

# Subsampling for Cost Efficiency with Spatially Explicit Capture-Recapture Models

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## Abstract

Genetic mark-recapture studies estimate animal abundance using non-invasive DNA identification methods to collect “captures” and “recaptures” from individuals that leave genetic material at trap sites. Due to the cost of genotypic analysis, researchers often choose to process only a subsample of this genetic material. Traditional (non-spatial) mark-recapture estimators of abundance have been shown to be biased in this case, especially when the study population displays a behavioral trap response that varies at the individual level. Less is known about the influence of subsampling genetic mark-recapture data, randomly or non-randomly, when using spatially explicit capture-recapture (SECR) models to estimate abundance. We analyzed hair-snare data obtained from a 2012 genetic mark-recapture study of black bears (*Ursus americanus*), where 1019 hair samples were successfully genotyped. We simulated the process of subsampling hair samples either randomly or non-randomly. Similar to non-spatial mark-recapture estimators, subsampling produced density estimates that were lower, on average, than the full data estimate; however, non-random subsampling had much less of an effect on estimator performance, particularly at small sample sizes. Thus, non-random subsampling may be preferable to random sampling, despite the inherent violations of SECR assumptions that may result.

## Acknowledgements

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## Non-technical Summary

Mark-recapture studies, in which animals are ‘tagged’ and released, are often used by wildlife managers to estimate animal abundance. Usually, this involves physically capturing the animal in a trap (net, snare, etc), and physically tagging the animal with a unique number combination, so that it can be identified later on. A newer method uses the same conceptual framework using the animal’s DNA as a unique identifier, which is often much less invasive and less costly than tagging by hand. Most of these methods involve hair snare traps - a baited lure is placed inside of a barbed wire perimeter, so that when the animal investigates the bait, they leave some hair behind which can be identified to determine the bear’s identity. However, contrary to previous methods where an individual’s identity could be determined simply by reading numbers on a tag, the hair samples need to be analyzed in a genetics lab to determine the bear’s identity - and this can very quickly use up the project’s budget. So, most of the time, managers subsample their hair samples to reduce their costs.

This sort of subsampling has been shown to be problematic for getting reliable population estimates, especially in species that have strong ‘personalities’ - for example, if one bear loves the bait, and leaves hundreds of samples, he is very likely to be included in a subsample. If a bear hated the whole experience, and left only one sample, he’s much less likely to be included. As a result, we usually underestimate populations when we subsample genetic mark-recapture data. Unfortunately, that might not be the only problem.

Traditionally, we would say an animal is ‘captured’ if we see it anywhere in our study area in a given time frame, regardless of where it was. As a result, a lot of the

data we analyze just confirms what we already knew - for example, we know bear X was in the area from May 10 to May 20 after we see one of his hair samples, and any more of his hair we analyze during that time frame is useless, because we already knew he was there. A relatively new estimator (spatially explicit capture recapture, or SECR) actually uses this useless data to describe where the animal was, which is used to determine the animal's likelihood of leaving a hair sample at each trap. Because of much of this formerly useless data gets thrown out when subsampling, we had reason to believe that SECR estimates may change quite a bit after the data is subsampled.

To investigate this, we subsampled some real hair snare data from northern Minnesota bears in a few different ways, and fit SECR models to those subsamples. We found that strategically subsampling could reduce these effects when compared to randomly subsampling - by choosing hair at different trap and time period combinations, our estimates using very small sample sizes were pretty close to estimates obtained by using *all* the samples at once.

While we can't make generalizations yet, because we don't truly know how many bears were out there when the hair samples were obtained, we argue that subsampling *is* problematic for SECR models. However, depending on the behavior of the animals being studied, the effects likely vary - if animals have a tendency to leave many samples at a single site, we predict that subsampling may be less of an issue. Regardless, this problem has not been given much attention yet, and our results that managers should give some thought into how they (or if they should) subsample in order to best manage animal populations.

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# Introduction

Mark-recapture studies are routinely used by wildlife managers to estimate animal abundance; especially in the case of endangered species and game animals, abundance and its associated temporal trends are of critical importance for making informed management decisions (Borchers *et al.* 2002; McCrea & Morgan 2014). In many cases, however, abundance estimates can be difficult to interpret without some understanding of the effective area sampled; extrapolation to a regional scale by way of density is almost always desired, if not necessary (Borchers *et al.* 2002; Royle *et al.* 2013). As such, abundance estimates without associated reliable density estimates may be of limited use to managers.

Density estimates have often been obtained from abundance estimates using ad-hoc methods that range widely in their biological relevance (Royle *et al.* 2013). Spatially-explicit capture recapture methods (SECR), by contrast, link abundance estimators to their associated study area in a statistically rigorous way (Efford *et al.* 2005; Borchers 2012; Royle *et al.* 2013). SECR estimates of abundance scale directly with a given sample area, potentially allowing for more standardization of estimates across space or time. SECR models also make better use of the capture-recapture data. In particular, SECR models utilize the information in the spatial capture histories to model detection probabilities as a function of the distance between each animal's activity center (AC) and the trapping grid. By accounting for each individual's movement characteristics relative to the distance between their AC and the trapping grid, SECR provides a way to account for an important source of individual heterogeneity in capture probabilities that is unaccounted for in traditional (non-spatial) mark-recapture estimators.

We explored a popular method for estimating abundance of mammal populations: genetic mark-recapture, where individuals are identified by sequencing the genome of residual genetic material left at a trap site (Boulanger *et al.* 2004; Petit & Valiere 2006; Gervasi *et al.* 2008; Buckworth & Territory 2012). Many studies aim to obtain hair samples, often by the use of baited traps and hair-snares, which provide a relatively non-invasive and efficient way to ascertain the identity of detected animals when compared to live capture. However, due to the costs of genotypic analysis, managers are often forced to subsample their hair clusters (Boulanger *et al.* 2004; Petit & Valiere 2006; Gervasi *et al.* 2008; Settlage *et al.* 2008).

Subsampling has been shown to be problematic for non-spatial mark-recapture estimators, especially when individuals exhibit a behavioral response to having been previously captured, and this behavioral response is not consistent across individuals (Tredick *et al.* 2007; Ebert *et al.* 2010; Augustine *et al.* 2014). In this case, individuals that leave many hair clusters are likely to be identified in a subsample, where individuals that leave few clusters are often excluded. In other words, clusters selected in a subsample are likely to come from individuals that are repeatedly captured. As a result, estimates of capture probability are biased high and abundance estimates are biased low; this effect is more pronounced as subsample size decreases (Augustine *et al.* 2014).

While subsampling generally reduces estimator precision, removal of redundant data has no effect on either SECR or non-spatial mark recapture models. Captures at the same site by session combination are frequently (SECR) or always (non-spatial mark-recapture) collapsed into a single capture, in which case each capture after the first (at a single site-session) provides no new information. Multiple captures at *different*

sites during the *same* period are also collapsed into a single capture event in the case of non-spatial mark-recapture. However, these captures provide information regarding the location and movement of that individual, and this information is used to estimate detection parameters in SECR models. Thus, samples that are redundant in a non-spatial model (captures at > 1 trap location in a single period) are of critical importance to SECR models. As a result, the effects of subsampling may be even more problematic for SECR models when compared to non-spatial capture-recapture models, as there are often fewer redundant samples to remove.

In response to the knowledge that multiple samples from one individual in the same period are redundant in non-spatial models, managers often avoid taking multiple samples from a single trap under the assumption that they are likely to be from the same individual, and thus not informative and not worth the cost of genotypic analysis. This strategy is effective for use with non-spatial models; analyzing several samples from the same site often leads to diminishing returns in precision and accuracy (Dreher *et al.* 2009). Instead, preference is given to samples from novel site by session combinations (hereafter referred to as site-sessions), because they are more likely to be new individuals. This non-random sampling could cause issues in SECR models by violating the assumption that the observed samples reflect the movement characteristics of the study population. A natural solution to this violation is to avoid preference for novel site-sessions (ie, simple random sampling), at the cost of identifying fewer unique individuals and analyzing more redundant data.

Various simulation and empirical studies have addressed the issue of subsampling

on non-spatial mark-recapture estimators, with a general conclusion being that subsampling genetic mark-recapture data results in estimators that are biased low, but that the magnitude of this bias depends on the actual data at hand and several assumptions such as erroneous genotyping rate and trap spacing (Tredick *et al.* 2007; Dreher *et al.* 2009; Augustine *et al.* 2014). The tradeoff between potential redundancy (using simple random sampling) and non-representation of movement characteristics (using non-random sampling) has not been investigated in the context of SECR models. **In this study, our objective was to use northern Minnesota genetic mark-recapture dataset with 1019 successful samples to compare abundance and density estimates using (1) various subsampling strategies utilized by wildlife managers and researchers and (2) various subsampling rates reflective of different budgetary constraints.** Using these results, we provide guidance for genetic mark-recapture estimates when budget constraints limit effective sample size.

