public Underst Sci 19:372–382. doi: 10.1177/0963662508098576

Lourenço R, del Mar Delgado M, Campioni L, et al (2018) Why do top predators engage in superpredation? From an empirical scenario to a theoretical framework. Oikos 127:1563–1574. doi: 10.1111/oik.05118

Luck M, Wu J (2002) A gradient analysis of urban landscape pattern: a case study from the Phoenix metropolitan region, Arizona, USA. Landsc Ecol 17:327-339

Luna C (1971) The handbook of transportation in America. Popular Library, New York, NY

Luniak M (2004) Synurbization–adaptation of animal wildlife to urban development. In: Proc. 4th Int. Symposium Urban Wildl. Conserv. Tucson. pp 50–55

Lynch GS, Kirby JD, Warren RJ, Conner LM (2008) Bobcat spatial distribution and habitat use relative to population reduction. J Wildl Manag 72:107–112. doi: 10.2193/2006-231

Lyons J, Mastromonaco G, Edwards DB, Schulte-Hostedde AI (2017) Fat and happy in the city: Eastern chipmunks in urban environments. Behav Ecol 28:1464–1471. doi: 10.1093/beheco/arx109

Macbeth BJ, Cattet MRL, Stenhouse GB, et al (2010) Hair cortisol concentration as a noninvasive measure of long-term stress in free-ranging grizzly bears (*Ursus arctos*): considerations with implications for other wildlife. Can J Zool 88:935–949. doi: 10.1139/Z10-057

Madliger CL, Cooke SJ, Love OP (2017) A call for more physiology at conservation conferences. Biodivers Conserv 26:2507–2515. doi: 10.1007/s10531-017-1364-2

Mahard TJ, Litvaitis JA, Tate P, et al (2016) An evaluation of hunter surveys to monitor relative abundance of bobcats. Wildl Soc Bull. doi: 10.1002/wsb.642

Manel S, Schwartz MK, Luikart G, Taberlet P (2003) Landscape genetics: combining landscape ecology and population genetics. Trends Ecol Evol 18:189–197. doi: 10.1016/S0169-5347(03)00008-9

Marston MA (1942) Winter Relations of Bobcats to White-Tailed Deer in Maine. J Wildl Manag 6:328-337.

Martin LB (2009) Stress and immunity in wild vertebrates: Timing is everything. Gen Comp Endocrinol 163:70–76. doi: 10.1016/j.ygcen.2009.03.008

Martinuzzi S, Stewart SI, Helmers DP, et al (2015) The 2010 wildland-urban interface of the conterminous United States. U.S. Department of Agriculture, Forest Service, Northern Research Station. https://doi.org/10.2737/NRS-RMAP-8. Accessed 18 Sept 2015

Mastromonaco GF, Gunn K, McCurdy-Adams H, et al (2014) Validation and use of hair cortisol as a measure of chronic stress in eastern chipmunks (*Tamias striatus*). Conserv Physiol 2:cou055. doi: 10.1093/conphys/cou055

Maurel D, Coutant C, Boissin-Agasse L, Boissin J (1986) Seasonal moulting patterns in three fur bearing mammals: the European badger (*Meles meles*), the red fox (*Vulpes vulpes*), and the mink (*Mustela vison*). A morphological and histological study. Can J Zool 64:1757–1764. doi: 10.1139/z86-265

McCarroll D, Loader NJ (2004) Stable isotopes in tree rings. Quat Sci Rev 23:771–801. doi: 10.1016/j.quascirev.2003.06.017

McClain C, Neeley L (2015) A critical evaluation of science outreach via social media: Its role and impact on scientists. F1000 Res 3:300. doi: 10.12688/f1000research.5918.2

McCune B (2006) Non-parametric habitat models with automatic interactions. J Veg Sci 17:819–830

McEwen BS (2005) Stressed or stressed out: what is the difference? J Psychiatry Neurosci JPN 30:315-318

McFadden KW, Sambrotto RN, Medellin RA, Gompper ME (2006) Feeding habits of endangered pygmy raccoons (*Procyon pygmaeus*) based on stable isotope and fecal analyses. J Mammal 87:501–509

McKinney ML (2002) Urbanization, biodiversity, and conservation. BioScience 52:883-890. doi: 10.1641/0006-3568(2002)052[0883:UBAC]2.0.CO;2

McRae BH, Beier P, Dewald LE, et al (2005) Habitat barriers limit gene flow and illuminate historical events in a wide-ranging carnivore, the American puma. Mol Ecol 14:1965–1977. doi: 10.1111/j.1365-294x.2005.02571.x

Meachen-Samuels J, Van Valkenburgh B (2009) Forelimb indicators of prey-size preference in the Felidae. J Morphol 270:729–744. doi: 10.1002/jmor.10712

Meisingset EL, Loe LE, Brekkum Ø, et al (2018) Spatial mismatch between management units and movement ecology of a partially migratory ungulate. J Appl Ecol 55:745–753. doi: 10.1111/1365-2664.13003

Menotti-Raymond M, David VA, Lyons LA, et al (1999) A genetic linkage map of microsatellites in the domestic cat (*Felis catus*). Genomics 57:9–23

Menotti-Raymond MA, David VA, Wachter LL, et al (2005) An STR forensic typing system for genetic individualization of domestic cat (*Felis catus*) samples. J Forensic Sci 50:1061–1070

Milas G, Šupe-Domić D, Drmić-Hofman I, et al (2018) Weather conditions: a neglected factor in human salivary cortisol research? Int J Biometeorol 62:165–175. doi: 10.1007/s00484-017-1436-8

Millions DG, Swanson BJ (2007) Impact of natural and artificial barriers to dispersal on the population structure of bobcats. J Wildl Manag 71:96–102

Mills LS, Zimova M, Oyler J, et al (2013) Camouflage mismatch in seasonal coat color due to decreased snow duration. Proc Natl Acad Sci 110:7360–7365. doi: 10.1073/pnas.1222724110

Millspaugh JJ, Woods RJ, Hunt KE, et al (2001) Fecal glucocorticoid assays and the physiological stress response in elk. Wildl Soc Bull 29:899–907

Misarti N, Finney B, Maschner H, Wooller MJ (2009) Changes in northeast Pacific marine ecosystems over the last 4500 years: evidence from stable isotope analysis of bone collagen from archeological middens. The Holocene 19:1139–1151. doi: 10.1177/0959683609345075

Moen AN (1976) Energy conservation by white-tailed deer in the winter. Ecology 57:192–198. doi: 10.2307/1936411

Moss WE, Alldredge MW, Pauli JN (2016) Quantifying risk and resource use for a large carnivore in an expanding urban-wildland interface. J Appl Ecol 53:371–378. doi: 10.1111/1365-2664.12563

Muir J (1911) My first summer in the Sierra. The Riverside Press, Cambridge, MA

Mukherjee S, Heithaus MR (2013) Dangerous prey and daring predators: a review. Biol Rev 88:550–563. doi: 10.1111/brv.12014

Nagylaki T (1985) Homozygosity, effective number of alleles, and interdeme differentiation in subdivided populations. Proc Natl Acad Sci 82:8611–8613

Nelson JL, Cypher BL, Bjurlin CD, Creel S (2007) Effects of habitat on competition between kit foxes and coyotes. J Wildl Manag 71:1467–1475. doi: 10.2193/2006-234

New Hampshire Fish and Game Department (2017) New Hampshire wildlife harvest summary. Concord, NH

Newbury RK, Hodges KE (2018) Regional differences in winter diets of bobcats in their northern range. Ecol Evol. 8:1-11 doi: 10.1002/ece3.4576

Newbury RK, Hodges KE (2019) A winter energetics model for bobcats in a deep snow environment. J Therm Biol. 80:56-63 doi: 10.1016/j.jtherbio.2019.01.006

Newig J, Fritsch O (2009) Environmental governance: participatory, multi-level, - and effective? Environ Policy Gov 19:197–214. doi: 10.1002/eet.509

Newsome SD, Bentall GB, Tinker MT, et al (2010) Variation in $d^{13}C$ and $d^{15}N$ diet–vibrissae trophic discrimination factors in a wild population of California sea otters. Ecol Appl 20:1744-1752

Newsome SD, Garbe HM, Wilson EC, Gehrt SD (2015a) Individual variation in anthropogenic resource use in an urban carnivore. Oecologia 178:115–128. doi: 10.1007/s00442-014-3205-2

Newsome TM, Dellinger JA, Pavey CR, et al (2015b) The ecological effects of providing resource subsidies to predators. Glob Ecol Biogeogr 24:1–11. doi: 10.1111/geb.12236

Nielsen CK, Bottom CR, Tebo RG, Greenspan E (2018) Habitat overlap among bobcats (*Lynx rufus*), coyotes (*Canis latrans*), and wild turkeys (*Meleagris gallopavo*) in an agricultural landscape. Can J Zool 96:486–496. doi: 10.1139/cjz-2017-0079

O'Connell TC, Hedges REM, Healey MA, Simpson AHRW (2001) Isotopic comparison of hair, nail and bone. J Archaeol Sci 28:1247–1255. doi: 10.1006/jasc.2001.0698

Ordeñana MA, Crooks KR, Boydston EE, et al (2010) Effects of urbanization on carnivore species distribution and richness. J Mammal 91:1322–1331. doi: 10.1644/09-MAMM-A-312.1

Palomares F, Caro TM (1999) Interspecific Killing among Mammalian Carnivores. Am Nat 153:492-508

Parng E, Crumpacker A, Kurle CM (2014) Variation in the stable carbon and nitrogen isotope discrimination factors from diet to fur in four felid species held on different diets. J Mammal 95:151–159. doi: 10.1644/13-MAMM-A-014.1

Parsons AW, Forrester T, Baker-Whatton MC, et al (2018) Mammal communities are larger and more diverse in moderately developed areas. eLife 7:e38012. doi: 10.7554/eLife.38012

Peakall R, Smouse PE (2012) GENALEX 6.5: genetic analysis in Excel. Population genetic software for teaching and research--an update. Bioinformatics 28:2537–2539. doi: 10.1093/bioinformatics/bts460

Peers MJL, Thornton DH, Murray DL (2013) Evidence for large-scale effects of competition: niche displacement in Canada lynx and bobcat. Proc R Soc B Biol Sci 280:20132495. doi: 10.1098/rspb.2013.2495

Peers MJL, Thornton DH, Murray DL (2012) Reconsidering the specialist-generalist paradigm in niche breadth dynamics: resource gradient selection by Canada lynx and bobcat. PLoS ONE 7:1–10. doi: 10.1371/journal.pone.0051488

Peery MZ, Kirby R, Reid BN, et al (2012) Reliability of genetic bottleneck tests for detecting recent population declines. Mol Ecol 21:3403–3418. doi: 10.1111/j.1365-294X.2012.05635.x

Pilot M, Jędrzejewski W, Sidorovich VE, et al (2012) Dietary differentiation and the evolution of population genetic structure in a highly mobile carnivore. PLoS ONE 7:e39341. doi: 10.1371/journal.pone.0039341

Piry S, Luikart G, Cornuet J. (1999) BOTTLENECK: A computer program for detecting recent reductions in the effective population size using allele frequency data. J Hered 90:502–503

Poessel SA, Burdett CL, Boydston EE, et al (2014) Roads influence movement and home ranges of a fragmentation-sensitive carnivore, the bobcat, in an urban landscape. Biol Conserv 180:224–232. doi: 10.1016/j.biocon.2014.10.010

Pokharel SS, Singh B, Seshagiri PB, Sukumar R (2018) Lower levels of glucocorticoids in crop-raiders: diet quality as a potential 'pacifier' against stress in free-ranging Asian elephants in a human-production habitat. Anim Conserv. doi: 10.1111/acv.12450

Pollentier CD, Lutz RS, Drake D (2017) Female wild turkey habitat selection in mixed forest-agricultural landscapes. J Wildl Mamag 81:487-497 doi:10.1002/jwmg.21214

Potter TI, Stannard HJ, Greenville AC, Dickman CR (2018) Understanding selective predation: Are energy and nutrients important? PLoS ONE 13:e0201300. doi: 10.1371/journal.pone.0201300

Powers JG, Mautz WW, Pekins PJ (1989) Nutrient and energy assimilation of prey by bobcats. J Wildl Manag 53:1004-1008. doi: 10.2307/3809602

Prange S, Gehrt SD, Wiggers EP (2003) Demographic factors contributing to high raccoon densities in urban landscapes. J Wildl Manag 67:324-333. doi: 10.2307/3802774

Prange S, Gehrt SD, Wiggers EP (2004) Influences of anthropogenic resources on raccoon (*Procyon lotor*) movements and spatial distribution. J Mammal 85:483–490. doi: 10.1644/1383946

Pritchard JK, Stephens M, Donnelly P (2000) Inference of population structure using multilocus genotype data. Genetics 155:945–959

Probert BL, Litvaitis JA (1996) Behavioral interactions between invading and endemic lagomorphs: Implications for conserving a declining species. Biol Conserv 76:289–295. doi: 10.1016/0006-3207(95)00127-1

R Core Team (2019) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna

Ratcliffe CS, Crowe TM (2001) The effects of agriculture and the availability of edge habitat on populations of Helmeted Guineafowl *Numida meleagris* and on the diversity and composition of associated bird assemblages in KwaZulu-Natal province, South Africa. Biodivers Conserv 10:2109–2127

Ray J, Sunquist M (2001) Trophic relations in a community of African rainforest carnivores. Oecologia 127:395–408. doi: 10.1007/s004420000604

Raymond M, Rousset F (1995) GENEPOP 1.2: population genetics software for exact tests and ecumenicism. J Hered 86:248–249

Reagan DP (2006) An ecological basis for integrated environmental management. Hum Ecol Risk Assess Int J 12:819–833. doi: 10.1080/10807030600848635

Rebolo-Ifrán N, Carrete M, Sanz-Aguilar A, et al (2015) Links between fear of humans, stress and survival support a non-random distribution of birds among urban and rural habitats. Sci Rep 5:13723. doi: 10.1038/srep13723

Reding DM, Bronikowski AM, Johnson WE, Clark WR (2012) Pleistocene and ecological effects on continental-scale genetic differentiation in the bobcat (*Lynx rufus*). Mol Ecol 21:3078–3093. doi: 10.1111/j.1365-294X.2012.05595.x

Reding DM, Carter CE, Hiller TL, Clark WR (2013a) Using population genetics for management of bobcats in Oregon. Wildl Soc Bull 37:342–351. doi: 10.1002/wsb.243

Reding DM, Cushman SA, Gosselink TE, Clark WR (2013b) Linking movement behavior and fine-scale genetic structure to model landscape connectivity for bobcats (*Lynx rufus*). Landsc Ecol 28:471–486. doi: 10.1007/s10980-012-9844-y

Reed GC (2013) Bobcats in New Hampshire: Understanding the relationships between habitat suitability, connectivity, and abundance in a changing landscape. Masters Thesis, University of New Hampshire

Reed GC, Litvaitis JA, Callahan C, et al (2016) Modeling landscape connectivity for bobcats using expert-opinion and empirically derived models: how well do they work? Anim Conserv 20:308–320. doi: 10.1111/acv.12325

Reed GC, Litvaitis JA, Ellingwood M, et al (2017) Describing habitat suitability of bobcats (*Lynx rufus*) using several sources of information obtained at multiple spatial scales. Mamm Biol 82:17–26. doi: 10.1016/j.mambio.2016.10.002

Rehnus M, Bollmann K (2016) Non-invasive genetic population density estimation of mountain hares (*Lepus timidus*) in the Alps: systematic or opportunistic sampling? Eur J Wildl Res 62:737–747. doi: 10.1007/s10344-016-1053-6

Reid AE (2006) Spatial genetic structure of four bobcat populations in the southeastern US. M.S. thesis, University of Georgia

Resasco J, Tuff KT, Cunningham SA, et al (2018) Generalist predator's niche shifts reveal ecosystem changes in an experimentally fragmented landscape. Ecography 41:1209–1219. doi: 10.1111/ecog.03476

Rice WR (1989) Analyzing tables of statistical tests. Evolution 43:223-225. doi: 10.2307/2409177

Riley SJ, Decker DJ, Carpenter LH, Organ JF (2002) The essence of wildlife management. Wildl Soc Bull 30:585-593

Riley SJ, Ford JK, Triezenberg HA, Lederle PE (2018) Stakeholder trust in a state wildlife agency. J Wildl Manag. doi: 10.1002/jwmg.21501

Riley SPD, Boydston EE, Crooks KR, Lyren LM (2010) Bobcats (*Lynx rufus*). In: Gehrt SD, Riley SPD, Cypher BL (eds) Urban carnivores: ecology, conflict, and conservation. Johns Hopkins University Press, Baltimore, pp 121–138

Riley SPD, Bromley C, Poppenga RH, et al (2007) Anticoagulant exposure and notoedric mange in bobcats and mountain lions in urban southern California. J Wildl Manag 71:1874–1884. doi: 10.2193/2005-615

Riley SPD, Pollinger JP, Sauvajot RM, et al (2006) A southern California freeway is a physical and social barrier to gene flow in carnivores. Mol Ecol 15:1733–1741. doi: 10.1111/j.1365-294X.2006.02907.x

Riley SPD, Sauvajot RM, Fuller TK, et al (2003) Effects of urbanization and habitat fragmentation on bobcats and coyotes in southern California. Conserv Biol 17:566–576

Roberts NM, Crimmins SM (2010) Bobcat population status and management in North America: evidence of large-scale population increase. J Fish Wildl Manag 1:169–174

Romero LM (2004) Physiological stress in ecology: lessons from biomedical research. Trends Ecol Evol 19:249–255. doi: 10.1016/j.tree.2004.03.008

