**Phase I Research Proposal**

**Minnesota DNR Wildlife Research**

**Project title:** Genetic-based estimates of bear populations: maximizing bang

for the buck

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**Date:** 30 January 2015

**Problem statement:** Genetic-based mark–recapture population estimates from hair-snaring are now routinely used for bears. The number of samples obtained typically far exceeds the budget allotted for genetic analysis, and moreover, many samples are likely to be redundant (same visit by same bear). No guidance presently exists for selecting which and how many samples to genotype. Sample selection is likely to significantly affect spatially-explicit capture-recapture models, which rely on the spatial distribution of capture samples.

**Background:**

During the spring and summer of 2012, we conducted a genetic capture-mark-recapture (CMR) of black bears using barbed-wire hair snares in the Chippewa National Forest. Our goal was to ascertain whether the population had declined over the past 20 years, and if so, by how much. We obtained CMR population estimates on the same study site during the 1980s from physical captures, and in the early-1990s from camera captures. Since then, various indicators provided evidence that the population had sharply declined (Garshelis and Noyce 2011).

Some important distinctions between the genetic CMR and physical/camera-based CMR exist, which must be reconciled in order to properly compare these estimates across time. One issue is that the study area is not geographically closed, meaning that bears regularly moved in and out (because their home ranges overlapped the arbitrary study area boundaries). This has long been recognized as an important consideration when interpreting mark–recapture estimates of abundance or when estimating density since the effective area sampled by a capture grid is typically unknown (White et al. 1982). Abundance estimates unadjusted for lack of closure would correspond to the “super-population” (Kendall and Nichols 1995) of all animals using the study area at some time, not the number of individuals present there simultaneously. If home range size changed from the 1980s to the present (due to changing food conditions, which we know occurred), this could impact the degree of closure and hence the super-population that is sampled. Thus, changes in the rate of movement in and out of the study area must be considered when estimating population trends.

For CMR estimates in the 1980-1990s, we converted abundance to density by employing a weighting based on the proportion of time that collared bears used the study area (Garshelis 1992). A form of this procedure is now a module in Program MARK (Ivan et al. 2013a). During the 2012 CMR, however, we had no telemetry data from this area, so could not employ the same adjustment. Instead, we plan to use a spatially-explicit capture-recapture (secr) model to obtain a density estimate. It is imperative, therefore, that the differing procedures for deriving density are comparable.

Secr estimates are based on the spatial distribution of the captures (Efford 2004, Efford et al. 2004, 2009, Gardner et al. 2010). This method has been likened to mark-recapture–distance-sampling, where animals closer to the observer (or trap) have a higher probability of detection, but that probability is not 1 even at distance 0 (i.e., some animals approach the trap but do not enter)(Borchers 2012). It seems evident that the spatial distribution of captures (unlike telemetry locations of collared bears) could be affected by the placement of the traps and behavioral responses of bears to the traps; a host of recent simulation papers have specifically investigated these issues (Pradel and Sanz-Aguilar 2012, Sollman et al. 2012, Efford and Fewster 2013, Sun et al. 2014, Wilton et al. 2014).

Another related issue, which occurs often in genetic CMR, is that far more hair samples are obtained than can be genotyped within budgetary constraints. Therefore, it becomes necessary to subsample the data in some way. Despite this ubiquitous problem, and its inherent similarity to the trap-spacing issue (i.e., both relate to probability of detection at points across the landscape), few studies have investigated how best to subsample the collected specimens, or how differing procedures could affect estimates. Tredick et al. (2007) compared abundance estimates generated by analyzing every black bear hair sample versus varying sorts of subsamples. They concluded that all subsampling procedures yielded low-biased estimates. They recommended maximizing capture rates through trap spacing and subsampling strategies, but provided no guidance as to how to do this. Moreover, some of their results may be attributable to the relatively small sample size to begin with (n = 157 and 397 total genotyped samples on 2 study areas). Dreher et al (2009) used a simulation procedure parameterized using empirical data and concluded, contrary to Tredick et al. (2007), that judicious subsampling did not introduce bias or diminish precision; they found that genotyping >3 samples per hair trap did not improve estimates. However, their results were specific to the dataset they emulated (including a relatively high genotyping error rate, which meant that increasing numbers of samples from the same bear could lead to an increasing chance of erroneously scoring these as 2 or more bears); accordingly subsampling procedures are likely specific to the actual data at hand. Laufenberg et al. (2013) found, like Tredick et al. (2007), that subsampling caused population underestimates, and moreover, that confidence intervals were narrower than they should have been — both due to smaller datasets being less able to detect capture heterogeneity. Indeed, Augustine et al. (2014) showed that Tredick et al.’s (2007) low-biased estimates were due to trap-shy bears being inadequately represented in the subsampled data. Laufenberg et al. (2013) indicated that samples from the most difficult to capture bears were most important for producing accurate and precise population estimates. None of these studies, though, provided guidelines for how to subsample when necessary for budgetary reasons.