## Methods

The subsections below describe the nature of the data analyzed and the procedure followed in this study. The resultant code can be found in the Appendix under subsection “Code Documentation”.

## Data

The data analyzed in this study come from a 2012 genetic mark-recapture study of American black bears (*Ursus americanus*) in northern Minnesota (Garshelis & Noyce 2013). Using stationary hair-snare traps baited with suspended bacon and scent lures,

the authors collected 1642 hair clusters (groups of hair samples obtained from adjacent barbs) from 121 sites over six trapping sessions from May through July 2012, each of ten day length. Of these 1642 clusters, 1113 were sent to a genetics laboratory for genotypic analysis, and 1019 samples were successfully linked to individual bears.

It is important to note that the 1113 samples analyzed were effectively a subsample to begin with; the authors initially chose samples from 377 unique site by session combinations (site-sessions), with the remaining 776 samples chosen randomly. Given that the majority of samples were analyzed (67.7%), and that the majority of these samples were chosen randomly from the original sample set, we will treat the dataset as if it is representative of the population of interest.

Camera traps fitted to a subset of the trap locations indicated that bears occasionally visited the same trap several times in a single session, often using several different entry locations to approach the bait hung at the center of the trap. This individual variation is evidenced in the number of samples left at a given site-session by individual bears; 47% of the time, bears left only a single sample at a given site-session, but some left as many as 11, and some may have left even more considering that 529 samples were not analyzed (Garshelis & Noyce 2013). Additionally, movement characteristics differed strongly between individuals; 53% of bears visited between one and five unique sites, but bears visited up to 24 unique sites over the 6 sample periods.

## Subsampling

The subsampling strategies chosen span from simple random sampling to a subsampling method that gives preference to unique site-sessions (Figure 2). These are described



Figure 1: A typical baited hair-snare trap in northern Minnesota, one of 121 sites in the study conducted by Garshelis and Noyce (2013). Between May and July 2012, black bears left a total of 1642 hair clusters at these sites.

below:

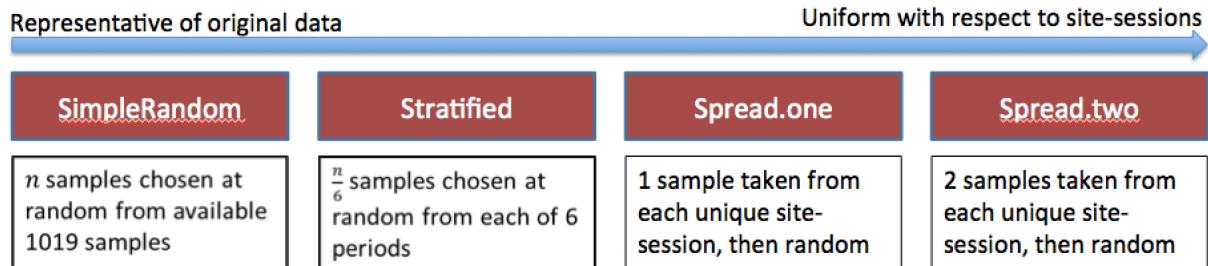


Figure 2: Subsampling types used to determine the effect of subsampling strategies on Spatially Explicit Capture Recapture models using hair snare data from northern Minnesota.

- SimpleRandom -  $n$  samples are chosen at random from the entire data set, without respect to period or site. This type of sampling is, on average, most representative of the original data set; for example, site-sessions that have a large number of samples would have the largest number of samples in the subsample, and

site-sessions with only one sample are unlikely to be chosen.

- Stratified -  $n/6$  samples are chosen at random from each of 6 sessions, without respect to site. It is important to note that this differs from a true stratified random sample, where the number of samples chosen from each session would be weighted by the number of samples in each session relative to the number of samples overall.
- Spread.one - one sample is chosen from each unique site-session. After this, samples are chosen randomly until  $n$  samples are selected. At  $n < 377$ , this strategy is identical to Spread.two.
- Spread.two - two samples are chosen from each unique site-session. After this, samples are chosen randomly until  $n$  samples are selected. This method is least representative of the original data, and effectively maximizes the number of site-sessions (and thus, unique individuals) included in analysis; for example, each unique site-session with only one or two samples have both of those samples chosen, and site-sessions with large amounts of samples are under-represented relative to the original dataset. At  $n < 377$ , this strategy is identical to Spread.one.

## Model Structure

A SECR model is unique from other mark-recapture models in that an animal's capture probability is derived using the animal's activity center (AC) (Borchers *et al.* 2002; Royle *et al.* 2013). Though many curves are used to characterize how detection probabilities change as a function of distance between an animal's activity center and a trap location, a common and readily understood choice is a half-normal curve, using two parameters:  $g_0$  and  $\sigma$ .  $g_0$  represents the probability of detecting an animal whose

activity center is located exactly at the trap location.  $\sigma$  represents the rate at which this probability decreases as an animal's homerange center moves further away from the trap.

Similar to other population models, these parameters can be allowed to vary by sex (Sex), time (t), and they may be allowed to change following an initial capture event (i.e., a behavioral trap response (b)). In figure 3,  $g_0$  was modeled as a function of time and sex ( $g_0 \sim t + \text{Sex}$ ) and  $\sigma$  varied by sex only ( $\sigma \sim \text{Sex}$ ); as such, each time and sex combination has its own intercept and capture probabilities decrease at different rates for males and females as a function of distance. Time effects may also be modelled in a structured, linear fashion (eg,  $g_0 \sim T$  instead of  $g_0 \sim t$ ), meaning that there is a trend in the change of intercept detection probability; this would be appropriate if detection probabilities decreased or increased monotonically over time.

## Model Fitting

We fit 5 SECR models, each with a different combination of explanatory variables, to each subsampled dataset. In each case, we assumed  $\sigma$  varied only by sex. We explored five models with different covariates influencing  $g_0$  (Table 1).

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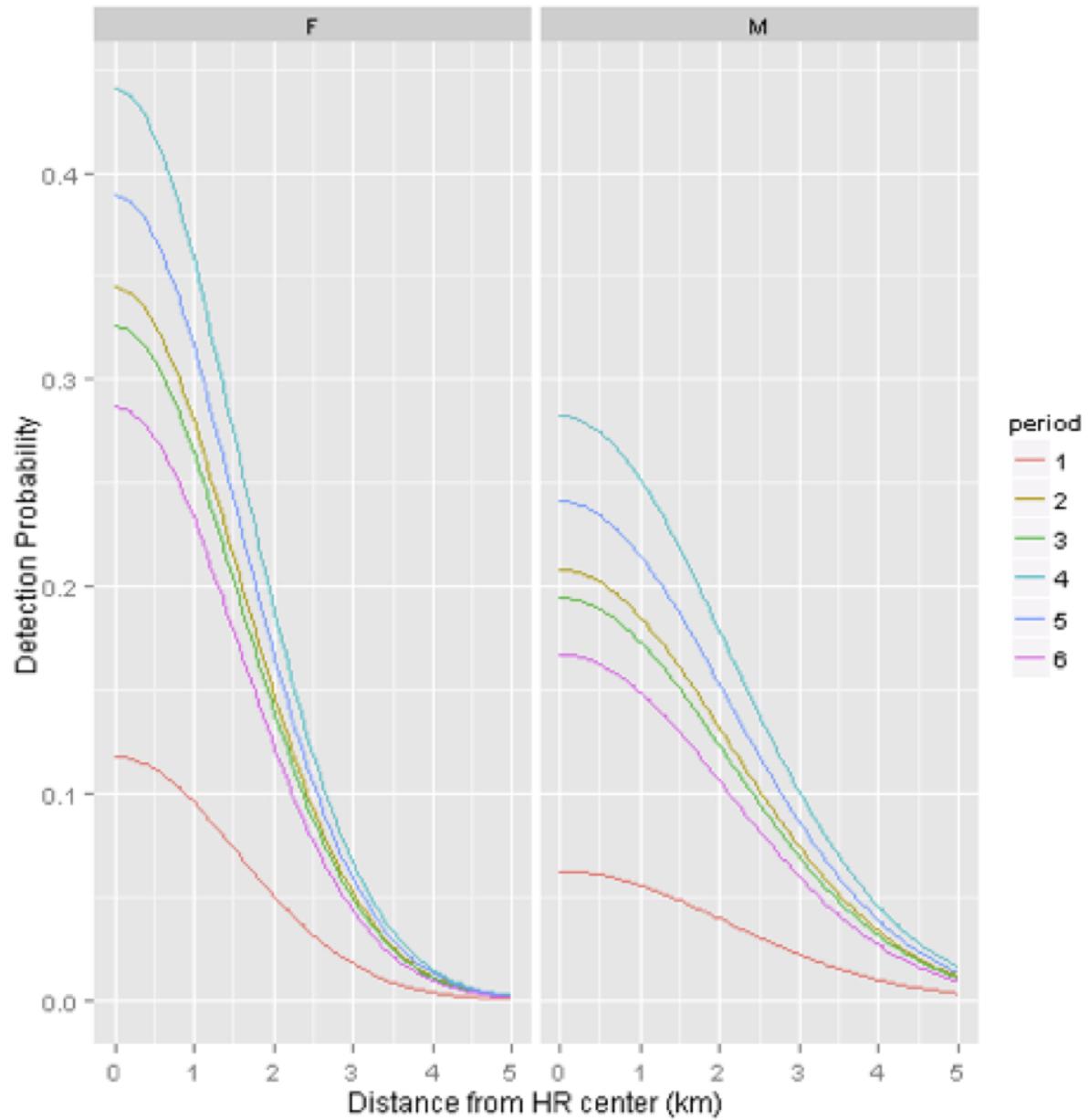