Rose C, Prange S (2015) Diet of the recovering Ohio bobcat (*Lynx rufus*) with a consideration of two subpopulations. Am Midl Nat 173:305–317

Roth JD, Hobson KA (2000) Stable carbon and nitrogen isotopic fractionation between diet and tissue of captive red fox: implications for dietary reconstruction. Can J Zool 78:848-852

Rucklidge GJ, Milne G, McGaw BA, et al (1992) Turnover rates of different collagen types measured by isotope ratio mass spectrometry. Biochim Biophys Acta BBA-Gen Subj 1156:57–61

Ruegg KC, Anderson EC, Harrigan RJ, et al (2017) Genetic assignment with isotopes and habitat suitability (GAIAH), a migratory bird case study. Methods Ecol Evol 8:1241-1252 doi: 10.1111/2041-210X.12800

Ruell EW, Riley SPD, Douglas MR, et al (2012) Urban habitat fragmentation and genetic population structure of bobcats in coastal southern California. Am Midl Nat 168:265–280. doi: 10.1674/0003-0031-168.2.265

Rueness EK, Stenseth NC, O'Donoghue M, et al (2003) Ecological and genetic spatial structuring in the Canadian lynx. Nature 425:69–72. doi: 10.1038/nature01942

Rundel CW, Wunder MB, Alvarado AH, et al (2013) Novel statistical methods for integrating genetic and stable isotope data to infer individual-level migratory connectivity. Mol Ecol 22:4163–4176. doi: 10.1111/mec.12393

Russ A, Reitemeier S, Weissmann A, et al (2015) Seasonal and urban effects on the endocrinology of a wild passerine. Ecol Evol 5:5698–5710. doi: 10.1002/ece3.1820

Russell E, Koren G, Rieder M, Van Uum S (2012) Hair cortisol as a biological marker of chronic stress: Current status, future directions and unanswered questions. Psychoneuroendocrinology 37:589–601. doi: 10.1016/j.psyneuen.2011.09.009

Sacks BN, Mitchell BR, Williams CL, Ernest HB (2005) Coyote movements and social structure along a cryptic population genetic subdivision. Mol Ecol 14:1241–1249. doi: 10.1111/j.1365-294X.2005.02473.x

Safner T, Miller MP, McRae BH, et al (2011) Comparison of bayesian clustering and edge detection methods for inferring boundaries in landscape genetics. Int J Mol Sci 12:865–889. doi: 10.3390/ijms12020865

Samarasin P, Shuter BJ, Wright SI, Rodd FH (2017) The problem of estimating recent genetic connectivity in a changing world. Conserv Biol 31:126–135. doi: 10.1111/cobi.12765

Scheel D (1993) Profitability, encounter rates, and prey choice of African lions. Behav Ecol 4:90–97. doi: 10.1093/beheco/4.1.90

Schwartz CC, Fortin JK, Teisberg JE, et al (2014) Body and diet composition of sympatric black and grizzly bears in the Greater Yellowstone Ecosystem. J Wildl Manag 78:68–78. doi: 10.1002/jwmg.633

Serieys LEK, Lea A, Pollinger JP, et al (2014) Disease and freeways drive genetic change in urban bobcat populations. Evol Appl 8:75–92. doi: 10.1111/eva.12226

Seton ET (1925) Lives of Game Animals: Cats, Wolves, and Foxes. Doubleday, Garden City, NY

Shipley LA, Forbey JS, Moore BD (2009) Revisiting the dietary niche: when is a mammalian herbivore a specialist? Integr Comp Biol 49:274–290. doi: 10.1093/icb/icp051

Smith JA, Thomas AC, Levi T, et al (2018) Human activity reduces niche partitioning among three widespread mesocarnivores. Oikos 127:890–901. doi: 10.1111/oik.04592

Spears BL, Ballard WB, Wallace MC, et al (2003) Coyote, *Canis latrans* - Rio Grande Turkey, *Meleagris gallopavo* intermedia, Interactions. Can Field-Nat 117:645-647. doi: 10.22621/cfn.v117i4.816

Stephens RB (2018) Small mammal community dynamics and the dispersal of mycorrhizal fungi. Ph.D. dissertation, University of New Hampshire

Stevenson ET, Gese EM, Neuman-Lee LA, French SS (2018) Levels of plasma and fecal glucocorticoid metabolites following an ACTH challenge in male and female coyotes (*Canis latrans*). J Comp Physiol B 188:345–358. doi: 10.1007/s00360-017-1125-2

Stock BC, Jackson AL, Ward EJ, et al (2018) Analyzing mixing systems using a new generation of Bayesian tracer mixing models. PeerJ 6:e5096. doi: 10.7717/peerj.5096

Svanbäck R, Quevedo M, Olsson J, Eklöv P (2015) Individuals in food webs: the relationships between trophic position, omnivory and among-individual diet variation. Oecologia 178:103–114. doi: 10.1007/s00442-014-3203-4

Szteren D, Aurioles-Gamboa D, Labrada-Martagón V, et al (2018) Historical age-class diet changes in South American fur seals and sea lions in Uruguay. Mar Biol 165:59. doi: 10.1007/s00227-018-3315-1

Terwissen CV, Mastromonaco GF, Murray DL (2014) Enzyme immunoassays as a method for quantifying hair reproductive hormones in two felid species. Conserv Physiol 2:cou044. doi: 10.1093/conphys/cou044

Terwissen CV, Mastromonaco GF, Murray DL (2013) Influence of adrenocorticotrophin hormone challenge and external factors (age, sex, and body region) on hair cortisol concentration in Canada lynx (*Lynx canadensis*). Gen Comp Endocrinol 194:162–167. doi: 10.1016/j.ygcen.2013.09.010

Tigas LA, Van Vuren DH, Sauvajot RM (2002) Behavioral responses of bobcats and coyotes to habitat fragmentation and corridors in an urban environment. Biol Conserv 108:299–306. doi: 10.1016/S0006-3207(02)00120-9

Tucker MA, Böhning-Gaese K, Fagan WF, et al (2018) Moving in the Anthropocene: global reductions in terrestrial mammalian movements. Science 359:466–469. doi: 10.1126/science.aam9712

U.S. Census Bureau (2018) Quick facts. https://www.census.gov/quickfacts/ Accessed 3 Jan 2019

U.S. Geological Survey (2011) NLCD 2011 land cover. US Geol Surv Sioux Falls, SD

VanOosterhout C, Hutchinson WF, Wills DPM, Shipley P (2004) MICRO-CHECKER: software for identifying and correcting genotyping errors in microsatellite data. Mol Ecol Notes 4:535–538. doi: 10.1111/j.1471-8286.2004.00684.x

Walski TW (2015) New Hampshire wild turkey assessment. New Hampshire Fish and Game Department

Waples RS, Do C (2008) LDNE: a program for estimating effective population size from data on linkage disequilibrium. Mol Ecol Resour 8:753–756. doi: 10.1111/j.1755-0998.2007.02061.x

Warsen SA, Frair JL, Teece MA (2014) Isotopic investigation of niche partitioning among native carnivores and the non-native coyote (*Canis latrans*). Isotopes Environ Health Stud 50:414–424. doi: 10.1080/10256016.2014.897946

Webb E, Thomson S, Nelson A, et al (2010) Assessing individual systemic stress through cortisol analysis of archaeological hair. J Archaeol Sci 37:807–812. doi: 10.1016/j.jas.2009.11.010

Williamson RD (1983) Identification of urban habitat components which affect eastern gray squirrel abundance. Urban Ecol 7:345–356. doi: 10.1016/0304-4009(83)90020-7

Wilson RR, Blankenship TL, Hooten MB, Shivik JA (2010) Prey-mediated avoidance of an intraguild predator by its intraguild prey. Oecologia 164:921–929. doi: 10.1007/s00442-010-1797-8

Wingfield JC, Romero LM (2011) Adrenocortical responses to stress and their modulation in free-living vertebrates. In: Terjung R (ed) Comprehensive Physiology. John Wiley & Sons, Inc., Hoboken, NJ, USA

Wolf TE, Valades GB, Simelane P, et al (2018) The relationship between physical injury, body condition and stress-related hormone concentrations in free-ranging giraffes. Wildl Biol 2018:wlb.00460. doi: 10.2981/wlb.00460

Woolf A, Hubert GF (1998) Status and management of bobcats in the United States over three decades: 1970s-1990s. Wildl Soc Bull 26:287–293

Young JK, Golla JM, Broman D, et al (2019) Estimating density of an elusive carnivore in urban areas: use of spatially explicit capture-recapture models for city-dwelling bobcats. Urban Ecosyst. doi: 10.1007/s11252-019-0834-6

APPENDICES

Appendix A.

UNH STABLE ISOTOPE LABORATORY ANALYTICAL METHODS

The ratio of sample analyses to in-house standards analyzed was less than 4:1. The measurement uncertainty of the instrument as determined by repeated analyses of in-house QA/QC standards was ± 0.10 ‰ (± 1σ) and ± 0.20 ‰ (± 1σ) for $\delta^{13}C$ and $\delta^{15}N$, respectively.

The measured ^{13}C abundance values are reported relative to (Vienna Pee Dee Belemnite) VPDB based on a 3-point normalization using contemporaneously analyzed in-house standards: Sorghum Flour ($\delta^{13}CVPDB$ = -13.81‰), Atlantic Cod ($\delta^{13}CVPDB$ = -17.95‰), and Black Spruce Needles ($\delta^{13}CVPDB$ = -27.98‰). Also, 3 additional in-house standards were analyzed as unknowns for QA/QC: Corn Gluten ($\delta^{13}CVPDB$ = -13.01‰), Tuna Muscle ($\delta^{13}CVPDB$ = -17.93‰), and NIST 1515 Apple Leaves ($\delta^{13}CVPDB$ = -27.04‰). Stable carbon isotopic values of in-house standards were quantified relative to VPDB on a scale normalized such that the $\delta^{13}C$ values of NBS 19 calcium carbonate and LSVEC lithium carbonate are +1.95 ‰ and –46.6 ‰, respectively, using a multi-point normalization (7 points) using the following international reference materials and isotopic values: IAEA-CH-7 ($\delta^{13}CVPDB$ = -32.151‰), NBS22 ($\delta^{13}CVPDB$ = -30.03‰), USGS40 ($\delta^{13}CVPDB$ = -26.39‰), USGS42 ($\delta^{13}CVPDB$ = -21.28‰), USGS43 ($\delta^{13}CVPDB$ = -21.09‰), IAEA-CH-6 ($\delta^{13}CVPDB$ = -10.449‰), and USGS41 ($\delta^{13}CVPDB$ = +37.63‰).

The measured ^{15}N abundance values are reported relative to atmospheric nitrogen (air) based on a 3-point normalization using contemporaneously analyzed in-house standards: Sorghum Flour (δ^{15}NAir = +1.75‰), Atlantic Cod (δ^{15}NAir = +13.60‰), and Black Spruce Needles (δ^{15}NAir = -7.68‰). Also, 3 additional in-house standards were analyzed as unknowns for QA/QC: Corn Gluten (δ^{15}NAir = +4.75‰), Tuna Muscle (δ^{15}NAir = +12.29‰), and NIST 1515 Apple Leaves (δ^{15}NAir = +0.53‰). Stable nitrogen isotopic values of in-house standards were quantified relative to atmospheric nitrogen using a multi-point normalization (7 points) using the following international reference materials and isotopic values: USGS25 (δ^{15}NAir = -30.40‰), USGS40 (δ^{15}NAir = -4.52‰), IAEA-N1 (δ^{15}NAir = +0.40‰), USGS42 (δ^{15}NAir = +8.05‰), USGS43 (δ^{15}NAir = +8.44‰), IAEA-N2 (δ^{15}NAir = +20.30‰), and USGS41 (δ^{15}NAir = +47.57‰).

Appendix B.

HISTORIC AND CONTEMPORARY GENETIC DATA

Data for genetic analyses in chapter 1 have been published in the online data depository Dryad and can be retrieved at: https://doi.org/10.5061/dryad.t77f1p4.

Appendix C.

BOBCAT ISOTOPE DATA

ID	Period	Type	Year	Season	State-Town	NHStPlX	NHStPlY	Sex	Age	Weight_kg	d13C	d15N	%N	%C	C:N
ACT155	Contemp	Hair	2015	Fall	NH-Mont Vernon	298701	44675	M	A	5.22	-22.88	7.41	0.15	0.45	3.05
ACT156	Contemp	Hair	2015	Fall	NH-Loudon	318283	91231	M	A	12.81	-22.84	6.15	0.15	0.45	3.02
ACT157	Contemp	Hair	2015	Spring	NH-Chester	333917	51983	F	J	7.71	-23.59	5.56	0.14	0.46	3.24
ACT158	Contemp	Hair	2015	Fall	NH-Cornish	247146	108416	M		13.83	-22.68	7.17	0.14	0.46	3.26
ACT159	Contemp	Hair	2015	Fall	NH-Grafton	275315	119574	M		13.83	-22.77	6.66	0.14	0.48	3.45
ACT160	Contemp	Hair	2015	Fall	NH-Pittsburg	332701	293720	F		8.73	-25.78	5.07	0.14	0.47	3.33
ACT161	Contemp	Hair	2016	Fall	NH-Ashland	302926	134970	M		9.98	-22.29	6.52	0.14	0.46	3.23
ACT162	Contemp	Hair	2015	Fall	NH-Laconia	315280	119152	M		12.25	-22.63	6.53	0.13	0.41	3.14
ACT163	Contemp	Hair	2015	Fall	NH-New Boston	298424	53028	F		8.85	-22.50	6.43	0.15	0.47	3.20
ACT164	Contemp	Hair	2016	Fall	NH-Gilford	322756	117577	F		6.35	-21.30	5.85	0.14	0.47	3.28
ACT165	Contemp	Hair	2015	Fall	NH-Pelham	328067	25987	M		9.98	-22.81	8.62	0.15	0.47	3.09
ACT166	Contemp	Hair	2016	Fall	NH-Hooksett	318748	63447	M		11.79	-22.98	8.70	0.14	0.49	3.43
ACT167	Contemp	Hair	2015	Fall	NH-Allenstown	323119	70888	M		10.09	-23.60	7.40	0.13	0.46	3.41
ACT168	Contemp	Hair	2015	Fall	NH-Lyme	263857	145113	M		14.06	-24.19	7.41	0.14	0.46	3.22
ACT169	Contemp	Hair	2016	Fall	NH-Merrimack	312087	39415	F		7.03	-23.68	7.96	0.15	0.47	3.14
ACT170	Contemp	Hair	2016	Fall	NH-Hancock	273151	52907				-23.50	7.83	0.14	0.49	3.48
ACT171	Contemp	Hair	2016	Fall	NH-Langdon	241893	74554	M		12.47	-23.07	9.34	0.14	0.45	3.26
ACT172	Contemp	Hair	2015	Fall	NH-Westmoreland	237570	52378	M		14.06	-22.40	7.17	0.14	0.46	3.23
ACT173	Contemp	Hair	2016	Fall	NH-Greenfield	283372	48903	F		7.94	-21.53	5.61	0.15	0.45	3.01
ACT174	Contemp	Hair	2013	Spring	NH-Unity	250973	88772	F		6.58	-21.81	7.27	0.14	0.48	3.36
ACT175	Contemp	Hair	2016	Fall	NH-Swanzey	248570	40459	F		7.26	-21.37	4.92	0.15	0.46	3.09
ACT177	Contemp	Hair	2015	Fall	NH-Charlestown	240924	83210	M		5.67	-23.00	6.64	0.14	0.47	3.32
ACT179	Contemp	Hair	2012	Spring	NH-Madbury	359014	75215	M		8.85	-23.23	6.39	0.15	0.45	3.04
ACT180	Contemp	Hair	2012	Spring	NH-Allenstown	323119	70888	M		15.42	-23.52	6.14	0.14	0.44	3.06
ACT181	Contemp	Hair	2012	Fall	NH-Hampton	367771	49070	M		15.65	-24.48	7.68	0.15	0.45	3.01
ACT182	Contemp	Hair	2012	Fall	NH-Concord	308703	81159	M		10.89	-22.23	6.57	0.14	0.45	3.12
ACT183	Contemp	Hair	2016	Fall	NH-Webster	295758	88845	F		5.44	-23.02	6.50	0.15	0.45	3.08