We are also not aware of any studies that have considered the effects of subsampling on secr estimates, even though the assumptions of secr methods would seem to make them more susceptible to subsampling biases (a recent comprehensive book on secr estimation did not mention subsampling of data; Royle et al. 2014). Whereas conventional abundance estimates only consider whether the individual was captured or not at ≥1 trap within a trapping session (multiple detections within a trapping session are redundant), secr estimates are based on capture frequencies at different traps (including multiple captures within trapping sessions). These capture frequencies are in turn assumed to be reflective of movement characteristics of the individual animals. Specifically, capture probabilities are assumed to decline as a function of distance from the center of an animal’s home range. Researchers often subsample hair samples with the intention of maximizing the number of unique individuals (e.g., by taking at least 1 hair from each unique trap by time session; e.g., Settlage et al. 2008). This method results in disproportionate sampling rates at traps and sampling occasions with few hair samples. As a result, realized capture frequencies will depend not just on an individual’s movements relative to its home range center, but also on the number of other bears leaving hair samples. Thus, even if this approach is reasonable for traditional abundance estimation, it may not be appropriate for secr density estimation.

We have an opportunity to use our data to investigate these potentially important issues about how sampling affects both bias and precision, thereby informing both the past (2012) and future genetic-based CMR estimates in Minnesota. Our team of investigators has particular expertise and interest in this subject, and the proposed project can be conducted at relatively little cost (especially compared to the cost of the collected data, and future such studies).

**Objectives:**

1. Compare abundance and density estimates and precision obtained from the 2012 genetic CMR using different subsamples of data — derive the best estimates from the existing data.
2. Assess effects of subsampling and behavioral characteristics of the bears on the bias and precision of genetic CMR estimates based on capture histories similar to that observed in 2012.
3. Provide guidance for study design of future genetic CMR estimates of bears in Minnesota.

**Methods:**

**Study area —** Chippewa National Forest

**Data collection —** This study employs data collected during the 2012 hair-snaring CMR. Noyce and Garshelis (2014) described methods and provided a summary of the data collected:

* Trapping area = 300 km2
* No. hair traps = 121
* No. sampling session = 6
* No. traps visited by bears each session: 30–79
* No. bear hair samples obtained = 2784 (barbs)
* No. sent to genetics lab = 1113: 1 from each site-session with hair (= 377) + random selection for the rest (selection from among clusters, not barbs, where cluster = group of adjacent barbs with hair, presumed to be 1 bear).
* No. genotyped = 1019 (92%)
* No. individuals identified = 43 (26M, 17F)
* No. individuals detected per session: 14–28
* No. detections at different hair traps by individuals = 1–22

Additionally, we employed camera traps at a number of hair-snare sites in 2012, and also erected 4 hair-traps with cameras in 2014. Cameras provided information on the number of repeat visits of individual bears to traps *within* a trapping session; this information is not obtainable from the genetic samples that were collected at 10-day intervals because multiple hair samples from the same bear could have been deposited during 1 or more visits. Cameras also provided information on bear visits that did not result in a hair sample. Further tests with cameras at hair traps will be conducted during summer 2015.

**Data analysis —**

1. Subsample the existing genotyped 2012 data in a number of ways, and compare resulting estimates of abundance (derived from Huggins model in Program MARK) and density (derived from secr).

1. Create a simulated data set, patterned after the existing data, with a known number of bears. Conduct a simulation analysis to test the effects of behavioral responses to the traps (as possibly evidenced in the existing data) and various schemes of subsampling the resulting hair captures.
2. Incorporate information from camera-trapping at hair-snare sites in the simulation model to discern whether that improves interpretation of the data, and possibly should be added as a study design component in future hair-snaring efforts.
3. A future analytical possibility will be to compare the secr-based density estimates with density estimates derived by incorporating telemetry data in the hair-snaring CMR. Ivan et al. (2013b) showed through simulations that telemetry-adjusted CMR estimates are more accurate than secr because the telemetry data include far more locations (both in and outside the trapping grid) and make no assumptions about home range shape or the influences of baited traps on animal movements. We did not have telemetry data accompanying the 2012 hair trapping, but we have plans to collect such data from GPS-collared bears on this same study site in 2016 (Garshelis and Forester, pending research proposal). Others have shown that telemetry data collected in years different than the CMR years are still valuable for calculating density (Dumond et al. 2015).

**Management Implications:**

Genetic CMR estimates have now become the standard for estimating bear populations (Proctor et al. 2010; see review by Garshelis and Noyce 2011). Looking forward, we expect there will be a need to employ this technique again in Minnesota. A better understanding of how behavioral and sampling issues impact both cost and estimator reliability is needed to design efficient and informative studies.

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**Timeline:**

Analysis completed by September 2015. Manuscript preparation during summer 2016.