Figure 3: Estimated half-normal detection curves for a SECR model fit to all 1019 genetic hair samples, where  $g_0$  varied by time and sex ( $g_0 \sim t + \text{Sex}$ ) and  $\sigma$  varied by sex only ( $\sigma \sim \text{Sex}$ ).

Table 1: Density estimates and Aikaike Information Criterion (AICc) scores associated with spatial-mark recapture (SECR) models fit to 1019 hair samples taken from black bears in Minnesota from May through July 2012.  $\Delta AICc$  represents the difference from the lowest scoring model and the compared model. All models were fit using the R programming language and package secr.

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<i>g0 Covariates</i>	AICc	$\Delta AICc$	Bears/100 sq mile( <i>95% Confidence Interval</i> )
b + t + Sex	3492	0	13.50 ( <i>9.86,18.48</i> )
t + Sex	3496	4	12.67 ( <i>9.30,17.26</i> )
b + t	3502	10	13.60 ( <i>9.93,19.64</i> )
t	3507	15	12.55 ( <i>9.22,17.08</i> )
b	3515	23	14.23 ( <i>10.41,19.46</i> )

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Models were fit using the R programming language (R Core Team 2015), package ‘secr’ for the fitting of the SECR models, and packages ‘foreach’ and ‘doParallel’ for optimization of model fitting using parallel processing (Analytics & Weston 2014, 2015; Efford 2015). The main function for fitting models to subsampled data is `secr.fit` in package ‘secr’. This function requires a capture history and a trapping grid to arrive at a derived density estimate and estimated parameters describing the effect of time, sex, and/or behavior on capture probabilities (Royle *et al.* 2013).

## Simulation

In this study, a single ‘simulation’ can be broadly defined as subsampling the full dataset using one of the subsampling strategies (Figure 2), fitting of five SECR models with varying covariates (Table 1), and saving model output for later comparison (Figure 4). Initially we varied the subsampling strategy while holding sample size constant at  $n = 450$  hair samples (Figure 2, 4B). This allowed us to evaluate the influence of subsampling strategy on the derived density estimate of each SECR model; these simulations are referred to as ‘subsampling trials’ in this document as well as in the accompanying code documentation.

We then considered two subsampling types (SimpleRandom and Spread.one) for further study. In a second set of ‘size trials’, we explored these two approaches across a range of sample sizes ( $n = 250$  to  $950$ , by  $100$ ) (Figure 4A).

## Results

### Notation

Let  $\hat{D}_{data,i}$  refer to the density estimate of a SECR model using  $data$  as the analyzed dataset, and  $i$  as the set of covariates for  $g0$ . For example,  $\hat{D}_{full,b}$  represents the density estimate using the full dataset and behavior as the sole covariate for  $g0$ .  $\hat{D}_{sr,b+t}$  represents a density estimate using a simple random sample and both behavior and time as covariates for  $g0$ ;  $\hat{D}_{so,t}$  represents a density estimate using the spread.one subsampling method and time as a covariate for  $g0$ .

Let  $M_i$  refer to a SECR model with  $i$  as the set of covariates for  $g0$ . For example,

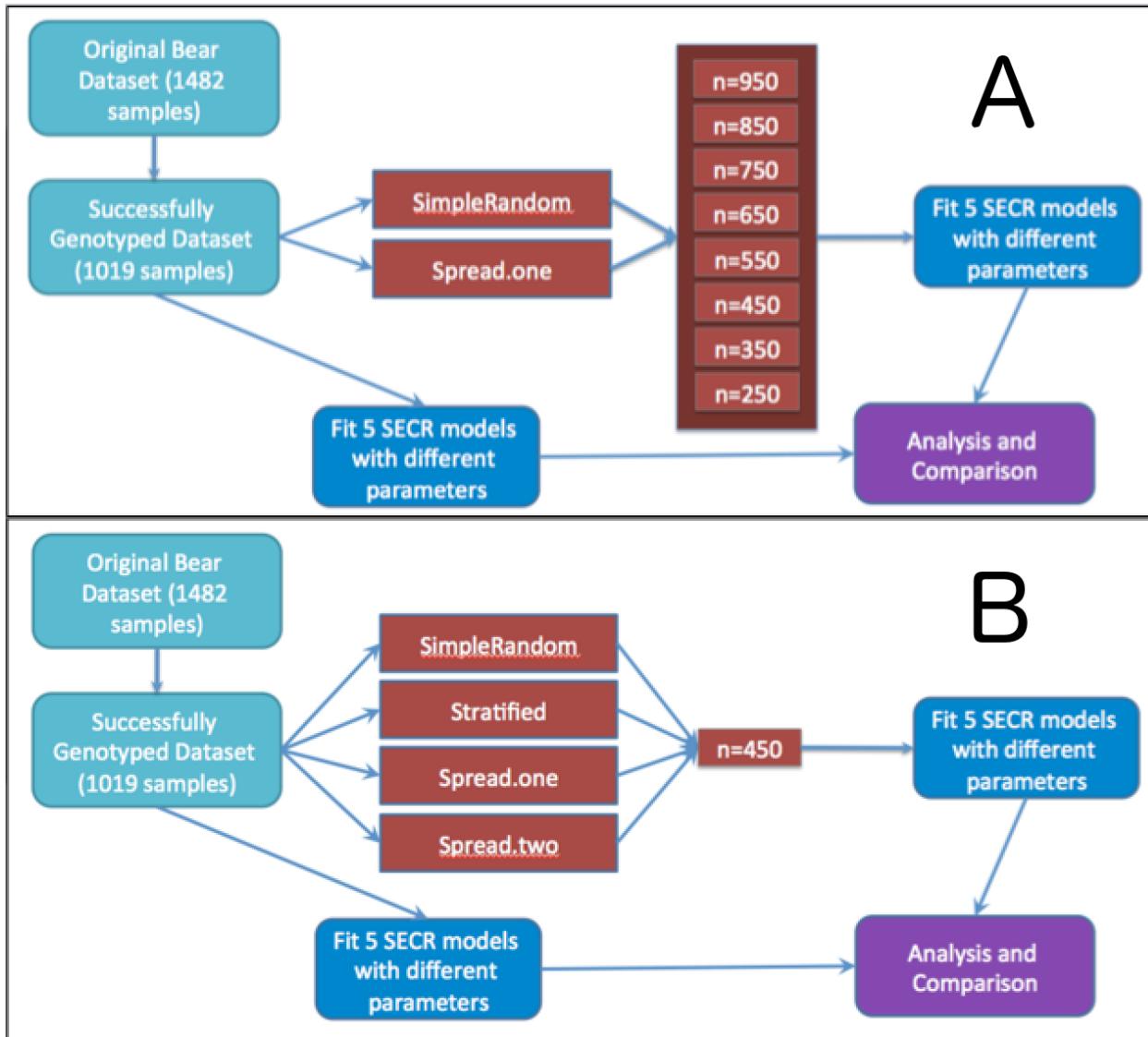


Figure 4: Visual representation of simulations performed in this study; We subsampled 1019 hair snare samples using a number of subsampling methods and size combinations for the purpose of comparing density estimates and associated biases.