ACT184	Contemp	Hair	2017	Fall	NH-Walpole	239677	64019	M		6.01	-22.66	7.11	0.15	0.45	3.11
ACT185	Contemp	Hair	2016	Fall	NH-Acworth	249629	79810	M		4.65	-21.88	6.19	0.15	0.45	3.02
ACT186	Contemp	Hair	2016	Spring	NH-Swanzey	248570	40459	F		6.35	-22.09	5.53	0.15	0.45	3.03
ACT187	Contemp	Hair	2016	Spring	NH-Walpole	239677	64019	M		4.54	-21.20	7.12	0.14	0.44	3.08
ACT188	Contemp	Hair	2016	Fall	NH-Surry	245905	58082	M		13.61	-23.23	7.61	0.15	0.44	3.04
ACT189	Contemp	Hair	2016	Fall	NH-Keene	248327	50109	M		9.98	-22.13	7.51	0.14	0.42	3.03
ACT190	Contemp	Hair	2016	Fall	NH-Washington	265640	75941	F		8.16	-21.60	5.77	0.15	0.44	3.04
ACT191	Contemp	Hair	2016	Fall	NH-New Ipswich	282974	27668	M		15.42	-22.51	7.34	0.15	0.44	3.02
ACT192	Contemp	Hair	2016	Fall	NH-Washington	265640	75941	M		14.51	-19.31	7.62	0.14	0.44	3.08
ACT193	Contemp	Hair	2016	Fall	NH-Conway	347698	167756	M		7.03	-22.74	6.64	0.14	0.45	3.14
ACT194	Contemp	Hair	2016	Fall	NH-Milan	335781	229703	F		3.06	-23.89	6.42	0.14	0.44	3.16
ACT195	Contemp	Hair	2016	Fall	NH-Franconia	300422	187118	F		3.86	-26.35	5.64	0.15	0.46	3.12
ACT196	Contemp	Hair	2016	Fall	NH-Berlin	332355	220823	F		5.44	-24.30	6.38	0.15	0.45	3.08
ACT197	Contemp	Hair	2017	Fall	NH-Wilton	291307	36824	F		4.99	-21.55	6.71	0.14	0.45	3.10
ALT001	Contemp	Hair	2010	Fall	NH-Richmond	250446	29685	F	J	6.80	-21.03	5.56	0.15	0.44	2.90
ALT002	Contemp	Hair	2010	Fall	NH-Antrim	274230	61517	F	J	7.50	-23.12	5.96	0.15	0.46	3.13
ALT026	Contemp	Hair	2009	Fall	NH-Gilsum	251292	60163	M	A	13.50	-24.05	7.39	0.14	0.46	3.33
ALT027	Contemp	Hair	2010	Fall	NH-Westmoreland	237570	52378	M	A	8.50	-20.65	6.33	0.15	0.47	3.10
ALT028	Contemp	Hair	2010	Fall	NH-Hancock	273151	52907	F	A	12.25	-22.72	7.56	0.14	0.44	3.15
ALT029	Contemp	Hair	2010	Fall	NH-Antrim	274230	61517	M	A	16.75	-23.09	6.34	0.15	0.46	3.07
ALT030	Contemp	Hair	2010	Fall	NH-Nelson	262918	54984	M	A	14.50	-22.61	7.42	0.14	0.45	3.09
ALT031	Contemp	Hair	2010	Fall	NH-Harrisville	265335	49139	M	A	12.70	-18.77	8.04	0.11	0.37	3.22
ALT032	Contemp	Hair	2010	Fall	NH-Harrisville	265335	49139	M	A	14.10	-24.57	7.55	0.13	0.50	3.83
ALT033	Contemp	Hair	2010	Fall	NH-Alstead	247666	68433	M	A	11.50	-22.39	7.26	0.14	0.42	3.14
ALT034	Contemp	Hair	2010	Fall	NH-Jaffrey	267871	36648	M	A	16.00	-22.98	7.29	0.15	0.44	3.04
ALT039	Contemp	Hair	2010	Fall	NH-Alstead	247666	68433	M	A	11.50	-23.09	6.85	0.16	0.47	2.94
ALT040	Contemp	Hair	2010	Fall	NH-Walpole	239677	64019	M	A	12.30	-22.49	7.95	0.15	0.45	2.95
MA101	Contemp	Hair	2010	Fall	MA-Williamstown	172584	22815				-23.84	6.71	0.15	0.47	3.12
ME011	Contemp	Hair	2016	Fall	ME-Berwick	366753	89273	M		11.34	-23.41	6.13	0.15	0.43	2.91
VT102	Contemp	Hair	2014	Fall	VT-BROOKFIELD	225818	170247	F	J	4.58	-25.15	6.56	0.16	0.46	2.82
VT107	Contemp	Hair	2014	Fall	VT-Greensboro	250622	233926	M	A	10.80	-25.54	6.22	0.15	0.45	2.94

VT116	Contemp	Hair	2014	Fall	VT-SHARON	238057	142796	M	A	7.89	-26.46	7.52	0.10	0.55	5.49
VT118	Contemp	Hair	2014	Fall	VT-TROY	243498	271201	F	A	7.48	-25.47	5.70	0.16	0.44	2.82
VT120	Contemp	Hair	2015	Fall	VT-WALDEN	254681	220279	F	J	3.08	-25.82	6.16	0.15	0.44	2.96
VT122	Contemp	Hair	2014	Fall	VT-WELLS	176757	104742	F	A	6.44	-22.91	6.34	0.14	0.44	3.06
VT123	Contemp	Hair	2014	Fall	VT-WEYBRIDGE	174961	173000	M	J	5.40	-23.87	8.68	0.16	0.45	2.83
VT124	Contemp	Hair	2014	Fall	VT-Whitingham	201796	32141	M	A	9.71	-22.95	7.76	0.15	0.44	2.85
VT126	Contemp	Hair	2014	Fall	VT-WINDSOR	238984	108809	F	A	7.71	-22.92	6.47	0.15	0.46	3.08
VT129	Contemp	Hair	2014	Fall	VT-SHARON	238057	142796	F	A	7.12	-22.90	6.82	0.15	0.46	3.11
VT130	Contemp	Hair	2014	Fall	VT-WHITING	176770	153559	M	J	3.40	-23.65	8.29	0.15	0.43	2.95
VT131	Contemp	Hair	2014	Fall	VT- Whitingham	201796	32141	F	A	7.08	-23.45	7.78	0.15	0.45	3.03
VT132	Contemp	Hair	2014	Fall	VT-MONKTON	182901	192972	M	J	4.40	-21.72	6.47	0.15	0.46	3.14
VT134	Contemp	Hair	2014	Fall	VT-MT HOLLY	207864	103847	M	A	11.75	-24.01	6.27	0.15	0.51	3.36
VT135	Contemp	Hair	2015	Fall	VT-ORWELL	169124	146400	M	A	9.53	-22.62	6.75	0.15	0.46	3.05
VT136	Contemp	Hair	2015	Fall	VT-SHOREHAM	167671	156242	F	A	7.71	-23.51	6.74	0.14	0.48	3.35
VT137	Contemp	Hair	2014	Fall	VT-W FAIRLEE	255019	160080	F	J	3.18	-22.89	6.87	0.14	0.45	3.20
VT138	Contemp	Hair	2014	Fall	VT-W FAIRLEE	255019	160080	F	A	6.30	-22.37	6.52	0.15	0.46	3.06
VT140	Contemp	Hair	2014	Fall	VT-DORSET	187560	85223	F	A	7.39	-23.54	6.68	0.15	0.46	3.04
VT141	Contemp	Hair	2014	Fall	VT-BARRE CITY	232707	189182	F	J	7.26	-24.03	7.41	0.15	0.45	2.97
VT142	Contemp	Hair	2014	Fall	VT-MONKTON	182901	192972	F	A	7.53	-23.60	6.72	0.15	0.46	3.11
VT143	Contemp	Hair	2014	Fall	VT-Starksboro	192212	192926	M	A	11.34	-21.43	8.70	0.15	0.45	3.01
VT144	Contemp	Hair	2014	Fall	VT-SUDBURY	178207	144561	M	A	11.34	-23.44	8.24	0.15	0.45	2.98
VT146	Contemp	Hair	2014	Fall	VT-SHOREHAM	167671	156242	M	J	4.35	-21.77	7.12	0.15	0.44	2.98
VT148	Contemp	Hair	2014	Fall	VT-W RUTLAND	187402	124675	M	A	9.84	-22.12	7.77	0.14	0.45	3.14
VT149	Contemp	Hair	2014	Fall	VT-MT HOLLY	207864	103847	M	A	10.80	-23.43	7.10	0.15	0.46	3.09
VT150	Contemp	Hair	2015	Fall	VT-SHOREHAM	167671	156242	F	A	6.44	-22.11	6.12	0.15	0.46	3.14
VT151	Contemp	Hair	2015	Fall	VT-SHOREHAM	167671	156242	F	A	6.89	-22.73	6.38	0.15	0.45	3.02
VT152	Contemp	Hair	2014	Fall	VT-BENNINGTON	173647	43968	F	A	7.17	-23.56	7.82	0.14	0.45	3.12
VT153	Contemp	Hair	2014	Fall	VT-WHITING	176770	153559	M	J	6.40	-23.87	8.53	0.15	0.48	3.23
VT162	Contemp	Hair	2015	Fall	VT-WESTMORE	271474	251169	F	J	5.72	-25.05	5.40	0.14	0.46	3.22
VT165	Contemp	Hair	2015	Fall	VT-BRISTOL	187637	181413	F	J	6.53	-22.60	6.30	0.15	0.47	3.11
VT166	Contemp	Hair	2016	Fall	VT-BELVIDERE	219733	251762	F	J	4.63	-23.53	6.07	0.14	0.46	3.19

VT167	Contemp	Hair	2015	Fall	VT-Weathersfield	234781	99007	F	A	4.04	-22.07	6.77	0.15	0.48	3.26
VT168	Contemp	Hair	2016	Fall	VT-Middlebury	183304	168158	M	A	2.45	-20.76	4.38	0.15	0.46	3.09
VT170	Contemp	Hair	2015	Fall	VT-TINMOUTH	187402	105894	M	J	10.43	-23.88	7.64	0.15	0.46	3.16
VT174	Contemp	Hair	2015	Fall	VT-ORANGE	243362	184211	F	A	5.76	-25.40	5.67	0.15	0.46	3.04
VT175	Contemp	Hair	2015	Fall	VT-ORWELL	169124	146400	M	J	8.85	-22.60	7.22	0.15	0.47	3.26
VT176	Contemp	Hair	2015	Fall	VT-BRISTOL	187637	181413	M	J	2.72	-22.55	6.65	0.15	0.47	3.17
VT177	Contemp	Hair	2016	Fall	VT-RUPERT	176285	85940	M	J	4.85	-21.91	6.00	0.14	0.44	3.12
VT178	Contemp	Hair	2016	Fall	VT-WELLS	176757	104742	F	A	7.57	-22.56	6.58	0.15	0.46	3.04
VT179	Contemp	Hair	2015	Fall	VT-RUPERT	176285	85940	M	J	3.36	-22.51	6.03	0.14	0.45	3.17
VT180	Contemp	Hair	2016	Fall	VT-SUDBURY	178207	144561	F	A	7.21	-21.68	8.19	0.15	0.45	3.04
VT181	Contemp	Hair	2015	Fall	VT-MONKTON	182901	192972	M	A	9.25	-22.58	6.22	0.15	0.46	3.13
VT182	Contemp	Hair	2015	Fall	VT-SALISBURY	183993	159103	F	J	6.71	-22.15	5.82	0.14	0.45	3.20
VT183	Contemp	Hair	2015	Fall	VT-LEICESTER	184989	153079	M	J	4.94	-21.78	5.65	0.15	0.46	3.13
VT184	Contemp	Hair	2016	Fall	VT-SUDBURY	178207	144561	F	A	7.21	-22.92	8.38	0.14	0.45	3.25
VT185	Contemp	Hair	2015	Fall	VT-Rockingham	232139	76039	M	A	9.98	-22.68	6.72	0.14	0.44	3.07
VT187	Contemp	Hair	2016	Fall	VT-ADDISON	165568	175951	M	J	7.53	-22.31	8.12	0.14	0.47	3.36
VT188	Contemp	Hair	2015	Fall	VT-MONKTON	182901	192972	F	J	8.30	-22.46	5.88	0.15	0.46	3.06
VT189	Contemp	Hair	2015	Fall	VT-GRAFTON	222613	76433	M	J	3.63	-22.00	6.04	0.14	0.45	3.19
VT190	Contemp	Hair	2015	Fall	VT-Middlebury	183304	168158	F	A	5.08	-21.69	4.22	0.15	0.47	3.21
VT191	Contemp	Hair	2015	Fall	VT-MONKTON	182901	192972	M	J	7.03	-20.93	4.21	0.15	0.45	3.06
VT192	Contemp	Hair	2015	Fall	VT-LEICESTER	184989	153079	F	A	6.26	-21.83	5.38	0.15	0.45	3.04
VT193	Contemp	Hair	2016	Fall	VT-NEWARK	279576	245340	F	A	6.12	-25.40	4.92	0.14	0.44	3.21
VT194	Contemp	Hair	2015	Fall	VT-POWNAL	173568	33581	M	A	8.53	-23.91	7.24	0.15	0.46	3.10
VT195	Contemp	Hair	2016	Fall	VT-ORWELL	169124	146400	M	J	11.39	-23.49	6.39	0.14	0.46	3.23
VT196	Contemp	Hair	2016	Fall	VT-WEYBRIDGE	174961	173000	M	A	5.99	-22.66	6.62	0.15	0.46	3.14
VT197	Contemp	Hair	2016	Fall	VT-NEWARK	279576	245340	M	J	3.36	-25.81	5.59	0.14	0.46	3.16
VT198	Contemp	Hair	2015	Fall	VT-PITTSFORD	189017	135344	F	J	9.80	-23.24	6.67	0.14	0.47	3.28
VT199	Contemp	Hair	2015	Fall	VT-PITTSFORD	189017	135344	F	A	7.21	-21.94	5.03	0.14	0.45	3.15
VT200	Contemp	Hair	2016	Fall	VT-DORSET	187560	85223	F	A	8.30	-23.56	6.52	0.15	0.44	3.01
VT201	Contemp	Hair	2017	Fall	VT-Middlebury	183304	168158	F	A	6.85	-20.99	6.29	0.21	0.63	2.98
VT202	Contemp	Hair	2017	Fall	VT-UNDERHILL	203084	227170	F		6.40	-23.80	4.67	0.14	0.43	2.99

VT203	Contemp	Hair	2016	Fall	VT-READING	225003	111270	F	A	6.21	-22.53	6.14	0.15	0.44	2.99
VT204	Contemp	Hair	2016	Fall	VT-GRAFTON	222613	76433	F	J	2.77	-20.91	6.70	0.15	0.44	3.02
VT205	Contemp	Hair	2016	Fall	VT-Rockingham	232139	76039	M	A	10.39	-23.16	6.74	0.15	0.44	2.98
VT206	Contemp	Hair	2016	Fall	VT-GROTON	252422	192842	F	A	5.67	-21.12	5.64	0.15	0.44	2.99
VT207	Contemp	Hair	2016	Fall	VT-GRANBY	295714	233572	M	A	10.84	-24.80	5.48	0.15	0.44	2.99
VT208	Contemp	Hair	2016	Fall	VT-BRISTOL	187637	181413	F	A	7.26	-20.81	7.40	0.15	0.44	2.98
VT209	Contemp	Hair	2016	Fall	VT-POWNAL	173568	33581	F	J	5.62	-22.82	6.46	0.15	0.44	2.99
VT210	Contemp	Hair	2016	Fall	VT-SPRINGFIELD	233916	88163	M	J	8.26	-23.27	7.23	0.14	0.43	2.96
VT211	Contemp	Hair	2017	Fall	VT-Middlebury	183304	168158	M	J	5.81	-21.11	7.04	0.14	0.44	3.03
VT213	Contemp	Hair	2016	Fall	VT-POULTNEY	176704	115846	F	J	6.17	-23.62	6.33	0.15	0.44	3.02
VT214	Contemp	Hair	2016	Fall	VT-BENSON	167773	136011	F	A	6.53	-22.42	6.31	0.15	0.45	2.94
VT215	Contemp	Hair	2016	Fall	VT-BRANDON	186251	145363	F	A	6.67	-22.75	6.41	0.15	0.45	2.92
VT216	Contemp	Hair	2016	Fall	VT-BENSON	167773	136011	M	A	11.52	-21.66	7.10	0.15	0.45	3.01
VT217	Contemp	Hair	2016	Fall	VT-CRAFTSBURY	242124	239511	M	J	10.66	-24.83	6.53	0.14	0.44	3.04
VT218	Contemp	Hair	2017	Fall	VT-CHARLOTTE	174791	202165	M	A	13.70	-22.07	7.23	0.15	0.45	2.97
VT219	Contemp	Hair	2017	Fall	VT-CORINTH	250038	171002	F	J	4.26	-23.99	6.38	0.15	0.45	2.95
VT220	Contemp	Hair	2016	Fall	VT-W FAIRLEE	255019	160080	M	J	4.58	-22.44	7.83	0.15	0.44	2.99
VT224	Contemp	Hair	2016	Fall	VT-LEICESTER	184989	153079	F	A	6.12	-20.64	6.11	0.15	0.45	3.02
VT225	Contemp	Hair	2016	Fall	VT-LEICESTER	184989	153079	M	J	4.17	-19.88	7.19	0.15	0.44	3.02
VT226	Contemp	Hair	2017	Fall	VT-SUDBURY	178207	144561	F	J	5.81	-23.54	6.46	0.15	0.44	2.95
VT227	Contemp	Hair	2017	Fall	VT-SHOREHAM	167671	156242	M	J	4.72	-21.56	7.00	0.15	0.44	3.02
VT228	Contemp	Hair	2017	Fall	VT-LEICESTER	184989	153079	F	A	5.94	-21.13	4.80	0.15	0.44	2.94
VT229	Contemp	Hair	2017	Fall	VT-SHOREHAM	167671	156242	F	J	5.58	-22.34	7.10	0.14	0.44	3.11
VT231	Contemp	Hair	2017	Fall	VT-Dummerston	224469	48230	F		5.44	-21.39	6.50	0.14	0.44	3.09
VT232	Contemp	Hair	2016	Spring	VT-VERNON	229669	29498	M	A	9.57	-22.41	6.76	0.14	0.42	3.00
VT233	Contemp	Hair	2015	Spring	VT-VERNON	229669	29498	M	J	3.76	-23.22	7.89	0.14	0.43	3.02
VT234	Contemp	Hair	2016	Fall	VT-RYEGATE	264203	191419	M	A	10.39	-23.82	6.94	0.15	0.44	2.96
VT235	Contemp	Hair	2016	Fall	VT-RYEGATE	264203	191419	F	A	5.76	-23.51	5.46	0.15	0.44	2.96
VT236	Contemp	Hair	2016	Fall	VT-CORINTH	250038	171002	M	J	9.71	-22.25	7.58	0.10	0.30	2.99
VT237	Contemp	Hair	2016	Fall	VT-CORINTH	250038	171002	M	A	11.79	-23.80	7.35	0.15	0.44	2.97
VT238	Contemp	Hair	2016	Fall	VT-CORINTH	250038	171002	M	A	7.76	-23.95	6.96	0.14	0.44	3.02

