

PROGRESS REPORT
for
COOPERATIVE BOBCAT RESEARCH PROJECT

Period Covered:
1 July – 30 September 2014

Prepared by

John A. Litvaitis, Tyler Mahard, Rory Carroll, and Marian K. Litvaitis
Department of Natural Resources
University of New Hampshire
Durham, NH
9 December 2014

SUMMARY BY STUDY OBJECTIVES

OBJECTIVE I -- DEVELOP PROTOCOL TO ESTIMATE CURRENT ABUNDANCE OF BOBCATS AND TRACK POPULATIONS STATEWIDE.

Approach #1: Use of transmitter-equipped bobcats to model suitable habitats and generate density estimate based on area requirements.

This portion of the project is complete. See Broman (2012) and Reed (2013).

Approach #2: Development of a method to monitor abundance of bobcats based on trail cameras and citizen scientist volunteers.

This portion of the project is complete. See attached draft of Mahard (2014).

Approach #3: Evaluate the application of population genetics using tissue from road-killed bobcats.

Genotyping continues on the 249 samples currently in our possession. In addition to genotyping several difficult/low quality samples that did not amplify in previous analyses, we are reanalyzing 10% of samples for quality assurance in the genetic data.

Recent analyses were conducted to assess the utility of resource selection probability function (RSPF) and expert opinion (EO) habitat suitability maps (Reed et al in review^A) in predicting functional connectivity for bobcats in New Hampshire (Reed et al in review^B). First, the Bayesian probability of population membership (Q) was calculated for each individual bobcat in New Hampshire using the program STRUCTURE (Pritchard et al 2000). The optimal number of putative populations in the state, as determined by the Evanno (2005) method, was four. A measure of genetic distance (Q distance; modified from Balkenhol et al. 2014) was calculated between each pair of individuals by summing the differences in probability of membership in each of the four populations. Next, individuals were placed on the RSPF and EO habitat suitability grids at the centroid of the township of capture. To calculate resistance distance, the program CIRCUITSCAPE (McRae and Beier 2007) was run between all pairwise locations with the RSPF or EO habitat suitability rasters as resistance surfaces. Finally, Q genetic distance, geographic distance, and resistance distance were correlated using Mantel and partial Mantel tests (Mantel 1967). Analyses were conducted using all individuals in the state as well as only individuals in two regions where the RSPF and EO models greatly differed, the southwestern region and north of the White Mountains (Table 1).

Table 1. Mantel and partial mantel test results. Tests were conducted using the *ecodist* package (Goslee and Urban 2007) in R (R Development Core Team 2013) with 1000 permutations. P-values are one-tailed; ** denotes significance at 0.05 level and * denotes significance at 0.10 level.

Population	Correlation	Mantel's r	P
All NH	Q ~ Geographic distance	0.305	0.001**
All NH	Q ~ RSPF resistance distance	0.114	0.017**
All NH	Q ~ Expert resistance distance	0.075	0.049**
All NH	Q ~ RSPF + Geographic distance	-0.153	0.999
All NH	Q ~ Expert + Geographic distance	-0.098	0.975
Southwestern	Q ~ Geographic distance	0.124	0.061*
Southwestern	Q ~ RSPF resistance distance	0.256	0.046**
Southwestern	Q ~ Expert resistance distance	0.127	0.158
Southwestern	Q ~ RSPF + Geographic distance	0.254	0.068*
Southwestern	Q ~ Expert + Geographic distance	0.080	0.230
North of White Mtns	Q ~ Geographic distance	0.254	0.033**
North of White Mtns	Q ~ RSPF resistance distance	0.103	0.200
North of White Mtns	Q ~ Expert resistance distance	0.255	0.016**
North of White Mtns	Q ~ RSPF + Geographic distance	-0.168	0.924
North of White Mtns	Q ~ Expert + Geographic distance	0.070	0.266

At the statewide scale, both RSPF and EO models were significantly correlated to genetic distance, but once geographic distance was partialled out, neither was significantly correlated. In the southwest region, the habitat suitability models differed in that RSPF contained no barriers to movement and a moderately high suitability whereas EO predicted excellent suitability but strong linear barriers along highway corridors. The latter predicted much lower connectivity. RSPF had the greatest correlations with genetic distance, and was significant even once geographic distance was partialled out (Table 1). This seems to suggest roads are not as strong of a barrier to bobcats as the EO model predicts. However, high-volume major highways are largely absent in this region. In the Northern regions, the EO model predicts much greater connectivity than RSPF. Here, the EO model was the single best correlate of genetic distance. RSPF predicted low connectivity here largely because the emphasis it places on snow cover. However, this variable is not likely to affect bobcat dispersal, which occurs most in spring and summer months when snowfall is not an issue. It should be noted that there are far fewer individuals in this region, so analyses are not as robust.

The genetic data do not offer great support to either model across the entire state, but tend to correlate best with the model with highest connectivity. Using genetic data to optimize the values of parameters determined to be significant may offer a better approach to understanding connectivity in the New Hampshire. Furthermore, incorporating species level dispersal characteristics of bobcats into models may increase efficacy. Autocorrelation plots (Fig. 1) based on genetic and geographic distance suggest that bobcats are significantly more related than would be expected due to chance up to a distance of about 65km. Effective dispersal events would have to exceed this threshold to prevent inbreeding effects and maintain genetic population integrity.