$M_{b+t+Sex}$  refers to a model with behavior, time and sex as covariates for  $g0$ .

Let  $g0_{full}$  refer to the estimate of  $g0$  using the full dataset, and let  $g0_{sr}$  and  $g0_{so}$  refer to  $g0$  estimates obtained when subsampling using SimpleRandom and Spread.one, respectively.  $g0b$  represents the difference between initial and recapture probabilities. Again, we will use subscripts to refer to the dataset and model used to estimate this parameter.

## Full Dataset Estimates

$M_{b+t+Sex}$  had the lowest AIC score of the five models investigated (Table 1). Estimates that included behavior as a parameter for  $g0$  (ie,  $\hat{D}_{full,b+t+Sex}$ ,  $\hat{D}_{full,b+t}$ , and  $\hat{D}_{full,b}$ ) resulted in larger density estimates than models that excluded behavior ( $\hat{D}_{full,t+Sex}$ , and  $\hat{D}_{full,t}$ ), with  $\hat{D}_{full,b}$  resulting in the largest density estimate (14.23) and  $\hat{D}_{full,t}$  resulting in the smallest density estimate (12.55) (Table 1).

## Simulation Study I: Subsampling Strategy

All distributions of  $\hat{D}_{sr,i}$  shifted towards lower values compared to  $\hat{D}_{full,i}$ , regardless of the model analyzed. Further, in all cases, sampling distributions of  $\hat{D}_{sr}$  were more variable than sampling distributions of  $\hat{D}_{so}$  (Figure 5).

Sampling distributions of  $\hat{D}_{so,b+t+Sex}$ ,  $\hat{D}_{so,b+t}$ , and  $\hat{D}_{so,b}$  at n=450 were centered on the corresponding estimates of the full dataset ( $\hat{D}_{full,b+t+Sex}$ ,  $\hat{D}_{full,b+t}$ , and  $\hat{D}_{full,b}$ ; Figure 5), whereas the sampling distributions for  $\hat{D}_{full,t+Sex}$  and  $\hat{D}_{full,t}$  were shifted towards lower values (Figure 5, bottom row).

## Simulation Study II: Sample Size

As expected, similar to non-spatial mark-recapture estimates, smaller sample sizes produced more variable estimates, with greater discrepancies between  $(\hat{D}_{sr,i}, \hat{D}_{so,i})$  and  $\hat{D}_{full,i}$ . However, models  $M_{b+t+Sex}$ ,  $M_{b+t}$ , and  $M_b$  resulted in sampling distributions of  $\hat{D}_{so,i}$  that were centered at the corresponding estimate of  $\hat{D}_{full}$ , regardless of sample size (Figure 6, bottom row). Similar to the previously discussed trends, distributions of  $\hat{D}_{so}$  were closer to  $\hat{D}_{full}$  in most cases, though this effect was somewhat diminished when a behavioral effect was not modelled ( $M_{t+Sex}$  and  $M_t$ ).

In order to investigate the effect of subsampling on intial capture and recapture probabilities, we compared estimates of these parameters across different sample sizes using  $M_{b+t+Sex}$ . Similar to the effects of subsampling on non-spatial mark-recapture parameter estimators, estimates of both  $g0_{sr}$  and  $g0_{so}$  were were, on average, larger than  $g0_{full}$ . Further, estimates of both  $g0b_{sr}$  and  $g0b_{so}$  were, on average, larger in absolute magnitude relative to  $g0b_{full}$ . These effects were more pronounced as subsample size decreased, and were also more pronounced when using SimpleRandom subsampling than when using Spread.one (Figure 7).

## Discussion

### Subsampling Performance

Our simulation results suggest that SECR density estimators, like their non-spatial counterparts, are biased low when applied to subsampled data (Tredick *et al.* 2007;

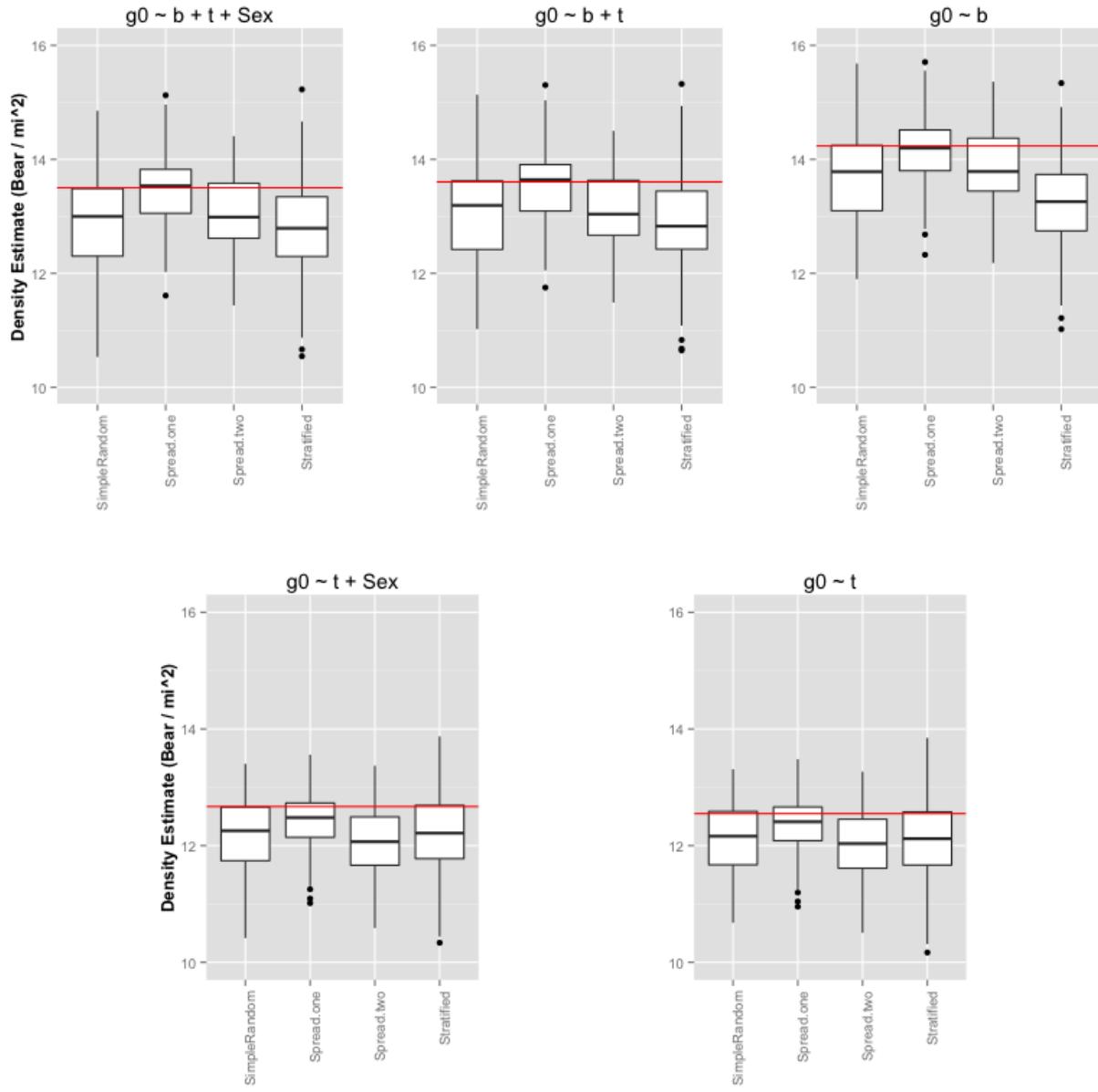


Figure 5: Derived density estimates of a spatially explicit capture-recapture model fitted to  $n=450$  subsamples of 1019 hair clusters using the four subsampling methods described in Figure 2. The red horizontal line represents the full dataset estimate ( $n=1019$ ) for each model.