VT239	Contemp	Hair	2016	Fall	VT-CORINTH	250038	171002	F	A	5.44	-23.90	5.68	0.15	0.46	3.02
VT240	Contemp	Hair	2017	Fall	VT-ORANGE	243362	184211	F	J	6.40	-24.91	5.56	0.15	0.44	2.96
VT241	Contemp	Hair	2016	Fall	VT-MIDDLESEX	223118	203423	F	J	6.53	-23.40	7.20	0.14	0.43	2.98
BS036	Historic	Bone	1952	Fall	NH-Hinsdale	231813	34670	M	A	14.37	-24.33	7.86	0.15	0.44	2.87
BS077	Historic	Bone	1954	Fall	NH-Epsom	326613	79462	M	A	10.57	-24.53	6.81	0.12	0.34	2.92
BS078	Historic	Bone	1954	Fall	NH-Deerfield	333338	70960	M	A	14.01	-23.46	6.58	0.15	0.44	2.86
BS107	Historic	Bone	1954	Fall	NH-Deerfield	333338	70960	F	A	7.88	-24.33	5.85	0.15	0.44	2.89
BS112	Historic	Bone	1954	Fall	NH-Greenfield	283372	48903	M	A	11.71	-23.68	7.39	0.12	0.34	2.85
BS226	Historic	Bone	1956	Fall	NH-Middleton	348387	109391	M	A	8.28	-23.55	7.20	0.16	0.44	2.83
BS233	Historic	Bone	1956	Fall	NH-Northumberland	311840	230640	F	A	9.48	-25.55	5.75	0.16	0.45	2.82
BS234	Historic	Bone	1956	Fall	NH-Carroll	312892	199958	F	A	5.99	-24.62	5.99	0.16	0.45	2.80
BS235	Historic	Bone	1956	Fall	NH-Jefferson	316088	210774	F	A	7.36	-24.90	6.38	0.16	0.45	2.83
BS236	Historic	Bone	1956	Fall	NH-Plainfield	250242	116943	F	A	6.76	-25.00	7.20	0.15	0.42	2.84
BS238	Historic	Bone	1956	Fall	NH-Loudon	318283	91231	F	A	6.93	-25.02	6.00	0.16	0.45	2.80
BS242	Historic	Bone	1956	Fall	NH-Jaffrey	267871	36648	M	A	7.69	-23.95	7.08	0.16	0.46	2.79
BS244	Historic	Bone	1956	Fall	NH-Jaffrey	267871	36648	F	A	7.54	-26.13	7.59	0.15	0.41	2.76
BS247	Historic	Bone	1956	Fall	NH-Gilmanton	324557	103072	M	A	10.44	-24.64	6.66	0.16	0.44	2.84
BS248	Historic	Bone	1957	Fall	NH-Gilmanton	324557	103072	M	A	10.40	-24.63	6.32	0.15	0.44	2.85
BS250	Historic	Bone	1957	Fall	NH-Enfield	263720	122060	F	A	8.12	-25.54	6.93	0.15	0.43	2.88
BS251	Historic	Bone	1957	Fall	NH-Amherst	304891	41166	M	A	6.10	-22.98	6.09	0.16	0.45	2.85
BS253	Historic	Bone	1957	Fall	NH-Amherst	304891	41166	F	A	6.84	-23.78	5.96	0.14	0.39	2.83
BS254	Historic	Bone	1957	Fall	NH-Pittsburg	332701	293720	F	A	8.18	-24.93	6.34	0.16	0.45	2.81
BS273	Historic	Bone	1957	Fall	NH-Weare	295502	64569	F	A	7.16	-24.42	6.46	0.16	0.44	2.81
BS274	Historic	Bone	1957	Fall	NH-Weare	295502	64569	F	A	6.39	-23.59	6.51	0.15	0.44	2.85
BS300	Historic	Bone	1957	Fall	NH-Alexandria	286649	124788	M	A	13.18	-24.07	7.59	0.16	0.45	2.83
BS312	Historic	Bone	1957	Fall	NH-Groton	284424	138342	M	A	15.20	-24.18	7.85	0.08	0.22	2.87
BS315	Historic	Bone	1958	Fall	NH-Clarksville	327773	278891	M	A	13.69	-24.50	7.53	0.16	0.44	2.80
BS326	Historic	Bone	1958	Fall	NH-Clarksville	327773	278891	F	A	10.66	-25.20	5.84	0.08	0.22	2.94
BS328	Historic	Bone	1958	Fall	NH-Pittsburg	332701	293720	F	A	5.43	-26.23	6.25	0.15	0.43	2.84
BS332	Historic	Bone	1958	Fall	NH-Columbia	315729	258405	F	A	3.05	-25.26	6.74	0.15	0.44	2.82
BS333	Historic	Bone	1958	Fall	NH-Pittsburg	332701	293720	F	A	5.20	-25.68	6.82	0.15	0.43	2.86

BS335	Historic	Bone	1958	Fall	NH-Plainfield	250242	116943	M	A	12.02	-24.41	7.59	0.16	0.44	2.79
BS336	Historic	Bone	1958	Fall	NH-Plainfield	250242	116943	M	A	4.07	-24.06	7.90	0.15	0.43	2.86
BS339	Historic	Bone	1958	Fall	NH-Orange	278104	128223	M	A	14.70	-24.91	7.09	0.13	0.37	2.84
BS341	Historic	Bone	1958	Fall	NH-Orange	278104	128223	F	A	6.10	-24.47	6.62	0.15	0.42	2.83
BS342	Historic	Bone	1958	Fall	NH-Plainfield	250242	116943	M	A	7.48	-24.66	7.68	0.15	0.43	2.86
BS346	Historic	Bone	1958	Fall	NH-Success	346875	223382	F	A	7.95	-24.72	5.88	0.14	0.41	2.82
BS349	Historic	Bone	1958	Fall	NH-Sutton	278674	93370	F	A	4.80	-23.74	7.21	0.15	0.43	2.82
BS352	Historic	Bone	1958	Spring	NH-Wilmot	279648	105762	M	A	7.48	-25.39	7.53	0.15	0.43	2.86
BS356	Historic	Bone	1958	Fall	NH-Millsfield	331385	251743	F	A	11.17	-24.30	6.58	0.13	0.37	2.83
BS370	Historic	Bone	1959	Fall	NH-Pittsburg	332701	293720	F	A	7.65	-25.31	6.01	0.15	0.43	2.82
BS371	Historic	Bone	1959	Fall	NH-Berlin	332355	220823	M	A	13.57	-24.96	7.08	0.13	0.35	2.82
BS375	Historic	Bone	1959	Fall	NH-Berlin	332355	220823	M	A	4.88	-24.57	7.10	0.15	0.43	2.83
BS383	Historic	Bone	1959	Fall	NH-Hancock	273151	52907	M	A	9.40	-22.93	5.89	0.15	0.43	2.80
BS384	Historic	Bone	1959	Fall	NH-Dublin	266872	43876	M	A	12.54	-23.75	7.43	0.15	0.43	2.81
BS385	Historic	Bone	1959	Fall	NH-Temple	284608	36512	M	A	11.39	-23.87	6.84	0.15	0.42	2.80
BS387	Historic	Bone	1959	Fall	NH-Dublin	266872	43876	F	A	5.85	-22.95	6.46	0.15	0.45	2.89
BS389	Historic	Bone	1959	Fall	NH-Temple	284608	36512	M	A	5.75	-23.11	6.73	0.15	0.43	2.83
BS397	Historic	Bone	1958	Fall	NH-Sandwich	317683	148805	M	A	9.03	-24.08	6.91	0.15	0.43	2.80
BS400	Historic	Bone	1959	Fall	NH-Dixville	331139	265257	M	A	13.60	-25.05	7.15	0.05	0.16	3.33
BS401	Historic	Bone	1959	Fall	NH-Randolph	327980	210854	M	A	12.12	-24.11	6.84	0.15	0.42	2.82
BS402	Historic	Bone	1959	Fall	NH-Milan	335781	229703	F	A	8.13	-25.00	5.82	0.15	0.42	2.82
BS405	Historic	Bone	1959	Fall	NH-Salisbury	292168	97900	M	A	17.55	-24.05	6.57	0.15	0.42	2.80
BS408	Historic	Bone	1959	Fall	NH-Cambridge	344394	239988	F	A	6.75	-25.23	5.80	0.09	0.26	2.90
BS413	Historic	Bone	1959	Fall	NH-Lisbon	284343	193301	F	A	8.35	-25.57	6.09	0.15	0.42	2.81
BS415	Historic	Bone	1960	Fall	NH-Northumberland	311840	230640	M	A	11.54	-24.31	7.64	0.15	0.42	2.81
BS416	Historic	Bone	1960	Fall	NH-Stratford	312006	245943	M	A	11.58	-24.57	7.23	0.16	0.44	2.81
BS417	Historic	Bone	1960	Fall	NH-Carroll	312892	199958	M	A	14.25	-24.87	7.14	0.15	0.41	2.79
BS418	Historic	Bone	1960	Fall	NH-Easton	289801	180661	M	A	6.31	-25.77	6.77	0.15	0.42	2.88
BS419	Historic	Bone	1960	Fall	NH-Lisbon	284343	193301	F	A	7.39	-25.99	6.14	0.15	0.42	2.83
BS422	Historic	Bone	1960	Fall	NH-Bath	274415	186684	F	A	7.55	-25.50	6.17	0.15	0.42	2.81
BS424	Historic	Bone	1960	Fall	NH-Stratford	312006	245943	M	A	6.31	-26.21	6.52	0.10	0.31	2.94

BS428	Historic	Bone	1960	Fall	NH-Milan	335781	229703	F	A	6.07	-25.01	5.56	0.15	0.43	2.86
BS430	Historic	Bone	1960	Fall	NH-Success	346875	223382	M	A	6.15	-24.86	7.37	0.15	0.42	2.88
BS431	Historic	Bone	1960	Fall	NH-Success	346875	223382	F	A	7.28	-24.65	5.92	0.10	0.29	2.85
BS433	Historic	Bone	1960	Fall	NH-Columbia	315729	258405	F	A	8.11	-25.00	6.11	0.15	0.42	2.78
BS436	Historic	Bone	1960	Fall	NH-Stratford	312006	245943	M	A	6.86	-25.95	6.38	0.15	0.42	2.83
BS441	Historic	Bone	1959	Fall	NH-Rindge	271851	28087	M	A	8.42	-24.06	6.99	0.15	0.42	2.83
BS442	Historic	Bone	1960	Fall	NH-Andover	289757	105175	F	A	8.19	-24.35	5.94	0.15	0.42	2.80
BS447	Historic	Bone	1959	Fall	NH-Greenfield	283372	48903	M	A	13.36	-24.10	7.32	0.15	0.42	2.80
BS449	Historic	Bone	1960	Fall	NH-Dublin	266872	43876	F	A	5.84	-24.31	6.65	0.15	0.42	2.85
BS450	Historic	Bone	1959	Fall	NH-New Ipswich	282974	27668	F	A	6.53	-22.79	6.44	0.11	0.32	2.82
BS451	Historic	Bone	1960	Fall	NH-Roxbury	256357	50399	F	A	6.74	-23.13	6.88	0.15	0.43	2.81
BS452	Historic	Bone	1960	Fall	NH-Nelson	262918	54984	F	A	6.28	-24.26	6.38	0.15	0.43	2.81
BS454	Historic	Bone	1959	Fall	NH-Jaffrey	267871	36648	F	A	6.83	-24.15	6.30	0.15	0.42	2.79
BS455	Historic	Bone	1960	Fall	NH-Swanzey	248570	40459	F	A	5.82	-22.94	7.34	0.15	0.42	2.81
BS455	Historic	Bone	1960	Fall	NH-Swanzey	248570	40459	F	A	5.82	-22.94	7.34	0.16	0.45	2.81
BS460	Historic	Bone	1960	Fall	NH-Wolfeboro	340044	123622	M	A	10.41	-24.48	7.15	0.15	0.43	2.79
BS465	Historic	Bone	1961	Fall	NH-Hanover	257745	135172	M	A	4.57	-26.84	6.40	0.14	0.44	3.10
BS467	Historic	Bone	1961	Fall	NH-Dorchester	274621	141213	M	A	9.97	-24.60	7.13	0.10	0.29	2.85
BS468	Historic	Bone	1961	Fall	NH-Canaan	269244	131009	M	A	12.34	-22.91	5.53	0.09	0.25	2.84
BS469	Historic	Bone	1961	Fall	NH-Orange	278104	128223	F	A	6.93	-25.21	6.34	0.15	0.42	2.79
BS473	Historic	Bone	1960	Fall	NH-Pittsburg	332701	293720	F	A	3.71	-24.85	6.34	0.16	0.44	2.86
BS479	Historic	Bone	1960	Fall	NH-Canterbury	309877	94735	F	A	7.14	-25.00	6.30	0.13	0.36	2.86
BS480	Historic	Bone	1961	Fall	NH-Harrisville	265335	49139	M	A	4.62	-23.34	6.65	0.15	0.44	3.01
BS482	Historic	Bone	1961	Fall	NH-Peterborough	277727	43415	M	A	5.06	-24.28	6.38	0.15	0.43	2.89
BS486	Historic	Bone	1961	Fall	NH-Harrisville	265335	49139	F	A	3.79	-23.74	6.51	0.15	0.43	2.81
BS493	Historic	Bone	1961	Fall	NH-Chatham	349463	185213	F	A	6.51	-24.76	5.80	0.15	0.43	2.79
BS496	Historic	Bone	1961	Fall	NH-Dummer	332837	239638	F	A	5.68	-25.52	6.36	0.15	0.45	2.90
BS497	Historic	Bone	1961	Fall	NH-Dummer	332837	239638	F	A	5.54	-25.54	6.34	0.15	0.43	2.84
BS500	Historic	Bone	1961	Fall	NH-Dummer	332837	239638	F	A	6.01	-25.04	5.20	0.15	0.43	2.80
BS507	Historic	Bone	1961	Fall	NH-Pittsburg	332701	293720	F	A	4.51	-25.65	6.08	0.15	0.41	2.81
BS512	Historic	Bone	1961	Fall	NH-Pittsburg	332701	293720	F	A	10.38	-25.47	5.73	0.15	0.42	2.79

BS514	Historic	Bone	1961	Fall	NH-Pittsburg	332701	293720	M	A	9.74	-25.33	5.90	0.09	0.25	2.87
BS516	Historic	Bone	1961	Fall	NH-Pittsburg	332701	293720	M	A	14.47	-25.45	6.93	0.09	0.25	2.83
BS517	Historic	Bone	1961	Fall	NH-Pittsburg	332701	293720	M	A	13.23	-24.99	7.72	0.06	0.18	2.88
BS522	Historic	Bone	1961	Fall	NH-Colebrook	319884	266567	F	A	9.61	-25.40	6.33	0.15	0.42	2.84
BS525	Historic	Bone	1961	Fall	NH-Beans Purchase	343746	198888	F	A	6.37	-25.04	6.09	0.15	0.43	2.80
BS527	Historic	Bone	1961	Fall	NH-Milan	335781	229703	F	A	7.60	-25.47	5.62	0.12	0.34	2.80
BS528	Historic	Bone	1961	Fall	NH-Stark	320760	233196	F	A	6.83	-24.79	5.80	0.15	0.43	2.81
BS533	Historic	Bone	1962	Fall	NH-Errol	342812	252047	F	A	4.89	-25.41	6.58	0.15	0.43	2.84
BS535	Historic	Bone	1961	Fall	NH-Clarksville	327773	278891	F	A	6.87	-25.09	6.58	0.15	0.43	2.78
BS536	Historic	Bone	1961	Fall	NH-Dummer	332837	239638	F	A	9.02	-25.12	6.33	0.15	0.44	2.87
BS538	Historic	Bone	1961	Fall	NH-Millsfield	331385	251743	M	A	10.08	-25.09	7.35	0.15	0.43	2.81
BS539	Historic	Bone	1961	Fall	NH-Pittsburg	332701	293720	F	A	10.70	-24.89	6.64	0.15	0.43	2.79
BS540	Historic	Bone	1961	Fall	NH-Dummer	332837	239638	M	A	12.35	-25.15	6.21	0.15	0.43	2.81
BS541	Historic	Bone	1961	Fall	NH-Milan	335781	229703	M	A	13.60	-24.48	7.24	0.15	0.43	2.79
BS559	Historic	Bone	1962	Fall	NH-Stewartstown	319963	273455	M	A	12.28	-24.80	7.84	0.08	0.23	2.85
BS565	Historic	Bone	1962	Fall	NH-Pittsburg	332701	293720	F	A	6.77	-25.15	6.90	0.15	0.41	2.78
BS582	Historic	Bone	1963	Fall	NH-Dummer	332837	239638	F	A	9.11	-25.25	6.58	0.10	0.28	2.93
BS584	Historic	Bone	1963	Fall	NH-Orford	267847	155107	F	A	4.26	-24.30	6.45	0.15	0.42	2.82
BS587	Historic	Bone	1964	Fall	NH-Grafton	275315	119574	M	A	5.99	-24.64	6.36	0.15	0.42	2.83
BS589	Historic	Bone	1964	Fall	NH-Danbury	283859	114151	F	A	7.92	-24.11	5.89	0.15	0.42	2.82
BS590	Historic	Bone	1964	Fall	NH-Warner	286849	86899	F	A	6.90	-24.08	6.56	0.15	0.42	2.80
BS591	Historic	Bone	1964	Fall	NH-Andover	289757	105175	F	A	4.61	-24.31	6.58	0.15	0.42	2.80
BS593	Historic	Bone	1964	Fall	NH-Whitefield	305962	208127	M	A	5.21	-24.40	7.62	0.16	0.45	2.84
BS597	Historic	Bone	1964	Fall	NH-Whitefield	305962	208127	M	A	9.60	-24.40	7.69	0.16	0.45	2.81
BS599	Historic	Bone	1964	Fall	NH-Whitefield	305962	208127	M	A	9.90	-24.61	6.80	0.16	0.45	2.82
BS600	Historic	Bone	1964	Fall	NH-Whitefield	305962	208127	M	A	9.61	-23.38	6.77	0.16	0.45	2.81
BS601	Historic	Bone	1964	Fall	NH-Whitefield	305962	208127	M	A	13.09	-24.47	7.29	0.16	0.45	2.79
BS602	Historic	Bone	1964	Fall	NH-Whitefield	305962	208127	M	A	13.53	-24.59	7.03	0.16	0.45	2.84
BS610	Historic	Bone	1964	Fall	NH-Berlin	332355	220823	M	A	10.47	-25.31	6.29	0.16	0.45	2.78
BS610	Historic	Bone	1964	Fall	NH-Berlin	332355	220823	M	A	10.47	-25.31	6.29	0.16	0.45	2.82

Appendix D.

