

## Developing a close-kin mark-recapture model to map black bear population numbers in Michigan's Upper Peninsula

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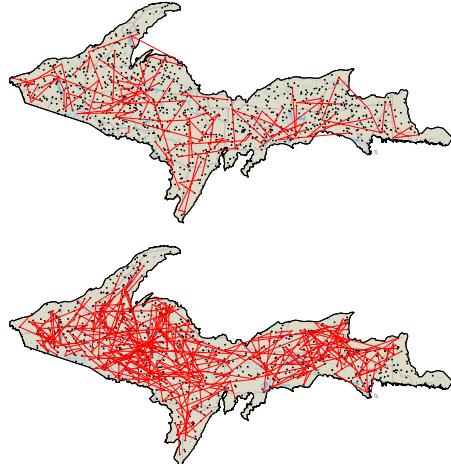
Accurate population size estimates for managed or threatened species are vital for implementing informed management strategies. In Michigan, black bears (*Ursus americanus*) are managed by harvesting, and estimates of the population size are used in determining the hunting license quota. Accurate, up-to-date estimates of the bear population size in the state – ideally, by age and by region – are therefore a necessary component of any effective management plan.

Recent bear population monitoring efforts in the state of Michigan have relied on capture-mark-recapture (CMR) methods, by which a sample of a population is initially marked, and an estimate of total population abundance can be made from the number of marked individuals that are subsequently recaptured (or harvested). However, traditional CMR methods are not ideal: they require extra fieldwork to do initial population marking; the tetracycline biomarker used in marking black bear individuals is no longer permitted; and there is a substantial wait time (1-3 years) after the initial marking period until population estimates can be made. Statistical catch-at-age analysis (SCAA) fits a demographic model to age and fecundity distributions estimated from harvested bears, thus allowing population size estimation without costly and time-intensive fieldwork<sup>1</sup>. However, since SCAA does not directly estimate absolute population size, to remain accurate it needs periodic recalibration with another method, e.g., CMR.

Genetic data from sampled individuals can be used to produce an accurate and cost-effective alternative to CMR for estimating population sizes<sup>2,3</sup>. Genetic mark-capture methods use an individual's genetic data in lieu of the initial marking phase in a standard CMR, and may therefore use data collected solely from harvested animals.

Close-kin mark-recapture (CKMR) models are an exciting class of genetic mark-recapture methods that leverage advances in molecular genetics to estimate population size from kinship patterns inferred in a genotyped sample<sup>4,5</sup>. To build an intuition for how relatedness between sampled individuals can be informative about total population size, we can consider the number of siblings in a sample. As depicted in Figure 1, a random sample from a population with a small number of breeding adults is more likely to contain siblings than that from a population with a large number of breeding adults; the number of sibling-pairs of various ages in a sample can therefore be used to infer the recent history of adult population sizes.

CKMR approaches offer a number of advantages over competing models. Like all genetic mark recapture models, a CKMR approach requires only a single round of sampling,



**Figure 1:** Locations of sampled bears (black points) and relationships of sampled half-sibs (red lines), in spatially explicit simulations of sexual, age-structured populations with local density-dependent population regulation, at two values of local population density. In the top figure, a total population of around 14,000 bears resulted in 73 half-sib pairs out of 1,000 harvested bears, while in the lower figure, a smaller total population of around 3,300 resulted in 216 half-sib pairs out of the same harvested number.

which can be achieved through a harvest. (It would be more accurate to refer to CKMR as a Close-Kin Capture method, as there is no marking phase, so it therefore requires no re-capture.) These methods also avoid some types of bias that can be introduced into CMR methods due to heterogeneity in capture/recapture probability. Moreover, by focusing on multiple pedigree connections (e.g., half-sib relationships, in addition to parent-offspring and full-sib) they allow a researcher to study unsampled individuals.

Here, we propose to develop a CKMR model for black bears in Michigan's Upper Peninsula (UP) for use by the Michigan Department of Natural Resources. This model, which will account for variable fecundity and capture probability, as well as non-sparse and non-uniform sampling, will generate population size estimates for the adult, pre-harvest black bear population in the UP. Because spatial structure in the bear population might impact population size estimates, we will also extend existing CKMR models to incorporate geography. In addition to generating estimates of total population size that are robust to the spatial structure of the pedigree, this spatial model will also generate maps of estimated population density, and has the potential to shed light on other demographic parameters as well. This model will be extensively tested using spatially explicit, forward-time simulations. To demonstrate the feasibility of this approach, we have included preliminary simulations of the bear population in the UP (Fig 1). These simulations, which were run with SLiM<sup>6</sup>, output both whole-genome genotypes and actual genealogical relationships, and have many realistic demographic features (e.g., nonuniform density and local post-natal dispersal) but are only proof-of-concept (code available at <https://github.com/petrelharp/howmanybears>). Biological parameters used to simulate these tests will be informed by previous research on Michigan black bears<sup>1,7</sup> and partner feedback. These simulations will be used both to validate the proposed inference procedure and to explore the sensitivity of the output to model assumptions (all model assumptions will be listed in the model documentation).

To disseminate the results of this new model, we will implement it in well-documented scripts that produce templated reports and graphical output for easy use by the DNR, and provide accompanying vignettes and a video walk-through demonstration. We will also engage in educational trainings with state biologists, and assist in outreach with administrators, commissioners, and stakeholders.

We are confident that we will be able to carry out the proposed work in the timeline below (Fig 2). Both PIs Bradburd and Ralph have extensive experience developing statistical methods<sup>8–10</sup> – with a particular focus on spatial population genetics<sup>11,12</sup> – and implementing them as documented software packages. In addition, the PIs have collaborated previously on black bear research<sup>10</sup> and on developing management plans for government agencies<sup>13</sup>, and have recently co-written a review discussing how to link properties of the pedigree to population demography and dynamics<sup>11</sup>.

Project timeline	2020			2021												2022							
	O	N	D	J	F	M	A	M	J	J	A	S	O	N	D	J	F	M	A	M	J	J	A
Hire and onboard personnel	■																						
Develop statistical inference methods				■■■■■																			
Develop spatial simulations of bear populations				■■■■■																			
Solicit partner feedback on simulations				■■■■■																			
Refine simulations based on partner feedback				■■■■■																			
Implement statistical inference methods				■■■■■																			
Test statistical inference methods				■■■■■																			
Apply to available bear data				■■■■■																			
Develop user-interface				■■■■■																			
Solicit partner feedback on user-interface				■■■■■																			
Refine user-interface				■■■■■																			
Develop user-interface trainings				■■■■■																			
Trainings and outreach				■■■■■																			

**Figure 2:** Timeline of proposed work.

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