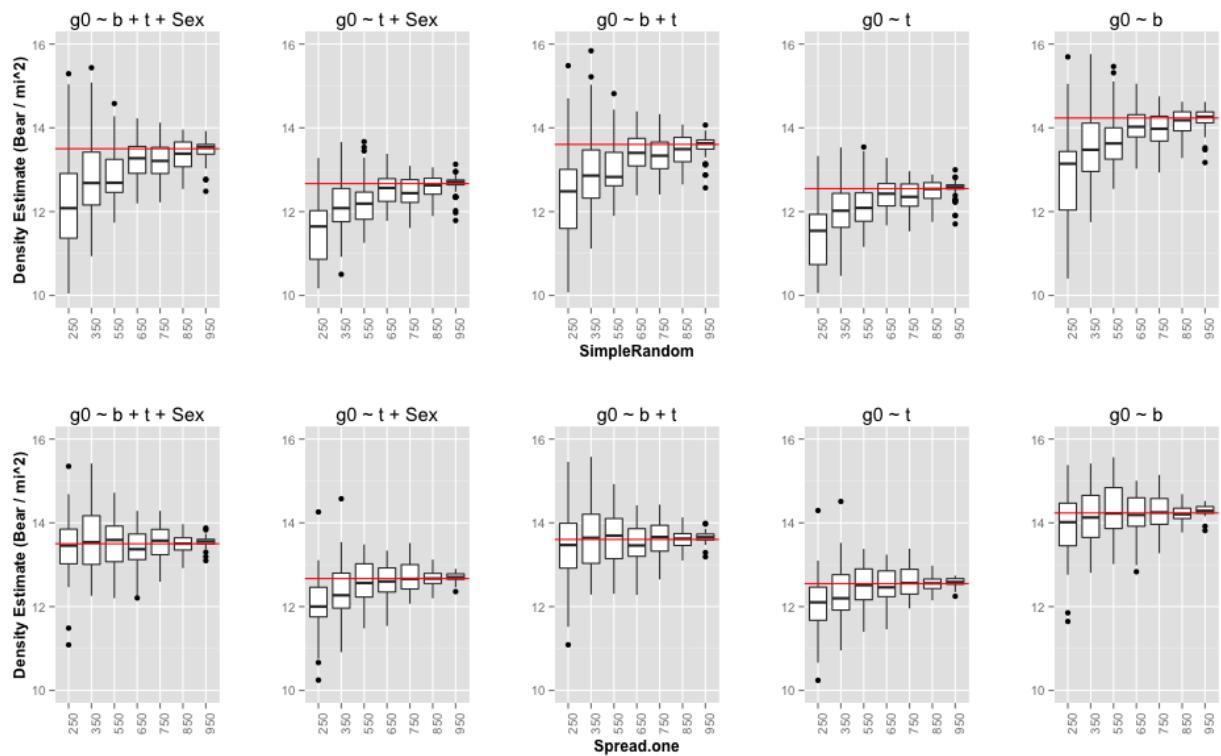


Figure 6: Derived density estimates of a SECR model fitted to various size subsamples (250 to 950 by 100) of 1019 hair clusters using one of two subsampling methods (SimpleRandom and Spread.one) described in Figure 2.

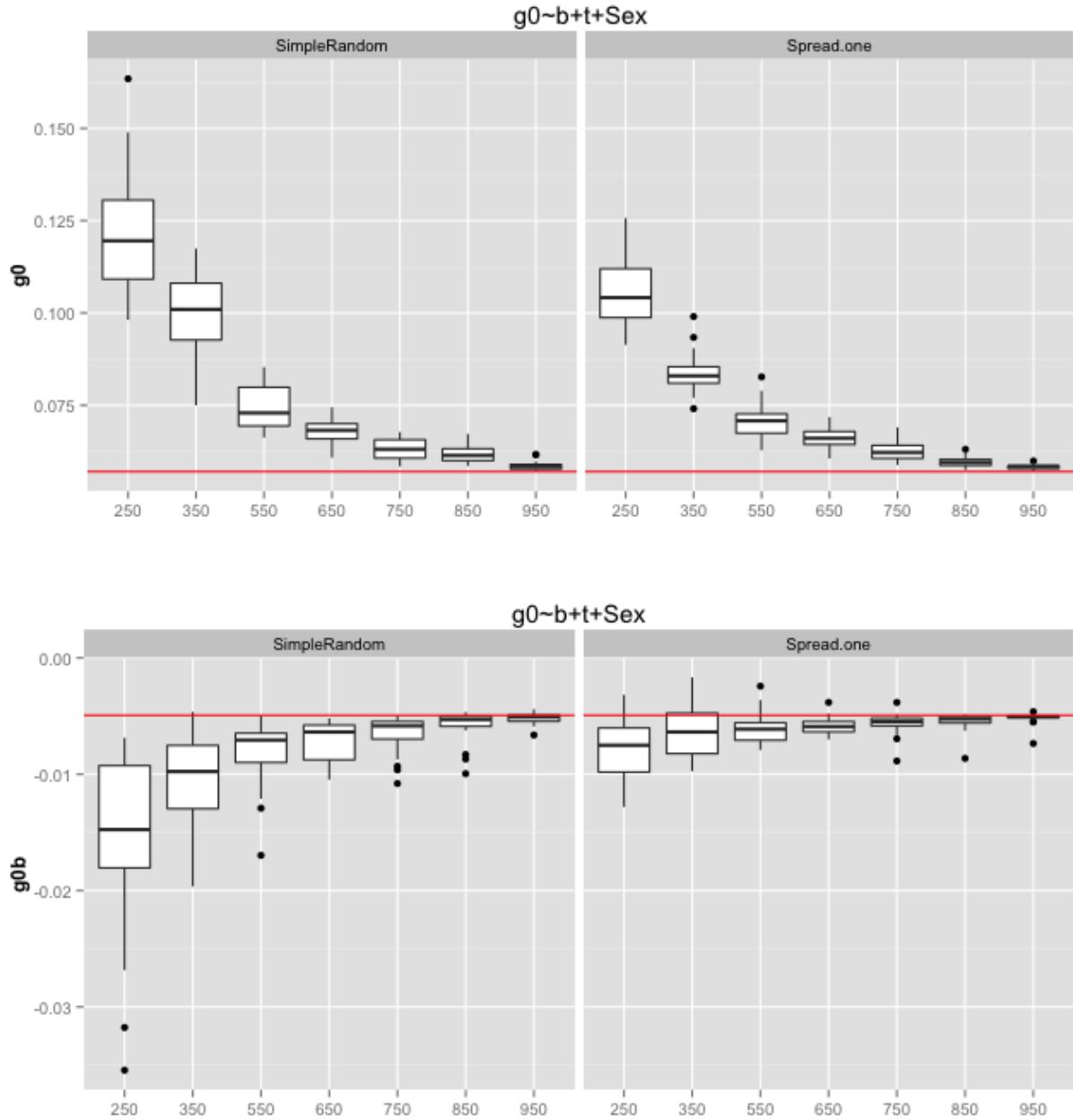


Figure 7: Estimated  $g0$  (initial capture probability) and  $g0b$  (difference between initial and recapture probability) for different sample sizes of two subsampling types, SimpleRandom and Spread.one (described in Figure 2). The horizontal red line indicates the value when fitting this model ( $g0 \sim b + t + Sex$ ) on the full dataset. The other four models displayed similar effects with respect to  $g0$ . The other two models which included a behavioral covariate for  $g0$  displayed similar trends with respect to  $g0b$ .

Augustine *et al.* 2014). However, using a subsampling method that gives preference to unique site-sessions (Spread.one) was more resistant to subsampling biases than a completely random subsampling method (SimpleRandom); Distributions of  $\hat{D}_{so}$  were closer to  $\hat{D}_{full}$  at most subsample sizes for each model (Figure 6), and similarly, estimates of  $g0_{so}$  and  $g0b_{so}$  were closer to their full dataset counterparts (Figure 7). Non-random sampling increased the number of uniquely identified individuals (especially those that left only one or two samples), which outweighed the inherent cost of violating SECR's assumption that the capture history provides an accurate description of individual movement characteristics.

Bears in this study exhibited considerable heterogeneity in their behavioral response (47% of the time, bears left only a single sample at a given site-session, but some left as many as 11; Garshelis & Noyce 2013). As a result, the random subsampling methods were much more likely to select redundant data from bears that tended to leave several samples at a single site-session. Conversely, non-random sampling likely performed well because much of the data it excluded from the full dataset was redundant (same bear, same site, same session), and thus had a higher percentage of novel samples.

Key assumptions in this study include the treatment of the full dataset as a representative sample from the population - Noyce and Garshelis (2013) successfully subsampled 67.7% of samples, so there is likely an unmodelled behavioral effect from the samples that were not originally analyzed when the study took place. Further, these analyzed hair samples were already non-random to a degree (377 non-random with preference to unique site-sessions and 776 completely random), so our analysis may be missing novel individuals or known individuals' locations that were similarly

not identified in the original genotypic analysis. However, it is also likely that many of these samples were redundant due to the strong individual heterogeneity noted in this study. Additionally, we analyzed only successful samples, and thus ignored the possibility of failure to identify individuals from a submitted sample; however, because our dataset was not simulated, there may have been false identification of individuals due to allelic dropout or false amplification (Dreher *et al.* 2009), or the ‘shadow effect’ - erroneously treating a novel individual as a recapture due to similarity in their genotype (Mills *et al.* 2000).