PREY GUILD ISOTOPE DATA

Scientific names of prey species are as follows: Opossum (*Didelphis virginiana*), Raccoon (*Procyon lotor*), Skunk (*Mephitis mephitis*), Stoat (*Mustela erminea*), Cottontail (*Sylvilagus* spp.), Hare (*Lepus americanus*), Deer (*Odocoileus virginianus*), Porcupine (*Erethizon dorsatum*), Chicken (*Gallus gallus domesticus*), Mouse (*Peromyscus* spp.), Shrew (*Blarina brevicauda*, *Sorex* spp.), Chipmunk (*Tamias striatus*), Flying squirrel (*Glaucomys* spp.), Gray squirrel (*Sciurus carolinensis*), Turkey (*Meleagris gallopavo*), Mink (*Neovison vison*), Woodchuck (*Marmota monax*), Common pheasant (*Phasianus colchicus*), Vole (*Myodes gapperi*, *Microtus* spp.)

Period	Species	Guild	d13C	d15N	%N	%C	C/N
Contemp	Opossum	Carnivores	-23.31	6.22	0.15	0.47	3.07
Contemp	Opossum	Carnivores	-22.80	6.98	0.15	0.46	3.02
Contemp	Opossum	Carnivores	-21.79	7.48	0.15	0.47	3.04
Contemp	Opossum	Carnivores	-21.61	5.45	0.17	0.51	3.06
Contemp	Raccoon	Carnivores	-23.21	7.65	0.16	0.48	3.00
Contemp	Raccoon	Carnivores	-22.69	5.72	0.16	0.49	3.00
Contemp	Raccoon	Carnivores	-21.52	6.30	0.16	0.49	2.98
Contemp	Raccoon	Carnivores	-21.31	7.50	0.16	0.47	3.04
Contemp	Raccoon	Carnivores	-20.65	6.95	0.16	0.47	3.02
Contemp	Raccoon	Carnivores	-19.31	9.05	0.16	0.49	3.08
Contemp	Skunk	Carnivores	-22.31	7.03	0.15	0.47	3.05
Contemp	Stoat	Carnivores	-21.26	5.63	0.15	0.48	3.23
Contemp	Cottontail	Lagomorphs	-28.43	2.72	0.15	0.46	3.01
Contemp	Cottontail	Lagomorphs	-27.87	0.97	0.14	0.44	3.05
Contemp	Cottontail	Lagomorphs	-27.42	2.41	0.15	0.45	3.02
Contemp	Cottontail	Lagomorphs	-24.79	2.93	0.15	0.45	3.04
Contemp	Hare	Lagomorphs	-29.70	-0.02	0.14	0.46	3.21
Contemp	Hare	Lagomorphs	-29.04	-0.35	0.14	0.45	3.12
Contemp	Hare	Lagomorphs	-28.88	-0.60	0.15	0.45	3.05
Contemp	Hare	Lagomorphs	-28.74	0.48	0.14	0.43	3.11
Contemp	Hare	Lagomorphs	-28.67	1.08	0.15	0.46	3.15
Contemp	Hare	Lagomorphs	-28.66	0.12	0.11	0.34	3.12
Contemp	Hare	Lagomorphs	-28.35	-0.30	0.15	0.46	3.03
Contemp	Hare	Lagomorphs	-28.34	0.44	0.15	0.47	3.17
Contemp	Hare	Lagomorphs	-28.31	0.84	0.15	0.46	3.16
Contemp	Hare	Lagomorphs	-28.31	1.73	0.15	0.46	3.03
Contemp	Hare	Lagomorphs	-27.55	-0.08	0.15	0.46	3.12
Contemp	Hare	Lagomorphs	-27.29	1.27	0.15	0.46	3.05

Contemp	Hare	Lagomorphs	-27.28	1.38	0.14	0.44	3.11
Contemp	Hare	Lagomorphs	-27.11	0.82	0.15	0.49	3.38
Contemp	Hare	Lagomorphs	-26.54	1.68	0.14	0.45	3.18
Contemp	Deer	LargeMammals	-28.11	2.72	0.09	0.58	6.75
Contemp	Deer	LargeMammals	-26.79	3.87	0.13	0.50	3.73
Contemp	Deer	LargeMammals	-26.54	5.42	0.14	0.48	3.32
Contemp	Deer	LargeMammals	-26.32	2.83	0.13	0.48	3.58
Contemp	Deer	LargeMammals	-26.27	4.79	0.14	0.48	3.46
Contemp	Deer	LargeMammals	-26.25	3.60	0.13	0.50	3.79
Contemp	Deer	LargeMammals	-26.25	3.65	0.13	0.52	3.88
Contemp	Deer	LargeMammals	-26.17	4.47	0.14	0.47	3.31
Contemp	Deer	LargeMammals	-26.13	5.28	0.14	0.48	3.46
Contemp	Deer	LargeMammals	-26.07	5.50	0.13	0.46	3.44
Contemp	Deer	LargeMammals	-25.88	5.46	0.12	0.50	4.03
Contemp	Deer	LargeMammals	-25.66	4.37	0.14	0.48	3.50
Contemp	Deer	LargeMammals	-25.20	4.56	0.14	0.45	3.31
Contemp	Deer	LargeMammals	-25.05	4.70	0.14	0.48	3.36
Contemp	Deer	LargeMammals	-25.01	5.55	0.14	0.47	3.31
Contemp	Deer	LargeMammals	-25.01	2.58	0.14	0.46	3.36
Contemp	Porcupine	LargeMammals	-25.07	3.90	0.15	0.47	3.07
Contemp	Porcupine	LargeMammals	-24.58	4.40	0.16	0.51	3.18
Contemp	Porcupine	LargeMammals	-24.21	3.16	0.16	0.48	3.01
Contemp	Porcupine	LargeMammals	-24.14	2.19	0.15	0.47	3.02
Contemp	Chicken	Poultry	-21.49	6.26	0.15	0.46	3.17
Contemp	Chicken	Poultry	-20.91	5.50	0.15	0.47	3.15
Contemp	Chicken	Poultry	-19.93	5.75	0.14	0.45	3.20
Contemp	Chicken	Poultry	-19.81	4.89	0.14	0.45	3.21
Contemp	Chicken	Poultry	-19.49	4.88	0.13	0.40	3.12
Contemp	Chicken	Poultry	-19.46	3.43	0.15	0.46	3.16
Contemp	Chicken	Poultry	-19.17	4.18	0.14	0.46	3.24
Contemp	Chicken	Poultry	-18.87	4.23	0.16	0.49	3.14
Contemp	Chicken	Poultry	-18.63	5.16	0.15	0.49	3.20
Contemp	Chicken	Poultry	-18.48	4.38	0.15	0.47	3.16
Contemp	Chicken	Poultry	-18.47	6.09	0.16	0.49	3.10
Contemp	Chicken	Poultry	-18.15	6.07	0.16	0.49	3.11
Contemp	Chicken	Poultry	-18.11	5.18	0.16	0.50	3.11
Contemp	Chicken	Poultry	-17.99	3.87	0.15	0.47	3.14
Contemp	Chicken	Poultry	-17.85	5.09	0.16	0.49	3.13
Contemp	Chicken	Poultry	-17.76	7.07	0.15	0.47	3.09
Contemp	Chicken	Poultry	-17.67	6.64	0.16	0.50	3.17

Contemp	Chicken	Poultry	-17.20	5.95	0.16	0.49	3.12
Contemp	Chicken	Poultry	-17.04	5.62	0.16	0.49	3.09
Contemp	Mouse	SmallMammals	-25.64	6.53	0.14	0.45	3.12
Contemp	Mouse	SmallMammals	-24.95	5.31	0.14	0.45	3.16
Contemp	Mouse	SmallMammals	-24.61	5.33	0.14	0.45	3.15
Contemp	Mouse	SmallMammals	-24.42	5.01	0.14	0.44	3.09
Contemp	Mouse	SmallMammals	-24.22	4.56	0.15	0.46	3.08
Contemp	Mouse	SmallMammals	-23.80	3.87	0.14	0.44	3.10
Contemp	Mouse	SmallMammals	-23.45	4.29	0.14	0.45	3.16
Contemp	Mouse	SmallMammals	-23.42	2.83	0.14	0.45	3.21
Contemp	Mouse	SmallMammals	-23.38	4.32	0.14	0.44	3.10
Contemp	Mouse	SmallMammals	-23.35	3.01	0.14	0.45	3.23
Contemp	Mouse	SmallMammals	-23.25	6.62	0.14	0.48	3.50
Contemp	Mouse	SmallMammals	-23.04	2.62	0.14	0.45	3.22
Contemp	Mouse	SmallMammals	-23.02	3.70	0.14	0.46	3.27
Contemp	Mouse	SmallMammals	-22.91	3.02	0.14	0.45	3.14
Contemp	Mouse	SmallMammals	-22.85	4.36	0.14	0.45	3.22
Contemp	Mouse	SmallMammals	-22.77	3.38	0.15	0.45	3.18
Contemp	Mouse	SmallMammals	-22.76	3.64	0.14	0.45	3.13
Contemp	Mouse	SmallMammals	-22.76	4.01	0.14	0.45	3.25
Contemp	Mouse	SmallMammals	-22.74	3.41	0.15	0.46	3.13
Contemp	Mouse	SmallMammals	-22.73	3.13	0.15	0.45	3.16
Contemp	Mouse	SmallMammals	-22.71	4.13	0.14	0.45	3.23
Contemp	Mouse	SmallMammals	-22.70	3.72	0.14	0.45	3.21
Contemp	Mouse	SmallMammals	-22.68	4.04	0.14	0.46	3.27
Contemp	Mouse	SmallMammals	-22.68	3.03	0.14	0.45	3.28
Contemp	Mouse	SmallMammals	-22.67	3.75	0.14	0.46	3.19
Contemp	Mouse	SmallMammals	-22.67	3.19	0.14	0.46	3.23
Contemp	Mouse	SmallMammals	-22.65	4.62	0.14	0.45	3.21
Contemp	Mouse	SmallMammals	-22.64	2.01	0.14	0.45	3.14
Contemp	Mouse	SmallMammals	-22.63	3.41	0.14	0.45	3.22
Contemp	Mouse	SmallMammals	-22.61	2.96	0.14	0.45	3.22
Contemp	Mouse	SmallMammals	-22.60	3.22	0.14	0.45	3.20
Contemp	Mouse	SmallMammals	-22.58	2.20	0.13	0.45	3.35
Contemp	Mouse	SmallMammals	-22.57	2.68	0.14	0.45	3.22
Contemp	Mouse	SmallMammals	-22.56	3.16	0.14	0.46	3.26
Contemp	Mouse	SmallMammals	-22.55	2.74	0.14	0.45	3.18
Contemp	Mouse	SmallMammals	-22.54	2.19	0.14	0.45	3.24
Contemp	Mouse	SmallMammals	-22.53	2.41	0.15	0.45	3.18
Contemp	Mouse	SmallMammals	-22.52	3.85	0.14	0.46	3.25

Contemp	Mouse	SmallMammals	-22.51	4.62	0.14	0.45	3.23
Contemp	Mouse	SmallMammals	-22.50	3.49	0.14	0.44	3.21
Contemp	Mouse	SmallMammals	-22.50	3.09	0.14	0.46	3.21
Contemp	Mouse	SmallMammals	-22.49	3.82	0.14	0.46	3.25
Contemp	Mouse	SmallMammals	-22.47	4.54	0.15	0.46	3.22
Contemp	Mouse	SmallMammals	-22.46	3.55	0.14	0.44	3.12
Contemp	Mouse	SmallMammals	-22.45	3.26	0.14	0.45	3.23
Contemp	Mouse	SmallMammals	-22.43	2.97	0.15	0.46	3.22
Contemp	Mouse	SmallMammals	-22.42	3.81	0.14	0.45	3.23
Contemp	Mouse	SmallMammals	-22.40	4.28	0.14	0.45	3.15
Contemp	Mouse	SmallMammals	-22.39	3.02	0.14	0.44	3.09
Contemp	Mouse	SmallMammals	-22.37	3.40	0.15	0.45	3.15
Contemp	Mouse	SmallMammals	-22.36	4.03	0.14	0.46	3.34
Contemp	Mouse	SmallMammals	-22.35	2.13	0.14	0.45	3.27
Contemp	Mouse	SmallMammals	-22.32	3.90	0.15	0.46	3.18
Contemp	Mouse	SmallMammals	-22.31	3.87	0.14	0.45	3.23
Contemp	Mouse	SmallMammals	-22.29	4.78	0.14	0.44	3.17
Contemp	Mouse	SmallMammals	-22.28	2.80	0.15	0.46	3.20
Contemp	Mouse	SmallMammals	-22.26	2.74	0.14	0.45	3.12
Contemp	Mouse	SmallMammals	-22.26	3.45	0.14	0.45	3.20
Contemp	Mouse	SmallMammals	-22.22	4.66	0.15	0.47	3.26
Contemp	Mouse	SmallMammals	-22.22	2.25	0.15	0.45	3.16
Contemp	Mouse	SmallMammals	-22.17	1.69	0.15	0.45	3.17
Contemp	Mouse	SmallMammals	-22.15	2.33	0.14	0.46	3.25
Contemp	Mouse	SmallMammals	-22.13	3.38	0.14	0.45	3.22
Contemp	Mouse	SmallMammals	-22.12	2.18	0.14	0.45	3.19
Contemp	Mouse	SmallMammals	-22.08	1.26	0.14	0.45	3.27
Contemp	Mouse	SmallMammals	-22.08	2.80	0.14	0.45	3.12
Contemp	Mouse	SmallMammals	-22.07	7.21	0.14	0.45	3.29
Contemp	Mouse	SmallMammals	-22.03	2.58	0.14	0.45	3.17
Contemp	Mouse	SmallMammals	-22.02	2.73	0.14	0.44	3.10
Contemp	Mouse	SmallMammals	-21.99	5.00	0.14	0.45	3.17
Contemp	Mouse	SmallMammals	-21.98	1.52	0.14	0.45	3.19
Contemp	Mouse	SmallMammals	-21.96	1.93	0.14	0.45	3.15
Contemp	Mouse	SmallMammals	-21.96	2.44	0.15	0.45	3.18
Contemp	Mouse	SmallMammals	-21.95	2.31	0.14	0.45	3.11
Contemp	Mouse	SmallMammals	-21.88	2.43	0.15	0.46	3.23
Contemp	Mouse	SmallMammals	-21.87	2.76	0.14	0.46	3.25
Contemp	Mouse	SmallMammals	-21.84	3.19	0.14	0.45	3.28
Contemp	Mouse	SmallMammals	-21.83	2.49	0.14	0.45	3.24