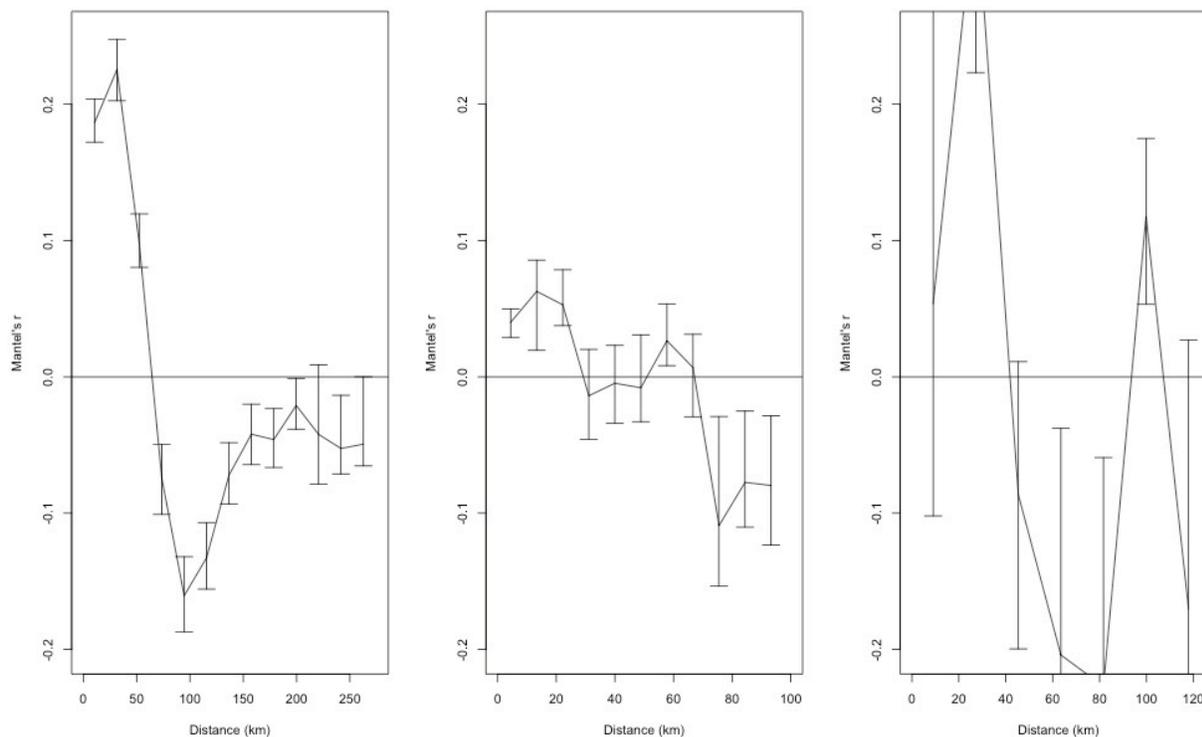


Figure 1. Spatial autocorrelation plots for all NH, southwest region, and north of the White Mountains. In all study areas, individuals are significantly more related at a distance less than 65 km. Large variation in the northern plot is due to a small sample size, but the trend is still evident.

Pertaining to our broader regional approach, solicitations for more samples from the current hunting/trapping seasons have been sent to agencies in Vermont, Massachusetts, and Quebec. Vermont is represented well in the data set, but both Massachusetts and Quebec have thus far contributed relatively few samples. A network of trappers, guides, hunters, and taxidermists has been established to collect tissues from Maine. Advertisements and flyers about the project have circulated in publications and at meetings of the Maine Trappers Association, Western Maine Trappers Association, Maine Professional Guides Association, and several taxidermists in the region. Hopefully, this network will be able to provide much needed representation from a region that appears to be critical to bobcat movement in New England and especially New Hampshire.

OBJECTIVE II -- COMPARE ABUNDANCE OF BOBCATS IN NEW HAMPSHIRE TO POPULATIONS IN ADJACENT STATES.

This portion of the project is complete, see Broman (2012) and Reed (2013).

OBJECTIVE III -- IDENTIFY POTENTIAL WILDLIFE CORRIDORS.

This portion of the project is complete, see Reed (2013).

LITERATURE CITED

- Balkenhol N, Holbrook JD, Onorato D, Zager P, White C, Waits LP (2014) A multi-method approach for analyzing hierarchical genetic structures: a case study with cougars *Puma concolor*. *Ecography* 37:552–563
- 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
- Goslee SC, Urban DL (2007) The ecodist package for dissimilarity-based analysis of ecological data. *J Stat Software* 22:1-19
- Mantel N (1967) The detection of disease clustering and a generalized regression approach. *Cancer Res* 27:209–220
- McRae BH, Beier, P. (2007). Circuit theory predicts gene flow in plant and animal populations. *Proc Nat Acad Sci* 104:19885-19890
- Pritchard JK, Stephens M, Donnelly P (2000) Inference of population structure using multilocus genotype data. *Genetics* 155:945–959
- R Development Core Team (2013) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria
- Reed GC, Litvaitis JA, Ellingwood M, Tate P, Broman DJA (in review^A) Hierarchical habitat selection by bobcats (*Lynx rufus*) based on two sources of information.
- Reed GC, Litvaitis JA, Callahan C, Carroll RP, Litvaitis MK, and Broman DJA (in review^B) Modeling landscape connectivity for mesocarnivores using expert opinion, radio telemetry, and bobcats (*Lynx rufus*) as a focal species: how well do they work?