## Future Analysis

The work presented here identifies an issue that has not previously been given much attention; that subsampling may be more problematic for SECR models than non-spatial mark-recapture estimates. Our simulations suggest that using a strategy to maximize site-sessions within an analyzed subsample may ameliorate these problems, but the optimal strategy likely depends on the characteristics of the observed study population. Further simulation is needed before we can make more general conclusions and recommendations regarding the effect of subsampling methodology on SECR estimates; this could be accomplished by simulating genetic mark-recapture data with varying degrees of behavioral responses and various genotypic error rates (both positive bias inducing, in the case of shadow effects, or negative, in the case of allelic dropout and false amplification) to see when the trade-offs between the subsampling methods presented here begin to favor random sampling. Yet, the insights we have gained through our simulations allow us to make several predictions.

In a simulated case with no redundant samples (eg, each bear that enters a trap leaves exactly one sample and leaves, and  $g0b = 0$ ), one might expect random sampling to perform better (less biased, more precise) than a non-random sample, as the former would be more representative of the actual biological processes affecting movement patterns, and thus better model the heterogeneity in capture probability that arises from those patterns. As redundant samples are introduced (eg, each bear that enters a trap leaves more than one sample and leaves), one might expect that preference to unique site-sessions would once again perform best, as it did in our simulations using empirical data.

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# **Code Documentation**

This section is meant to document and explain various functions and scripts that were created in my (Nick Gondek) spring 2016 thesis project with John Fieberg and Dave Garshelis.

Generally, the process is broken down into three steps - subsampling (BearSubsample), data transformation (BearSumFunc), and model fitting/storage (BearParallelModelFit). Three functions perform these three steps, and one function aggregates them into a single overarching function (BearParallelSubSECR). Two scripts use this function in a loop to perform many iterations of this process, one varying the subsampling type, and one varying subsampling type while also varying subsample size (FloridaScript.R and MankatoScript.R, respectively).

In the document below, various chunks will represent different R scripts and functions, and will be annotated in order to explain how each contributes to the final product.

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## Subsampling Function

### I. BearSubsample.R

#### a. Summary

This function takes in a sample observation data frame (which is constructed both in DataExplorationUpdated.R and the eventual funtion BearParallelSubSECR.R) and subsamples it according to the four methods that were chosen, explained in greater detail below. The input is a large data frame of sample observations (~1000), and the output is a subsampled data frame of sample observations (Usually ~450, but this varies later on).

#### b. Arguments

*data* - A sample observation data frame to be subsampled. This is constructed both in DataExplorationUpdated.R and the eventual funtion BearParallelSubSECR.R.

*type* - The subsampling type to be used (“SimpleRandom”, “Stratified”, “Spread.one”, “Spread.two”).

- a) SimpleRandom - takes a random sample of size n from the entire data set, without any respect to sites or sessions. This is done by using mosaic's sample function, which works on data frames.
- b) Stratified - a stratified sample taking  $n/6$  random samples from each of the 6 periods. Note the difference between a **true stratified random sample** in that the samples are taken disproportionately from each period - instead of weighting each period based on their number of samples, a constant  $n/6$  are taken from each period. This is performed using a for loop which iterates over the 6 periods and using the same mosaic sample function as above.

- c) Spread.one - takes a single sample from each site x period combination. This is done using mutate, by creating a new variable called uniqueID which is a numeric of site x period. The data is then subsetted using a logical vector (!duplicated(uniqueID)) to take every unique combination, and then filled out with a random sample of the leftovers.
- d) Spread.two - takes two samples from each site x period combination. This is done using mutate, by creating a new variable called uniqueID which is a numeric of site x period. The data is then subsetted twice in a for loop using a logical vector (!duplicated(uniqueID)) to take every unique combination, and then filled out with a random sample of the leftovers.

*n* - The number of observations to be ‘genotyped’ - for the initial subsampling types, this was fixed at 450.

```
BearSubsample<-function(data, type, n){
  require(dplyr)
  if (type=="SimpleRandom"){ ##Simple random (all n taken at random with no regard to period or site)
    selected<-mosaic::sample(data, size=n)
  }

  if (type=="Stratified"){##For each of the six periods
    selected<-NULL
    for (i in (1:6)){
      new<-mosaic::sample(data[data$Period==i,], size = n/6)
      selected<-rbind(selected, new)
      selected<-filter(selected, !(is.na(Period)))
    }
  }

  if (type=="Spread.one"){##First take 1 from each site X period, then random
    selected<-NULL
    droprow<-NULL
    data<-mutate(data, uniqueID=(site*as.numeric(Period)))
    data<-sample(data)##Mix them up, then take the first one from each uniqueID

    selected<-data[!duplicated(data$uniqueID),]
    droprow<-(!duplicated(data$uniqueID)) * c(1:nrow(data))
    data<- data[-droprow,]

    selected<-rbind(selected, mosaic::sample(data, size=(n-nrow(selected))))
  }

  if (type=="Spread.two"){##First take 2 from each site X period, then random
    selected<-NULL
    droprow<-NULL
    data<-mutate(data, uniqueID=(site*as.numeric(Period)))
    data<-sample(data)##Mix them up, then take the first one from each uniqueID
  }
}
```

```

for (s in (1:2)){ ##Do it twice this time
  selected<-rbind(data[!duplicated(data$uniqueID),], selected)
  droprow<-(!duplicated(data$uniqueID)) * c(1:nrow(data))
  data<- data[-droprow,]
}

selected<-rbind(selected, mosaic::sample(data, size=(n-nrow(selected))))
}

return(selected)
}

```

## SECR Functions

### II. BearSumFunc.R

#### a. Summary

This function takes in a data frame of sample observations (subsampled or not, it does not matter) and transforms it into a SECR friendly proximity detector capture history file, to be used in the next step of fitting the SECR models and saving their resultant objects and outputs.

#### b. Arguments

*data* - a csv file of sample observations, which may be the full sample set or the subsampled sample set, saved as a temp file

*summary* - if TRUE, function outputs various metrics related to the input sample observations - these are largely from John's DataExplorationUpdated.R. This argument defaults to FALSE, to avoid cluttering the console when scripting.

*output.csv* - if NULL, function ouputs the proximity detector itself as a data frame. If a file path is set, function outputs a csv of this same data frame.

*type* - default is "proximity", and this is unchanged over the course of these initial iterations (Pre-April 2016). John's initial proposal had expressed interest in multi detectors ("multi"), so I incorporated this functionality for ease of future use. Any other type inputted results in an error.

```

BearSumFunc <- function(data, summary=FALSE, output.csv = NULL, type="proximity"){
  library(dplyr)
  library(mosaic)##Required Libraries
  sampobs<-read.csv(data) ##Reading in data

  #Gender: Sex = 204.25 -> Male, Sex= 250.25 ->Female
  sampobs$Group<-rep("M",nrow(sampobs))
  sampobs$Group[sampobs$Sex==250.25]<-"F"

  #Create a data set that contains a count of the number of times each bear
  #was seen for each unique site x period combination. Also determine

```

```

#sex of each individual and tabulate the number of males and females
caphist<- sampobs%>%group_by(Individual, site, Period)%>%
  summarize(Count= n())
sexid<-unique(select(sampobs, Individual, Group))
table(sexid$Group)
caphist2<-merge(caphist, sexid, all=FALSE)

##optional summary output
if(summary==TRUE){
  sum.out<-matrix(NA, 3, 4)
  rownames(sum.out)<- c("Same bear, site, period", "n detections per site & period", "Unique")
  colnames(sum.out)<- c("Max", "Mean", "sd", "n")

  capnums<-caphist%>%group_by(site, Period)%>% summarize(ncap=n() )
  timecap<-caphist%>%group_by(Period)%>% summarize(nbears=n_distinct(Individual) )
  sitecap<-caphist%>%group_by(site)%>% summarize(nbears=n_distinct(Individual) )

  sum.out[1,]<-as.double(favstats(caphist$Count)[5:8]) #same bear, site, period
  sum.out[2,]<-as.double(favstats(capnums$ncap)[5:8]) #n detections per site&period
  sum.out[3,]<-as.double(favstats(sitecap$nbears)[5:8]) #n detections per site&period

  outputsummary<-list(Captures.by.Period=timecap, Summary=sum.out)
  print(outputsummary)
}

#Write out proximity detector (if a path is set, write csv, otherwise just output the data f
bearCH<-data.frame(Session="BearMR", ID=caphist$Individual, Occassion=caphist2$Period, Detect
bearCHP<-data.frame(Session="BearMR", ID=sampobs$Individual, Occassion=sampobs$Period, Detect
# names(bearCH)<-c("Session", "ID", "Occasion", "Detector", "Count", "Sex") ##
if (!(is.null(output.csv))){
  if (type=="proximity"){
    write.table(bearCH, file=output.csv, row.names=FALSE, col.names=FALSE, sep=",")
  } else if (type=="multi"){
    write.table(bearCHP, file=output.csv, row.names=FALSE, col.names=FALSE, sep=",")
  } else print("Unrecognized detection type")
}

if (is.null(output.csv)){
  if (type=="proximity"){
    return(bearCH)
  } else if (type=="multi"){
    return(bearCHP)
  } else print("Unrecognized detection type")
}
}

```

### III. BearParallelModelFit.R

#### a. Summary

This function runs the computationally intensive process of secr model fitting independently on each available processor to cut down on the processing time dramatically. There are some minor nuances that are different from a typical for loop, and they are explained in comments below. Following the model fitting, the resultant output are saved in the form of a single csv, which is appended as needed with new entries, and RDS files of the models themselves are saved into their corresponding folder, as seen in the directory image below (or within the SpatialMR folder itself).