Contemp	Mouse	SmallMammals	-21.83	2.64	0.14	0.44	3.16
Contemp	Mouse	SmallMammals	-21.79	3.10	0.14	0.45	3.23
Contemp	Mouse	SmallMammals	-21.78	3.71	0.14	0.46	3.27
Contemp	Mouse	SmallMammals	-21.75	4.10	0.14	0.46	3.24
Contemp	Mouse	SmallMammals	-21.71	4.81	0.14	0.46	3.21
Contemp	Mouse	SmallMammals	-21.71	2.04	0.14	0.45	3.18
Contemp	Mouse	SmallMammals	-21.71	2.45	0.14	0.45	3.26
Contemp	Mouse	SmallMammals	-21.65	1.27	0.14	0.46	3.20
Contemp	Mouse	SmallMammals	-21.65	3.16	0.14	0.45	3.26
Contemp	Mouse	SmallMammals	-21.53	1.28	0.14	0.45	3.15
Contemp	Mouse	SmallMammals	-21.51	2.26	0.15	0.45	3.15
Contemp	Mouse	SmallMammals	-21.48	4.23	0.14	0.46	3.26
Contemp	Mouse	SmallMammals	-21.40	2.15	0.15	0.46	3.21
Contemp	Mouse	SmallMammals	-21.29	5.50	0.14	0.44	3.12
Contemp	Mouse	SmallMammals	-21.19	2.46	0.14	0.44	3.16
Contemp	Mouse	SmallMammals	-21.12	1.84	0.15	0.45	3.14
Contemp	Mouse	SmallMammals	-20.87	2.65	0.14	0.45	3.12
Contemp	Mouse	SmallMammals	-14.52	7.69	0.14	0.45	3.13
Contemp	Shrew	SmallMammals	-23.30	5.98	0.13	0.46	3.47
Contemp	Chipmunk	Squirrels	-24.04	3.26	0.14	0.45	3.15
Contemp	Chipmunk	Squirrels	-23.40	2.23	0.14	0.44	3.12
Contemp	Chipmunk	Squirrels	-23.30	3.01	0.15	0.47	3.16
Contemp	Chipmunk	Squirrels	-23.23	2.38	0.14	0.46	3.16
Contemp	Chipmunk	Squirrels	-23.22	1.63	0.15	0.45	3.05
Contemp	Chipmunk	Squirrels	-23.20	3.01	0.14	0.45	3.15
Contemp	Chipmunk	Squirrels	-22.95	2.09	0.15	0.45	3.10
Contemp	Chipmunk	Squirrels	-22.91	2.62	0.15	0.46	3.13
Contemp	Chipmunk	Squirrels	-22.90	2.13	0.15	0.46	3.10
Contemp	Chipmunk	Squirrels	-22.87	2.63	0.15	0.46	3.16
Contemp	Chipmunk	Squirrels	-22.84	2.37	0.15	0.46	3.14
Contemp	Chipmunk	Squirrels	-22.82	2.84	0.15	0.46	3.13
Contemp	Chipmunk	Squirrels	-22.74	2.43	0.15	0.46	3.13
Contemp	Chipmunk	Squirrels	-21.77	2.24	0.15	0.45	3.00
Contemp	Chipmunk	Squirrels	-21.70	3.34	0.15	0.45	3.12
Contemp	Chipmunk	Squirrels	-21.69	0.74	0.15	0.45	3.02
Contemp	Chipmunk	Squirrels	-21.66	2.09	0.15	0.45	3.08
Contemp	Chipmunk	Squirrels	-21.64	0.69	0.15	0.45	3.04
Contemp	Chipmunk	Squirrels	-21.27	0.91	0.15	0.45	3.08
Contemp	Chipmunk	Squirrels	-21.15	0.63	0.15	0.44	2.99
Contemp	Chipmunk	Squirrels	-21.02	0.50	0.15	0.45	3.05

Contemp	Chipmunk	Squirrels	-20.91	1.58	0.15	0.45	3.01
Contemp	Flying squirrel	Squirrels	-23.46	1.04	0.15	0.49	3.29
Contemp	Flying squirrel	Squirrels	-22.81	-0.87	0.15	0.46	3.16
Contemp	Flying squirrel	Squirrels	-22.16	-0.83	0.15	0.47	3.12
Contemp	Flying squirrel	Squirrels	-22.16	2.22	0.15	0.48	3.23
Contemp	Flying squirrel	Squirrels	-22.01	2.67	0.15	0.47	3.07
Contemp	Flying squirrel	Squirrels	-20.36	3.92	0.15	0.46	3.09
Contemp	Gray squirrel	Squirrels	-23.80	1.39	0.14	0.46	3.22
Contemp	Gray squirrel	Squirrels	-22.43	4.11	0.15	0.49	3.17
Contemp	Gray squirrel	Squirrels	-22.15	0.71	0.16	0.48	3.05
Contemp	Gray squirrel	Squirrels	-22.00	4.84	0.15	0.46	3.14
Contemp	Gray squirrel	Squirrels	-20.66	3.76	0.16	0.49	3.16
Contemp	Turkey	SubsidizedTurkeys	-23.14	5.42	0.15	0.48	3.29
Contemp	Turkey	SubsidizedTurkeys	-23.08	5.67	0.15	0.48	3.11
Contemp	Turkey	SubsidizedTurkeys	-22.75	3.54	0.15	0.47	3.21
Contemp	Turkey	SubsidizedTurkeys	-22.56	5.22	0.15	0.48	3.10
Contemp	Turkey	SubsidizedTurkeys	-22.36	5.77	0.15	0.47	3.19
Contemp	Turkey	SubsidizedTurkeys	-21.99	7.32	0.15	0.48	3.28
Contemp	Turkey	SubsidizedTurkeys	-21.77	4.80	0.15	0.49	3.24
Contemp	Turkey	SubsidizedTurkeys	-21.73	5.94	0.15	0.48	3.23
Contemp	Turkey	SubsidizedTurkeys	-21.44	6.16	0.15	0.47	3.25
Contemp	Turkey	SubsidizedTurkeys	-21.37	4.43	0.15	0.48	3.21
Contemp	Turkey	SubsidizedTurkeys	-21.18	5.43	0.18	0.56	3.02
Contemp	Turkey	SubsidizedTurkeys	-21.05	6.04	0.15	0.49	3.27
Contemp	Turkey	SubsidizedTurkeys	-20.46	5.62	0.15	0.48	3.14
Contemp	Turkey	SubsidizedTurkeys	-20.39	5.81	0.15	0.47	3.19
Contemp	Turkey	SubsidizedTurkeys	-19.44	4.45	0.15	0.48	3.23
Contemp	Turkey	SubsidizedTurkeys	-19.35	3.75	0.15	0.47	3.21
Contemp	Turkey	SubsidizedTurkeys	-19.32	6.47	0.15	0.50	3.27
Contemp	Turkey	SubsidizedTurkeys	-19.27	5.22	0.15	0.48	3.23
Contemp	Turkey	SubsidizedTurkeys	-19.12	6.35	0.15	0.47	3.22
Contemp	Turkey	SubsidizedTurkeys	-18.82	6.15	0.15	0.47	3.21
Contemp	Turkey	SubsidizedTurkeys	-17.97	3.93	0.15	0.48	3.17
Contemp	Turkey	SubsidizedTurkeys	-17.10	4.58	0.15	0.48	3.22
Contemp	Turkey	Turkeys	-26.42	4.32	0.14	0.46	3.20
Contemp	Turkey	Turkeys	-26.39	5.28	0.15	0.49	3.29
Contemp	Turkey	Turkeys	-26.21	3.82	0.15	0.48	3.23
Contemp	Turkey	Turkeys	-26.21	6.27	0.14	0.47	3.28
Contemp	Turkey	Turkeys	-26.12	4.72	0.14	0.47	3.32
Contemp	Turkey	Turkeys	-26.03	3.15	0.15	0.49	3.25

Contemp	Turkey	Turkeys	-26.03	4.84	0.15	0.48	3.23
Contemp	Turkey	Turkeys	-25.68	6.99	0.15	0.49	3.27
Contemp	Turkey	Turkeys	-25.66	6.03	0.14	0.46	3.27
Contemp	Turkey	Turkeys	-25.53	4.51	0.15	0.47	3.26
Contemp	Turkey	Turkeys	-25.03	4.29	0.14	0.47	3.25
Contemp	Turkey	Turkeys	-24.92	5.69	0.15	0.49	3.29
Contemp	Turkey	Turkeys	-24.84	4.94	0.15	0.49	3.25
Contemp	Turkey	Turkeys	-24.81	4.87	0.15	0.49	3.24
Contemp	Turkey	Turkeys	-24.81	4.94	0.15	0.48	3.26
Contemp	Turkey	Turkeys	-24.55	6.60	0.15	0.47	3.19
Contemp	Turkey	Turkeys	-24.02	5.70	0.15	0.49	3.23
Historic	Mink	Carnivores	-24.20	10.79	0.15	0.45	2.99
Historic	Mink	Carnivores	-23.72	9.57	0.15	0.46	2.99
Historic	Mink	Carnivores	-16.03	10.62	0.16	0.47	2.98
Historic	Opossum	Carnivores	-22.74	11.50	0.15	0.44	3.06
Historic	Opossum	Carnivores	-22.52	7.92	0.15	0.46	3.04
Historic	Opossum	Carnivores	-21.16	7.49	0.13	0.41	3.13
Historic	Opossum	Carnivores	-20.82	7.09	0.13	0.39	3.06
Historic	Opossum	Carnivores	-19.06	9.26	0.15	0.44	3.01
Historic	Raccoon	Carnivores	-20.15	7.66	0.14	0.45	3.12
Historic	Raccoon	Carnivores	-19.34	8.76	0.15	0.46	2.97
Historic	Raccoon	Carnivores	-18.87	6.51	0.15	0.45	2.98
Historic	Skunk	Carnivores	-22.56	7.84	0.15	0.46	3.01
Historic	Skunk	Carnivores	-22.19	9.23	0.15	0.47	3.15
Historic	Skunk	Carnivores	-22.05	8.30	0.15	0.46	3.13
Historic	Stoat	Carnivores	-25.47	9.02	0.14	0.42	3.06
Historic	Stoat	Carnivores	-22.21	7.71	0.15	0.45	3.06
Historic	Stoat	Carnivores	-21.09	9.82	0.16	0.49	3.07
Historic	Cottontail	Lagomorphs	-29.26	2.97	0.15	0.45	3.07
Historic	Cottontail	Lagomorphs	-28.52	2.47	0.15	0.46	3.10
Historic	Cottontail	Lagomorphs	-28.45	2.38	0.14	0.46	3.23
Historic	Cottontail	Lagomorphs	-28.28	2.52	0.14	0.44	3.16
Historic	Cottontail	Lagomorphs	-27.89	4.69	0.12	0.38	3.18
Historic	Cottontail	Lagomorphs	-27.80	4.10	0.13	0.42	3.24
Historic	Cottontail	Lagomorphs	-21.27	3.70	0.14	0.43	3.12
Historic	Hare	Lagomorphs	-28.77	1.88	0.13	0.41	3.06
Historic	Hare	Lagomorphs	-28.14	1.33	0.15	0.45	3.08
Historic	Hare	Lagomorphs	-27.74	3.03	0.15	0.46	3.08
Historic	Hare	Lagomorphs	-27.68	2.05	0.15	0.45	3.09
Historic	Hare	Lagomorphs	-27.00	3.11	0.15	0.45	3.10

Historic	Deer	LargeMammals	-26.45	3.69	0.11	0.33	2.98
Historic	Porcupine	LargeMammals	-24.98	3.53	0.14	0.42	3.05
Historic	Porcupine	LargeMammals	-24.44	3.58	0.15	0.46	3.09
Historic	Porcupine	LargeMammals	-24.22	3.43	0.14	0.42	3.04
Historic	Woodchuck	LargeMammals	-27.18	2.52	0.15	0.45	3.12
Historic	Woodchuck	LargeMammals	-27.14	4.11	0.14	0.47	3.37
Historic	Woodchuck	LargeMammals	-27.13	5.05	0.15	0.44	2.96
Historic	Woodchuck	LargeMammals	-27.09	3.30	0.13	0.49	3.76
Historic	Woodchuck	LargeMammals	-26.81	3.34	0.15	0.46	3.01
Historic	Woodchuck	LargeMammals	-26.43	3.73	0.15	0.45	2.94
Historic	Woodchuck	LargeMammals	-26.42	5.18	0.14	0.40	2.97
Historic	Common pheasant	Poultry	-23.61	8.98	0.12	0.36	3.11
Historic	Common pheasant	Poultry	-20.20	8.27	0.15	0.46	3.01
Historic	Common pheasant	Poultry	-19.01	5.58	0.16	0.48	3.08
Historic	Common pheasant	Poultry	-18.73	9.16	0.12	0.39	3.15
Historic	Common pheasant	Poultry	-15.73	5.52	0.15	0.48	3.20
Historic	Mouse	SmallMammals	-27.11	8.28	0.15	0.47	3.12
Historic	Mouse	SmallMammals	-26.20	5.08	0.15	0.48	3.28
Historic	Mouse	SmallMammals	-26.12	3.23	0.14	0.48	3.34
Historic	Mouse	SmallMammals	-25.69	4.00	0.14	0.42	3.03
Historic	Mouse	SmallMammals	-25.17	6.60	0.15	0.48	3.23
Historic	Mouse	SmallMammals	-24.94	2.75	0.15	0.48	3.11
Historic	Mouse	SmallMammals	-24.61	4.43	0.14	0.48	3.36
Historic	Mouse	SmallMammals	-23.64	2.68	0.15	0.48	3.21
Historic	Mouse	SmallMammals	-23.49	2.94	0.15	0.48	3.20
Historic	Mouse	SmallMammals	-21.83	3.50	0.15	0.48	3.25
Historic	Mouse	SmallMammals	-21.80	3.02	0.14	0.47	3.34
Historic	Mouse	SmallMammals	-21.52	4.27	0.15	0.47	3.15
Historic	Mouse	SmallMammals	-21.33	5.57	0.14	0.47	3.28
Historic	Shrew	SmallMammals	-26.55	7.27	0.13	0.47	3.51
Historic	Shrew	SmallMammals	-24.96	7.64	0.13	0.47	3.46
Historic	Shrew	SmallMammals	-24.27	8.22	0.14	0.45	3.27
Historic	Shrew	SmallMammals	-24.06	6.75	0.14	0.45	3.25
Historic	Shrew	SmallMammals	-23.99	6.41	0.14	0.51	3.54
Historic	Shrew	SmallMammals	-23.01	4.71	0.14	0.45	3.26
Historic	Shrew	SmallMammals	-22.95	5.71	0.14	0.49	3.40
Historic	Vole	SmallMammals	-26.72	5.56	0.13	0.48	3.57
Historic	Vole	SmallMammals	-26.69	6.28	0.14	0.49	3.57
Historic	Vole	SmallMammals	-26.63	6.35	0.14	0.47	3.45
Historic	Vole	SmallMammals	-25.55	5.24	0.14	0.48	3.45

Historic	Vole	SmallMammals	-25.43	5.04	0.14	0.46	3.30
Historic	Vole	SmallMammals	-24.66	2.90	0.15	0.46	3.12
Historic	Vole	SmallMammals	-24.46	3.10	0.14	0.50	3.50
Historic	Vole	SmallMammals	-24.20	7.14	0.13	0.47	3.68
Historic	Vole	SmallMammals	-23.67	7.01	0.14	0.47	3.30
Historic	Vole	SmallMammals	-23.57	4.83	0.15	0.47	3.20
Historic	Vole	SmallMammals	-22.40	6.39	0.14	0.48	3.54
Historic	Chipmunk	Squirrels	-23.52	-0.13	0.15	0.44	3.04
Historic	Chipmunk	Squirrels	-22.81	8.69	0.15	0.45	2.98
Historic	Chipmunk	Squirrels	-22.46	4.81	0.15	0.45	2.97
Historic	Chipmunk	Squirrels	-22.23	4.94	0.15	0.47	3.05
Historic	Chipmunk	Squirrels	-21.73	6.01	0.16	0.47	2.90
Historic	Flying squirrel	Squirrels	-23.80	5.94	0.15	0.48	3.25
Historic	Flying squirrel	Squirrels	-22.66	1.34	0.15	0.49	3.29
Historic	Flying squirrel	Squirrels	-21.37	4.72	0.15	0.47	3.21
Historic	Flying squirrel	Squirrels	-21.31	1.35	0.15	0.48	3.21
Historic	Flying squirrel	Squirrels	-21.19	4.59	0.15	0.47	3.16
Historic	Gray squirrel	Squirrels	-24.08	2.68	0.17	0.53	3.14
Historic	Gray squirrel	Squirrels	-23.60	3.65	0.15	0.48	3.25
Historic	Gray squirrel	Squirrels	-22.56	5.75	0.15	0.46	3.15
Historic	Gray squirrel	Squirrels	-21.69	6.66	0.15	0.48	3.22
Historic	Gray squirrel	Squirrels	-21.29	6.95	0.15	0.46	3.17
Historic	Gray squirrel	Squirrels	-20.76	2.34	0.15	0.48	3.15

Appendix E.