Also, there is a density conversion function tucked at the top of this script - I didn't feel it was substantial enough to warrant its own script.

#### b. Arguments

*trapgrid* - the trapgrid file that is to be used for the secr fitting. For the purposes of this initial analysis, we use the trapgrid from the field, but I integrated this to allow use of a simulated trapgrid.

*subtype* - the subtype used in the previous step of subsampling - note that no subsampling actually happens in this step, but it is needed to provide the correct path to save the model output.

*iteration* - the iteration of the loop, not for use interactively, but to save the model fit rds file with a new number.

*size* - another argument to save models in the correct folders - if size = 450, the output gets put into the SubsamplingData folder, else, it gets put into the SizeData folder.

```
desnconv<-function(x){  
  100*x/3861.022  
}  
  
library(secr)  
library(secrdesign)  
library(scrbook)  
  
BearParallelModelFit<-function(trapgrid="..../data/detectorfileScaled.csv", subtype=NULL, iteration=1, size=450){  
  output<-subtype  
  library(foreach)  
  #library(doMC)  
  library(doParallel)  
  #proxdata path and caphist  
  if(size==450){proxdata<-paste(..../data/SubsamplingData/, subtype, "/TempCapHist.csv", sep="")}  
  if(size!=450){proxdata<-paste(..../data/SizeData/, subtype, "/TempCapHist.csv", sep="")}  
  
  bearCH<-read.capthist(captfile = proxdata, trapgrid, detector= 'proximity', covnames="Sex",  
    sex="Sex", b="b", t="t", g0="g0", g1="g1", g2="g2", g3="g3", g4="g4", g5="g5",  
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```

```

#setup parallel backend to use all processors - note that this is not generally recommended for
#computers that are actually in use, but since this was run primarily on a server and/or broke
#laptop, I opted to use all cores, because I didn't need any cores to run other tasks.
cl<-makeCluster(detectCores()) #make a processing cluster of ALL available cores
registerDoParallel(cl) #tell foreach loop that we are using these cores

#start time
strt<-Sys.time()

#foreach loop, parallel (%do% operator runs systematically, %dopar% is parallel)
foreach(d=1:5) %dopar% {
  #import packages, need to be loaded on each processor independently
  library(foreach)
  library(doParallel)
  library(secr)
  library(secrdesign)
  library(scrbook)
  source('~/Google Drive/spatialMR/Rscripts/BearParallelModelFit.R')
  secrNew<-NULL
  modelEval<-models[[d]] #which model this core is actually going to process
  secrNew <- secr.fit(bearCH, model=modelEval, buffer = 10, trace = FALSE, CL=TRUE)

  if (!(is.null(secrNew)))
  { print(dN<-derived(secrNew))
    ##pathNew<-paste("../data/SubsamplingData/", output,"/", whichMod[d],"/",output, whichMod[d])
    ##This was the old method of saving values from secr. I am going to keep the paths for the o
    ##but save all of the data in a single csv file with three additional categorical var,
    ##the model letter, the subtype, and the subsample ID.

    if(size==450){ #if the size is exactly 450, must be a subsampling trial
      pathNew<-(("../data/SubsamplingData/FinalBearEst.csv")
      nrowSub<- nrow(read.csv("../data/SubsamplingData/SubsampleLabID.csv"))
    }

    if(size!=450){ #if the size is not exactly 450, must be a size trial
      pathNew<-(("../data/SizeData/FinalBearEst.csv")
      nrowSub<- nrow(read.csv("../data/SizeData/SubsampleLabID.csv"))
    }

    densNew<-desnconv(dN[2,c(1,3,4)]) #converting density

    if(size==450){
      write.table(c(nrowSub, densNew, subtype, whichMod[d]), file =pathNew, append = TRUE, col.na
      pathNew<-paste("../data/SubsamplingData/", output,"/", whichMod[d],"/secr", iteration, ".rds"
    }
  }
}

```

```

if(size!=450){
  write.table(c(nrowSub, densNew, subtype, whichMod[d], size), file =pathNew, append = TRUE,
  pathNew<-paste("../data/SizeData/", output,"/", whichMod[d],"./secr", iteration, ".rds", sep
  )}

  saveRDS(secrNew, file=pathNew)  }
}

#end time
print(Sys.time()-strt) #print how long the fitting took
print(Sys.time()) #print the current time (to check for stalling)
stopCluster(cl) #stop processing cluster
}

```

**c. File Structure** Files not referenced below are either remnants of previous iterations of this process, or are temporary files that are used in the model fitting process (these are named as such).

- Green - This is the final bear estimates csv using SECR, which contains bear estimates and associated confidence intervals, model letter (A-E), and the subsample ID. The rds files, further along in their respective Subtype folder and model letter folder, are the output lists of the secr model fitting. For each subtype for both SizeData and SubsamplingData, there are model letter folders where these rds files are kept.
- Red - These are conflict files created by google drive - to be honest, I am not sure what causes them, but they do not seem to affect the above FinalBearEst.csv in any way. To be safe, I have not deleted them.
- Yellow - This is the final bear estimates csv using Huggins p and c, which is in progress now (Mar 25, 2016).
- Purple - This is the csv containing the LabID numbers for each of the subsamples, so that they can be processed with huggins, and the resultant outputs can be directly compared using the same subsamples.

## IV. BearSubParallelSECR.R

### a. Summary

This function was created to complete the entire process of subsampling and model fitting in one line, so that it may be used in a script later on. As such, there isn't much else going on that is not covered by the above three functions. The first half of the function is from John's DataExplorationUpdated.R, cleaning up the samples data frame and filtering to only use successful samples.

### b. Arguments

*subtype* - the desired subsampling type - both passed onto BearSubsample, to use the correct subsampling type, as well as to BearParallelModelFit, in order to save the models in the correct directory.

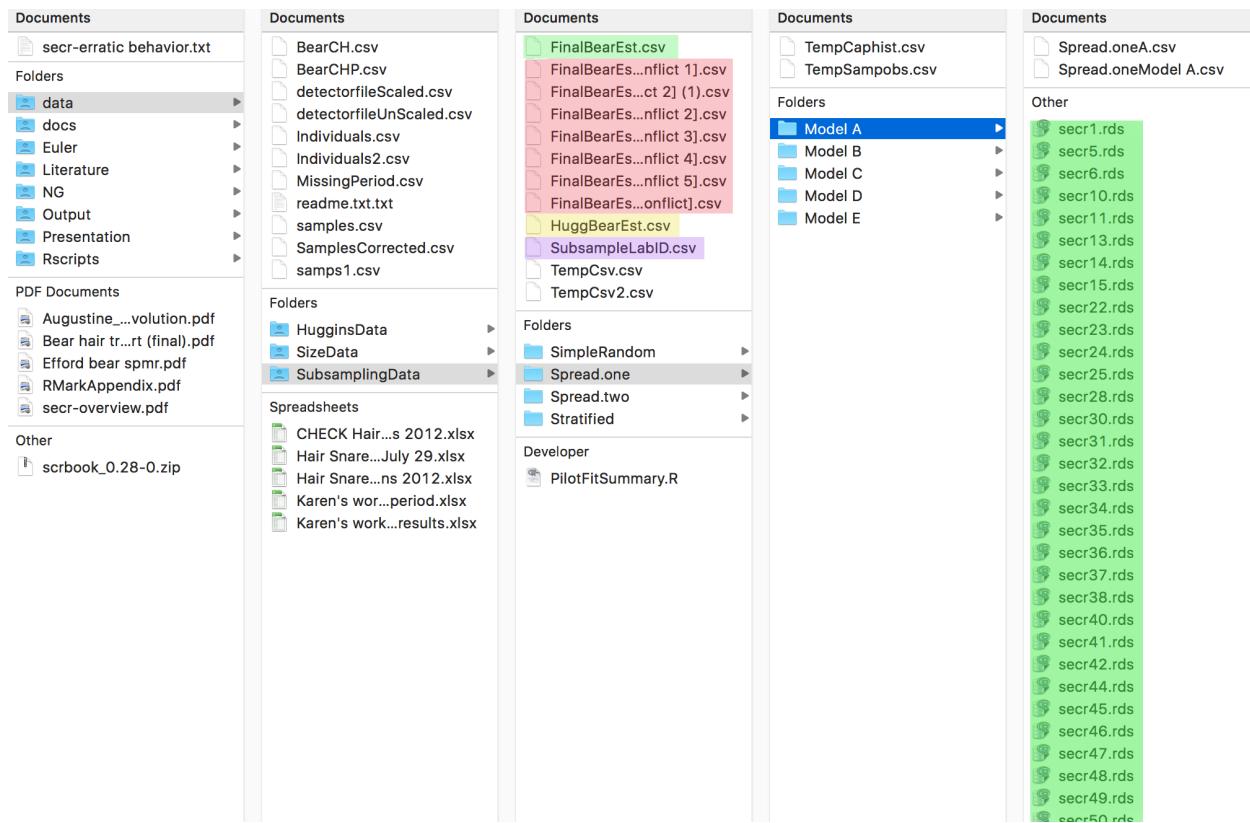


Figure 1: DirectoryFormat

*iterNo* - the iteration of the loop, not for use interactively, but to save the model fit rds file with a new number - this is passed onto BearParallelModelFit.

*size* - the desired number of samples obtained via subsampling. Also used to save models in the correct folders - if size = 450, the output gets put into the SubsamplingData folder, else, it gets put into the SizeData folder.