BOBCAT HAIR CORTISOL DATA

ID	BodyLoc	AgeClass	Sex	Weight	State-Town	WMU	HairMonth	HairYear	HairWt(mg)	Log(ng cort/g hair)
ACT156	Foot	A	Male	12.81	NH-Loudon	NH-J2	Oct	2015	53.0	1.072
ACT157	Foot	J	Female	7.71	NH-Chester	NH-M	Apr	2015	38.7	1.139
ACT159	Foot		Male	13.83	NH-Grafton	NH-G	Oct	2015	15.6	1.097
ACT160	Foot		Female	8.73	NH-Pittsburg	NH-A	Oct	2015	25.6	1.279
ACT161	Flank		Male	9.98	NH-Ashland	NH-F	Oct	2015	19.3	1.108
ACT162	Foot		Male	12.25	NH-Laconia	NH-J2	Oct	2015	9.8	1.411
ACT163	Flank		Female	8.85	NH-New Boston	NH-K	Oct	2015	9.9	1.010
ACT164	Flank		Female	6.35	NH-Gilford	NH-J2	Oct	2015	28.8	1.349
ACT165	Foot		Male	9.98	NH-Pelham	NH-M	Oct	2015	37.3	0.987
ACT166	Foot		Male	11.79	NH-Hooksett	NH-L	Oct	2015	58.9	1.016
ACT167	Foot		Male	10.09	NH-Allenstown	NH-L	Oct	2015	51.1	0.641
ACT168	Foot		Male	14.06	NH-Lyme	NH-G	Oct	2015	33.8	1.156
ACT169	Foot		Female	7.03	NH-Merrimack	NH-M	Oct	2015	29.6	1.464
ACT171	Foot		Male	12.47	NH-Langdon	NH-H1	Oct	2015	41.6	0.826
ACT172	Foot		Male	14.06	NH-Westmoreland	NH-H2N	Oct	2015	23.1	1.122
ACT173	Foot		Female	7.94	NH-Greenfield	NH-K	Oct	2015	20.0	1.159
ACT174	Foot		Female	6.58	NH-Unity	NH-H1	Apr	2013	31.9	1.193
ACT175	Foot		Female	7.26	NH-Swanzey	NH-H2S	Oct	2015	25.1	1.462
ACT177	Foot		Male	5.67	NH-Charlestown	NH-H1	Oct	2015	30.9	1.032
ACT181	Flank		Male	15.65	NH-Hampton	NH-M	Oct	2016	19.9	1.020
ACT183	Flank		Female	5.44	NH-Webster	NH-I1	Oct	2012	23.4	1.317
ACT184	Flank		Male	6.01	NH-Walpole	NH-H2N	Oct	2012	43.0	1.428
ACT185	Flank		Male	4.65	NH-Acworth	NH-H2N	Oct	2012	20.6	1.175
ACT186	Flank		Female	6.35	NH-Swanzey	NH-H2S	Apr	2012	34.0	1.081

ACT187	Flank		Male	4.54	NH-Walpole	NH-H2N	Apr	2012	26.2	1.058
ACT189	Flank		Male	9.98	NH-Keene	NH-H2N	Oct	2012	35.6	0.961
ACT190	Flank		Female	8.16	NH-Washington	NH-I2	Oct	2012	33.9	1.338
ACT191	Flank		Male	15.42	NH-New Ipswich	NH-K	Oct	2012	41.2	1.134
ACT192	Flank		Male	14.51	NH-Washington	NH-I2	Oct	2012	40.8	1.073
ACT194	Flank		Female	3.06	NH-Milan	NH-C2	Oct	2012	42.4	1.158
ACT195	Flank		Female	3.86	NH-Franconia	NH-E	Oct	2011	41.1	1.375
ACT197	Flank		Female	4.99	NH-Wilton	NH-K	Oct	2016	32.4	1.448
ALT035	Flank	A	Female	8.50	NH-Jaffrey	NH-H2S	Oct	2009	15.0	1.483
ALT039	Flank	A	Male	11.50	NH-Alstead	NH-H2N	Oct	2009	16.2	1.438
ALT040	Flank	A	Male	12.30	NH-Walpole	NH-H2N	Oct	2009	9.5	1.320
ME011	Foot	A	Male	11.34	ME-Berwick	ME-20	Oct	2015	41.6	1.602
ME012	Flank	A	Female	7.71	ME-Berwick	ME-20	Oct	2015	16.5	1.343
VT102	Foot	J	Female	5.04	VT-BROOKFIELD	VT-J1	Oct	2014	23.4	1.308
VT104	Foot	A	Female	8.33	VT-CONCORD	VT-J2	Oct	2014	27.7	1.415
VT107	Foot	A	Male	11.88	VT-GREENSBORO	VT-D1	Oct	2014	36.6	1.397
VT116	Foot	A	Male	8.68	VT-SHARON	VT-J2	Oct	2014	35.8	1.490
VT118	Foot	A	Female	8.23	VT-TROY	VT-D1	Oct	2014	25.6	1.425
VT120	Foot	J	Female	3.39	VT-WALDEN	VT-D2	Oct	2014	22.0	1.414
VT122	Foot	A	Female	7.09	VT-WELLS	VT-K	Oct	2014	38.5	1.753
VT123	Foot	J	Male	5.94	VT-WEYBRIDGE	VT-F1	Oct	2014	26.0	1.184
VT130	Foot		Male	3.74	VT-WHITING	VT-F2	Oct	2014	40.4	1.092
VT132	Foot	J	Male	4.84	VT-MONKTON	VT-F2	Oct	2014	32.5	1.330
VT133	Foot	J	Male	11.57	VT-HARDWICK	VT-D1	Oct	2014	42.0	1.232
VT137	Foot	J	Female	3.49	VT-WEST FAIRLEE	VT-J2	Oct	2014	28.9	1.241
VT139	Foot	J	Male	10.56	VT-CORINTH	VT-J2	Oct	2014	33.9	1.060
VT140	Foot	A	Female	7.39	VT-DORSET	VT-N	Oct	2014	33.4	0.855
VT141	Foot	J	Female	7.98	VT-BARRE town	VT-J1	Oct	2014	39.1	1.184
VT142	Foot	A	Female	8.28	VT-MONKTON	VT-F2	Oct	2014	27.0	1.435

VT143	Foot	A	Male	12.47	VT-STARKSBORO	VT-G	Oct	2014	35.6	1.145
VT144	Foot	A	Male	12.47	VT-SUDBURY	VT-K	Oct	2014	41.6	1.166
VT145	Foot	A	Female	8.28	VT-SHOREHAM	VT-F1	Oct	2014	24.3	1.488
VT146	Foot	J	Male	4.79	VT-SHOREHAM	VT-F1	Oct	2014	33.1	1.157
VT147	Foot	J	Female	6.49	VT-NEW HAVEN	VT-F2	Oct	2014	29.2	1.495
VT148	Foot	A	Male	10.83	VT-WEST RUTLAND	VT-K	Oct	2014	14.2	1.794
VT150	Foot	A	Female	7.09	VT-SHOREHAM	VT-F1	Oct	2014	43.9	1.218
VT151	Foot	A	Female	7.58	VT-SHOREHAM	VT-F1	Oct	2014	45.2	1.134
VT152	Foot	A	Female	7.88	VT-BENNINGTON	VT-N	Oct	2014	41.0	1.412
VT153	Foot	J	Male	7.04	VT-WHITING	VT-F2	Oct	2014	28.2	1.087
VT155	Foot	J	Female	7.92	VT-STANNARD	VT-D2	Oct	2015	34.2	1.351
VT162	Foot	A	Female	6.29	VT-WESTMORE	VT-D2	Oct	2015	25.4	1.023
VT165	Foot	A	Female	7.18	VT-BRISTOL	VT-I	Oct	2015	33.6	1.354
VT166	Foot	J	Female	5.09	VT-BELVIDERE	VT-C	Oct	2015	31.7	1.133
VT170	Foot	A	Male	11.48	VT-TINMOUTH	VT-K	Oct	2015	42.2	1.074
VT173	Foot	A	Female	7.83	VT-BELVIDERE	VT-C	Oct	2015	31.2	1.236
VT174	Foot	A	Female	6.34	VT-ORANGE	VT-H	Oct	2015	26.5	1.288
VT175	Foot	A	Male	9.73	VT-ORWELL	VT-F2	Oct	2015	31.6	1.219
VT176	Foot	J	Male	2.99	VT-BRISTOL	VT-I	Oct	2015	22.5	1.211
VT178	Foot	J	Female	8.33	VT-WELLS	VT-K	Oct	2015	27.7	1.152
VT179	Foot	J	Male	3.69	VT-RUPERT	VT-N	Oct	2015	15.9	1.861
VT181	Foot	A	Male	10.18	VT-MONKTON	VT-F2	Oct	2015	32.2	1.266
VT182	Foot	J	Female	7.38	VT-SALISBURY	VT-F2	Oct	2015	34.9	1.079
VT183	Foot	J	Male	5.44	VT-LEICESTER	VT-F2	Oct	2015	38.3	1.104
VT184	Foot	J	Female	7.93	VT-SUDBURY	VT-K	Oct	2015	25.4	1.123
VT185	Foot	A	Male	10.98	VT-ROCKINGHAM	VT-O	Oct	2015	19.8	1.069
VT187	Foot	J	Male	8.28	VT-ADDISON	VT-F1	Oct	2015	36.2	1.095
VT188	Foot	A	Female	9.13	VT-MONKTON	VT-F2	Oct	2015	41.3	1.185
VT192	Foot	A	Female	6.89	VT-LEICESTER	VT-F2	Oct	2015	25.0	1.733

VT193	Foot	A	Female	6.74	VT-NEWARK	VT-D2	Oct	2015	39.5	1.144
VT194	Foot	J	Male	9.38	VT-POWNAL	VT-P	Oct	2015	36.0	1.733
VT195	Foot	A	Male	12.52	VT-ORWELL	VT-F2	Oct	2015	38.9	1.082
VT196	Foot	J	Male	6.59	VT-WEYBRIDGE	VT-F1	Oct	2015	36.5	1.356
VT197	Foot	J	Male	3.69	VT-NEWARK	VT-D2	Oct	2015	37.0	1.249
VT200	Foot	A	Female	9.13	VT-DORSET	VT-N	Oct	2016	16.7	0.998
VT201	Foot	A	Female	7.53	VT-MIDDLEBURY	VT-F2	Oct	2016	40.2	1.054
VT202	Foot		Female	7.04	VT-UNDERHILL	VT-B	Oct	2016	45.2	1.117
VT203	Foot	A	Female	6.84	VT-READING	VT-M	Oct	2016	39.6	1.108
VT204	Foot	J	Female	3.04	VT-GRAFTON	VT-M	Oct	2015	31.3	1.358
VT205	Foot	A	Male	11.43	VT-ROCKINGHAM	VT-O	Oct	2016	40.5	1.188
VT206	Foot	A	Female	6.24	VT-GROTON	VT-H	Oct	2016	38.6	1.256
VT207	Foot	A	Male	11.92	VT-GRANBY	VT-E2	Oct	2016	41.9	1.058
VT208	Foot	A	Female	7.98	VT-BRISTOL	VT-I	Oct	2016	39.5	1.436
VT209	Foot	J	Female	6.19	VT-POWNAL	VT-P	Oct	2016	40.5	1.377
VT210	Foot	J	Male	9.08	VT-SPRINGFIELD	VT-O	Oct	2016	41.1	1.056
VT211	Foot	J	Male	6.39	VT-MIDDLEBURY	VT-F2	Oct	2016	40.0	1.388
VT213	Foot	J	Female	6.79	VT-POULTNEY	VT-K	Oct	2016	40.8	0.951
VT214	Foot	A	Female	7.18	VT-BENSON	VT-K	Oct	2016	40.0	1.423
VT215	Foot	A	Female	7.33	VT-BRANDON	VT-I	Oct	2016	32.5	1.608
VT216	Foot	A	Male	12.67	VT-BENSON	VT-K	Oct	2016	34.7	1.732
VT217	Foot	J	Male	11.73	VT-CRAFTSBURY	VT-D1	Oct	2016	32.9	0.990
VT218	Foot	A	Male	15.07	VT-CHARLOTTE	VT-F1	Oct	2016	31.7	1.340
VT219	Foot	J	Female	4.69	VT-CORINTH	VT-J2	Oct	2016	39.5	1.715
VT220	Foot	J	Male	5.04	VT-WEST FAIRLEE	VT-J2	Oct	2016	37.0	1.349
VT224	Foot	A	Female	6.74	VT-LEICESTER	VT-F2	Oct	2016	42.3	1.434
VT225	Foot	J	Male	4.59	VT-LEICESTER	VT-F2	Oct	2016	39.5	1.627
VT226	Foot	J	Female	6.39	VT-SUDBURY	VT-K	Oct	2016	25.4	1.366
VT227	Foot	J	Male	5.19	VT-SHOREHAM	VT-F1	Oct	2016	40.8	1.336

VT228	Foot	A	Female	6.54	VT-LEICESTER	VT-F2	Oct	2016	40.5	1.293
VT229	Foot	J	Female	6.14	VT-SHOREHAM	VT-F1	Oct	2016	8.0	1.130
VT231	Flank		Female	5.99	VT-DUMMERSTON	VT-O	Oct	2016	14.9	1.515
VT232	Foot	A	Male	10.53	VT-VERNON	VT-O	Apr	2016	28.9	0.912
VT233	Foot	J	Male	4.14	VT-VERNON	VT-O	Apr	2015	37.1	1.331
VT234	Foot	A	Male	11.43	VT-RYEGATE	VT-J2	Oct	2016	38.4	1.149
VT235	Foot	A	Female	6.34	VT-RYEGATE	VT-J2	Oct	2016	41.1	1.301
VT236	Foot	J	Male	10.68	VT-CORINTH	VT-J2	Oct	2016	42.5	1.137
VT237	Foot	A	Male	12.97	VT-CORINTH	VT-J2	Oct	2016	36.6	1.136
VT238	Foot	A	Male	8.53	VT-CORINTH	VT-J2	Oct	2016	29.2	1.299
VT239	Foot	A	Female	5.99	VT-CORINTH	VT-J2	Oct	2016	40.8	1.426
VT240	Foot	J	Female	7.04	VT-ORANGE	VT-H	Oct	2016	42.1	1.317
VT241	Foot	J	Female	7.18	VT-MIDDLESEX	VT-H	Oct	2015	41.7	1.047

Appendix F.

COMBINED DATA FOR INTEGRATED ANALYSES

ID	Town	NHStPl_X	NHStPl_Y	Sex	Pop	pLago	pLgMamm	pSmMamm	pSquirrel	d13C	d15N	Log(ngCort/gHair)
ACT156	NH-Loudon	318283	91231	M	S	0.173	0.175	0.255	0.397	-22.837	6.146	1.072
ACT157	NH-Chester	333917	51983	F	S	0.294	0.153	0.196	0.357	-23.587	5.559	1.139
ACT159	NH-Grafton	275315	119574	M	E	0.162	0.203	0.29	0.345	-22.897	6.504	1.097
ACT160	NH-Pittsburg	332701	293720	F	NC	0.618	0.114	0.117	0.152	-25.663	4.991	1.279
ACT161	NH-Ashland	302926	134970	M	E	0.114	0.148	0.312	0.426	-22.088	6.383	1.108
ACT162	NH-Laconia	315280	119152	M	E	0.129	0.185	0.313	0.373	-22.470	6.581	1.411
ACT163	NH-New Boston	298424	53028	F	S	0.136	0.171	0.296	0.397	-22.497	6.431	1.010
ACT164	NH-Gilford	322756	117577	F	E	0.081	0.091	0.251	0.577	-21.151	5.790	1.349
ACT165	NH-Pelham	328067	25987	M	E	0.071	0.335	0.431	0.163	-22.806	8.620	0.987
ACT166	NH-Hooksett	318748	63447	M	S	0.097	0.379	0.335	0.189	-23.296	8.021	1.016
ACT167	NH-Allenstown	323119	70888	M	S	0.146	0.327	0.296	0.231	-23.465	7.261	0.641
ACT168	NH-Lyme	263857	145113	M	NC	0.164	0.431	0.231	0.174	-24.194	7.412	1.156
ACT169	NH-Merrimack	312087	39415	F	S	0.11	0.432	0.284	0.174	-23.679	7.961	1.464
ACT171	NH-Langdon	241893	74554	M	S	0.052	0.38	0.455	0.113	-22.828	9.460	0.826
ACT172	NH-Westmoreland	237570	52378	M	S	0.117	0.231	0.358	0.294	-22.640	7.129	1.122
ACT173	NH-Greenfield	283372	48903	F	S	0.197	0.156	0.236	0.412	-22.908	5.837	1.159
ACT174	NH-Unity	250973	88772	F	S	0.083	0.164	0.422	0.331	-21.812	7.270	1.193
ACT175	NH-Swanzey	248570	40459	F	S	0.087	0.076	0.173	0.663	-21.368	4.920	1.462
ACT177	NH-Charlestown	240924	83210	M	S	0.16	0.227	0.294	0.318	-22.996	6.640	1.032
ACT181	NH-Hampton	367771	49070	M	E	0.147	0.495	0.205	0.153	-24.483	7.677	1.020
ACT183	NH-Webster	295758	88845	F	S	0.17	0.215	0.285	0.33	-23.025	6.498	1.317
ACT184	NH-Walpole	239677	64019	M	S	0.118	0.236	0.342	0.304	-22.661	7.113	1.428
ACT185	NH-Acworth	249629	79810	M	S	0.106	0.133	0.295	0.467	-21.878	6.185	1.175
ACT186	NH-Swanzey	248570	40459	F	S	0.128	0.111	0.222	0.539	-22.091	5.531	1.081

ACT187	NH-Walpole	239677	64019	M	S	0.069	0.122	0.424	0.385	-21.195	7.121	1.058
ACT189	NH-Keene	248327	50109	M	S	0.087	0.195	0.428	0.289	-22.125	7.507	0.961
ACT190	NH-Washington	265640	75941	F	S	0.1	0.103	0.252	0.545	-21.598	5.765	1.338
ACT191	NH-New Ipswich	282974	27668	M	S	0.106	0.229	0.378	0.287	-22.512	7.342	1.134
ACT192	NH-Washington	265640	75941	M	S	0.04	0.061	0.53	0.37	-19.314	7.621	1.073
ACT194	NH-Milan	335781	229703	F	E	0.258	0.257	0.228	0.258	-23.892	6.418	1.158
ACT195	NH-Franconia	300422	187118	F	NC	0.625	0.148	0.11	0.117	-26.350	5.641	1.375
ACT197	NH-Wilton	291307	36824	F	S	0.085	0.132	0.369	0.415	-21.553	6.706	1.448
ALT039	NH-Alstead	247666	68433	M	S	0.153	0.254	0.303	0.29	-23.086	6.851	1.438
ALT040	NH-Walpole	239677	64019	M	S	0.082	0.263	0.432	0.222	-22.490	7.946	1.320
ME011	ME-Berwick	366753	89273	M	E	0.229	0.203	0.238	0.33	-23.410	6.127	1.602
VT102	VT-BROOKFIELD	225818	170247	F	NC	0.355	0.326	0.163	0.157	-25.147	6.560	1.308
VT107	VT-GREENSBORO	250622	233926	M	NW	0.461	0.242	0.15	0.147	-25.535	6.215	1.397
VT116	VT-SHARON	238057	142796	M	VL	0.271	0.538	0.105	0.087	-26.456	7.517	1.490
VT118	VT-TROY	243498	271201	F	NW	0.526	0.174	0.139	0.16	-25.471	5.699	1.425
VT120	VT-WALDEN	254681	220279	F	NC	0.508	0.223	0.136	0.133	-25.816	6.165	1.414
VT122	VT-WELLS	176757	104742	F	S	0.169	0.19	0.277	0.364	-22.908	6.342	1.753
VT123	VT-WEYBRIDGE	174961	173000	M	VL	0.078	0.536	0.26	0.126	-23.866	8.681	1.184
VT130	VT-WHITING	176770	153559	M	S	0.09	0.471	0.285	0.153	-23.649	8.294	1.092
VT132	VT-MONKTON	182901	192972	M	VL	0.096	0.128	0.334	0.443	-21.723	6.465	1.330
VT137	VT-WEST FAIRLEE	255019	160080	F	NC	0.139	0.239	0.319	0.303	-22.891	6.869	1.241
VT140	VT-DORSET	187560	85223	F	S	0.201	0.269	0.264	0.267	-23.542	6.681	0.855
VT141	VT-BARRE CITY	232707	189182	F	NC	0.162	0.408	0.241	0.189	-24.029	7.408	1.184
VT142	VT-MONKTON	182901	192972	F	VL	0.198	0.277	0.257	0.268	-23.596	6.721	1.435
VT143	VT-STARKSBORO	192212	192926	M	VL	0.053	0.14	0.625	0.182	-21.429	8.696	1.145
VT144	VT-SUDBURY	178207	144561	M	S	0.088	0.43	0.32	0.161	-23.436	8.239	1.166
VT146	VT-SHOREHAM	167671	156242	M	S	0.086	0.158	0.399	0.357	-21.775	7.123	1.157

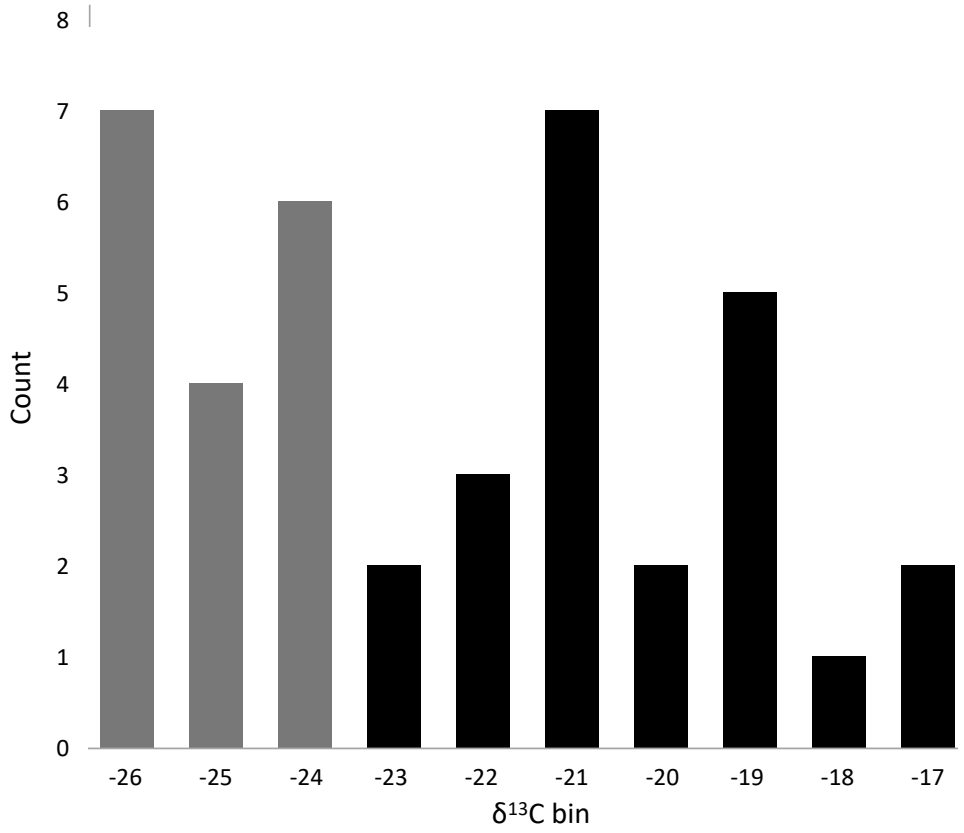
VT148	VT-WEST RUTLAND	187402	124675	M	S	0.082	0.206	0.448	0.264	-22.124	7.765	1.794
VT150	VT-SHOREHAM	167671	156242	F	S	0.121	0.141	0.282	0.456	-22.111	6.115	1.218
VT151	VT-SHOREHAM	167671	156242	F	S	0.152	0.182	0.286	0.38	-22.732	6.383	1.134
VT152	VT-BENNINGTON	173647	43968	F	S	0.114	0.406	0.296	0.184	-23.563	7.821	1.412
VT153	VT-WHITING	176770	153559	M	S	0.084	0.518	0.264	0.134	-23.867	8.526	1.087
VT162	VT-WESTMORE	271474	251169	F	NC	0.519	0.148	0.142	0.19	-25.050	5.401	1.023
VT165	VT-BRISTOL	187637	181413	F	VL	0.146	0.171	0.282	0.401	-22.604	6.303	1.354
VT166	VT-BELVIDERE	219733	251762	F	NW	0.249	0.202	0.225	0.324	-23.535	6.066	1.133
VT170	VT-TINMOUTH	187402	105894	M	S	0.131	0.429	0.258	0.182	-23.878	7.641	1.074
VT174	VT-ORANGE	243362	184211	F	NC	0.52	0.174	0.138	0.168	-25.399	5.667	1.288
VT175	VT-ORWELL	169124	146400	M	S	0.11	0.236	0.363	0.29	-22.605	7.223	1.219
VT176	VT-BRISTOL	187637	181413	M	VL	0.127	0.197	0.318	0.359	-22.554	6.650	1.211
VT178	VT-WELLS	176757	104742	F	S	0.135	0.188	0.313	0.365	-22.564	6.583	1.152
VT179	VT-RUPERT	176285	85940	M	S	0.15	0.153	0.26	0.437	-22.509	6.034	1.861
VT181	VT-MONKTON	182901	192972	M	VL	0.151	0.167	0.275	0.408	-22.584	6.224	1.266
VT182	VT-SALISBURY	183993	159103	F	S	0.128	0.125	0.243	0.503	-22.148	5.819	1.079
VT183	VT-LEICESTER	184989	153079	M	S	0.107	0.105	0.235	0.553	-21.778	5.652	1.104
VT184	VT-SUDBURY	178207	144561	F	S	0.079	0.354	0.396	0.171	-22.922	8.383	1.123
VT185	VT-ROCKINGHAM	232139	76039	M	S	0.134	0.208	0.319	0.339	-22.680	6.723	1.069
VT187	VT-ADDISON	165568	175951	M	VL	0.074	0.236	0.471	0.219	-22.305	8.123	1.095
VT188	VT-MONKTON	182901	192972	F	VL	0.15	0.142	0.246	0.462	-22.461	5.877	1.185
VT192	VT-LEICESTER	184989	153079	F	S	0.11	0.098	0.21	0.581	-21.827	5.382	1.733
VT193	VT-NEWARK	279576	245340	F	NC	0.603	0.116	0.118	0.163	-25.401	4.918	1.144
VT194	VT-POWNAL	173568	33581	M	S	0.17	0.374	0.253	0.203	-23.914	7.243	1.733
VT195	VT-ORWELL	169124	146400	M	S	0.215	0.237	0.245	0.303	-23.493	6.386	1.082
VT196	VT-WEYBRIDGE	174961	173000	M	VL	0.136	0.199	0.314	0.352	-22.659	6.622	1.356
VT197	VT-NEWARK	279576	245340	M	NC	0.574	0.158	0.128	0.14	-25.812	5.587	1.249

VT200	VT-DORSET	187560	85223	F	S	0.211	0.25	0.25	0.289	-23.562	6.519	0.998
VT201	VT-MIDDLEBURY	183304	168158	F	S	0.072	0.094	0.312	0.522	-20.988	6.286	1.054
VT202	VT-UNDERHILL	203084	227170	F	NW	0.391	0.102	0.138	0.369	-23.801	4.665	1.117
VT203	VT-READING	225003	111270	F	S	0.145	0.159	0.267	0.429	-22.534	6.138	1.108
VT204	VT-GRAFTON	222613	76433	F	S	0.067	0.1	0.373	0.46	-20.909	6.697	1.358
VT205	VT-ROCKINGHAM	232139	76039	M	S	0.163	0.251	0.286	0.299	-23.163	6.741	1.188
VT206	VT-GROTON	252422	192842	F	NC	0.081	0.091	0.23	0.598	-21.125	5.637	1.256
VT207	VT-GRANBY	295714	233572	M	NC	0.474	0.162	0.15	0.214	-24.799	5.485	1.058
VT208	VT-BRISTOL	187637	181413	F	VL	0.06	0.103	0.481	0.356	-20.806	7.398	1.436
VT209	VT-POWNAL	173568	33581	F	S	0.157	0.198	0.287	0.359	-22.815	6.458	1.377
VT210	VT-SPRINGFIELD	233916	88163	M	S	0.136	0.308	0.308	0.247	-23.272	7.232	1.056
VT211	VT-MIDDLEBURY	183304	168158	M	S	0.071	0.114	0.421	0.395	-21.113	7.036	1.388
VT213	VT-POULTNEY	176704	115846	F	S	0.236	0.227	0.246	0.292	-23.619	6.327	0.951
VT214	VT-BENSON	167773	136011	F	S	0.13	0.164	0.293	0.412	-22.420	6.310	1.423
VT215	VT-BRANDON	186251	145363	F	S	0.153	0.191	0.291	0.364	-22.754	6.409	1.608
VT216	VT-BENSON	167773	136011	M	S	0.083	0.15	0.404	0.362	-21.661	7.097	1.732
VT217	VT-CRAFTSBURY	242124	239511	M	NW	0.344	0.297	0.181	0.178	-24.833	6.533	0.990
VT218	VT-CHARLOTTE	174791	202165	M	VL	0.09	0.186	0.399	0.325	-22.070	7.233	1.340
VT219	VT-CORINTH	250038	171002	F	NC	0.272	0.253	0.227	0.247	-23.991	6.379	1.715
VT220	VT-W FAIRLEE	255019	160080	M	NC	0.085	0.245	0.431	0.239	-22.436	7.834	1.349
VT224	VT-LEICESTER	184989	153079	F	S	0.067	0.083	0.287	0.564	-20.643	6.110	1.434
VT225	VT-LEICESTER	184989	153079	M	S	0.048	0.07	0.449	0.434	-19.880	7.194	1.627
VT226	VT-SUDBURY	178207	144561	F	S	0.218	0.244	0.248	0.29	-23.538	6.461	1.366
VT227	VT-SHOREHAM	167671	156242	M	S	0.081	0.139	0.403	0.376	-21.562	7.001	1.336
VT228	VT-LEICESTER	184989	153079	F	S	0.078	0.072	0.159	0.692	-21.132	4.802	1.293
VT229	VT-SHOREHAM	167671	156242	F	S	0.102	0.201	0.375	0.322	-22.338	7.103	1.130

VT231	VT-DUMMERSTON	224469	48230	F	S	0.083	0.116	0.348	0.453	-21.394	6.496	1.515
VT232	VT-VERNON	229669	29498	M	S	0.116	0.188	0.331	0.364	-22.362	6.763	0.912
VT233	VT-VERNON	229669	29498	M	S	0.099	0.341	0.355	0.204	-23.108	7.887	1.331
VT234	VT-RYEGATE	264203	191419	M	NC	0.194	0.326	0.25	0.23	-23.815	6.941	1.149
VT235	VT-RYEGATE	264203	191419	F	NC	0.291	0.144	0.188	0.377	-23.514	5.459	1.301
VT236	VT-CORINTH	250038	171002	M	NC	0.088	0.211	0.428	0.273	-22.249	7.575	1.137
VT237	VT-CORINTH	250038	171002	M	NC	0.152	0.38	0.262	0.205	-23.801	7.353	1.136
VT238	VT-CORINTH	250038	171002	M	NC	0.198	0.34	0.242	0.221	-23.949	6.961	1.299
VT239	VT-CORINTH	250038	171002	F	NC	0.333	0.17	0.196	0.302	-23.899	5.682	1.426
VT240	VT-ORANGE	243362	184211	F	NC	0.481	0.166	0.152	0.2	-24.911	5.555	1.317
VT241	VT-MIDDLESEX	223118	203423	F	NW	0.147	0.321	0.288	0.244	-23.405	7.200	1.047

Appendix G.

HISTOGRAM OF TURKEY CARBON ISOTOPE RATIOS

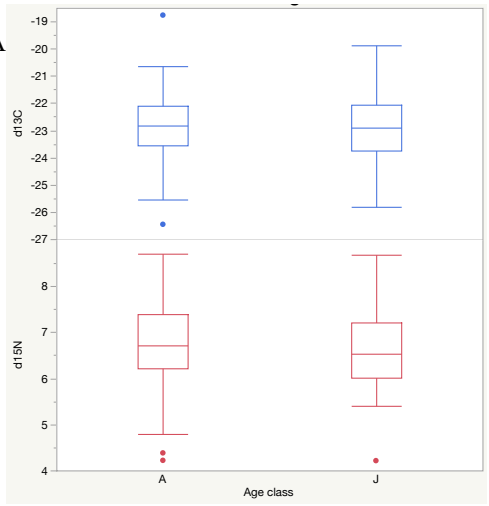


Turkeys (*Meleagris gallopavo*) were bimodally distributed in terms of d13C, so were split into two guilds for contemporary mixing model analyses. Individuals were assigned to the turkey or subsidized turkey guilds based on hierarchical clustering in JMP. Individuals that clustered with the turkey guild are represented by gray bars and subsidized turkeys are represented by black bars.

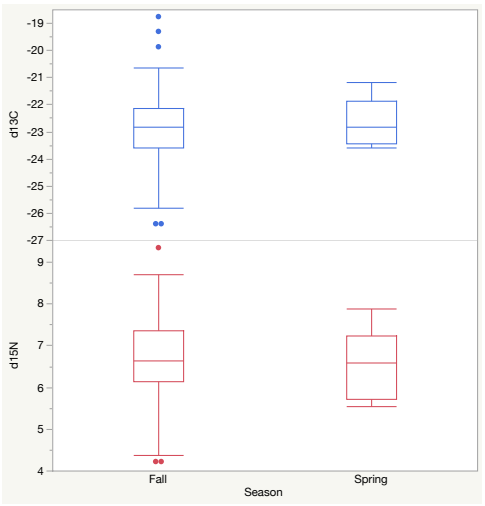
Appendix H.

BOX PLOTS OF ORGANISMAL LEVEL FACTORS INFLUENCING ISOTOPIC DATA

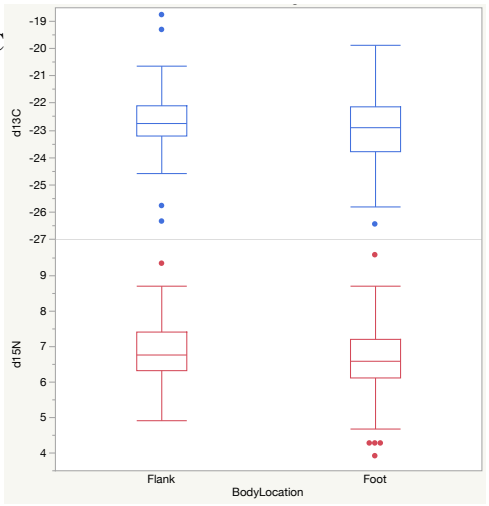
A



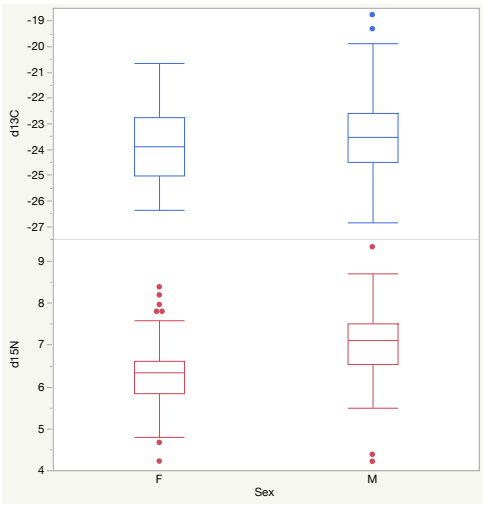
B



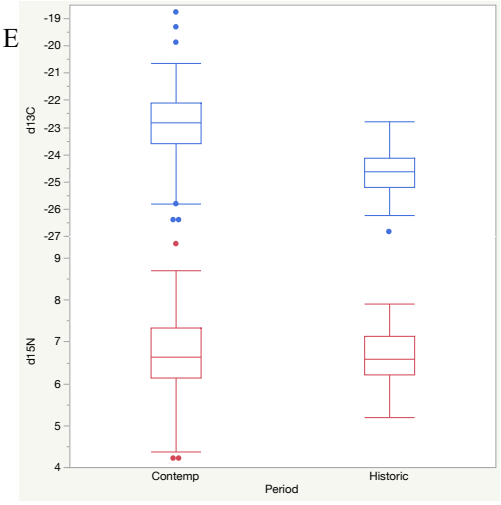
C



D



E



In chapter 2, I used t-tests to test for differences in $\delta^{13}C$ and $\delta^{15}N$ between adult and juvenile age classes (A), season of collection (B), body location (rear flank or foot) from which hair was collected (C), sex (D), and time period (E). Period was a significant factor for $\delta^{13}C$ but not $\delta^{15}N$. Both isotopes differeb between the sexes. No differences were found between age classes, seasons, or body locations.