```
BearSubParallelSECR<- function(subtype, iterNo, size=450) {  
  source('~/Google Drive/spatialMR/Rscripts/BearParallelModelFit.R')  
  source('~/Google Drive/spatialMR/Rscripts/BearSubsample.R')  
  source('~/Google Drive/spatialMR/Rscripts/BearSumFunc.R')  
  
  #' Loading necessary libraries.  
  
  library(dplyr)  
  library(secr)  
  library(secrdesign)  
  library(scrbook)  
  library(mosaic)  
  
  #' Read in raw data on samples and individuals tab (saved as .csv files)  
  ind<-read.csv("../data/Individuals2.csv")  
  samps<-read.csv("../data/samplesCorrected.csv")  
  
  #' Note: on July 23, David sent a file with corrections made to a few observations that were  
  #' or had period="6?". This program uses the corrected "samples" tab from that spreadsheet.  
  #' main difference from the DataExploration.R file.  
  #'  
  
  #' Look at event IDs & Periods. Use strsplit to determine the site associated with each samp  
  
  events<-unlist(strsplit(as.character(samps$Event.ID), "-"))  
  samps$site<-as.numeric(sapply(strsplit(as.character(samps$Event.ID), "-"), `[, 1]))  
  suppressWarnings(samps$cid<-as.numeric(sapply(strsplit(as.character(samps$Event.ID), "-"),`  
  table(samps$site)  
  
  #' Focus only on observations that were sampled successfully.  
  sampobs<-filter(samps, Class=="sample")  
  
  #' Fix the 6? entries, turn this variable into a numeric variable  
  sampobs$Period[sampobs$Period=="6?"]<-"6"  
  
  #' For now, drop observations that are missing Period. Eventually, however, we will want to  
  #' observations that were highlighted earlier. The remaining 7 of these 9 observations corre  
  sampobs<-filter(sampobs, Period!="")  
  
  #' Subsampling of the sampobs data.  
  sampobs2 <- BearSubsample(sampobs, subtype, size)
```

```

#' NEW 1/14/16 - saving the subsample labID for later use in huggins models,
#' that way the same subsample can be reused.
if (size==450){
  write.table(matrix(sampobs2$Lab.ID, 1, size), file = "../data/SubsamplingData/SubsampleLabID.csv")
}
if (size!=450){
  write.table(matrix(sampobs2$Lab.ID, 1, size), file = "../data/SizeData/SubsampleLabID.csv")
}
#' Now, turn Period into a numeric variable
#sampobs2$Period<-droplevels(sampobs2$Period)
sampobs2$Period<-as.numeric(sampobs2$Period)
table(sampobs2$Period)

#' Drop several of the columns that we will not need.
sampobs3<-sampobs2[,c(1:9, 16,18,42:44)]

#' Setting csv pathways, Write this file out
if (size==450){
  pathcsv1<-paste("../data/SubsamplingData/", subtype, "/TempSampobs.csv", sep = "")
  pathcsv2<-paste("../data/SubsamplingData/", subtype, "/TempCaphist.csv", sep = "")
  write.csv(sampobs3, file=pathcsv1, row.names=FALSE)
}

if (size!=450){
  pathcsv1<-paste("../data/SizeData/", subtype, "/TempSampobs.csv", sep = "")
  pathcsv2<-paste("../data/SizeData/", subtype, "/TempCaphist.csv", sep = "")
  write.csv(sampobs3, file=pathcsv1, row.names=FALSE)
}

#' Apply the capture history transformation necessary for secr models
BearSumFunc(data=pathcsv1, summary = FALSE, output=pathcsv2)

#' Run the model fitting and storage function.
BearParallelModelFit(subtype = subtype, iteration=iterNo, size= size)
print(paste(subtype,iterNo, "done!"))
}

```

## Huggins Function

### V. BearHugginsParallel.R

This is still in progress - more later, when it is complete. Essentially, it will function similarly to BearParallelModelFit, using the huggins code from John's HuggyBear.R, and roughly analogous parameters to Models A-E in the SECR trials above.

## Looping Scripts

### VI. FloridaScript.R

A very straightforward script meant to run ‘subsampling trials’ - a for loop that performs a secr model fitting on each of the four subsampling types, and then repeats. The upper bound of the for loop is fairly arbitrary, as this was run almost continuously throughout the month of January 2016.

```
source('~/Google Drive/spatialMR/Rscripts/BearSubParallelSECR.R')
for (iter in 150:1000){ ## This lower bound is changed interactively based on the number of the
  BearSubParallelSECR("Stratified", iterNo=iter)
  BearSubParallelSECR("Spread.one", iterNo=iter)
  BearSubParallelSECR("Spread.two", iterNo=iter)
  BearSubParallelSECR("SimpleRandom", iterNo=iter)
}
```

### VII. MankatoScript.R

A script designed to run ‘size trials’ - for loop that executes two different subsampling types (chosen based on results of the previous script) with varying sizes. Try functionality added because at very low n, secr occasionally fails (not entirely sure why yet). Again, the upper bound of the outer loop is fairly arbitrary.

```
source('~/Google Drive/spatialMR/Rscripts/BearSubParallelSECR.R')
for (s in 130:1000) ## This lower bound is changed interactively based on the number of the last
{
  testSizes<-seq(400, 240, -10)
  for (x in 1:17){
    try({BearSubParallelSECR("Spread.one", iterNo=s, size = testSizes[x])})
    try({BearSubParallelSECR("SimpleRandom", iterNo=s, size = testSizes[x])})
  }
}
```

## Analysis Scripts

### VIII. EstimateSummary.R

These are the graphs and summaries that were used for my presentation on Feb 9 2016 at the Wildlife Society Conference in Mankato. The script reads in the final bear estimate (FinalBearEst.csv) from the SubsamplingData folder and compares them using box and whisker plots in gg, with a red line indicating what the ‘full model’ (all ~1000 samples) put out. Then, bar graphs representing the residual between this full model estimate and the avg estimate for each subtype. Lastly, anova to see whether the density estimates are significantly different from one another, holding model constant.

```
#'This script will read in the existing Bear Est data and compare them, using a bwplot.
#'(1/21/16)
library(mosaic)
```

```

BearEst<-read.csv("../data/SubsamplingData/FinalBearEst.csv")
colnames(BearEst)<-c("SubID", "densEstimate", "ucl", "lcl", "Subtype", "Model")

#'Number of Observations for each subtype X model. As of 1/21, there are ~16 for each.
#'As of 1/22, almost 25 for each. 100 should be attainable by around the 30th of Jan.
tally(Subtype~Model, data=BearEst)

#'Full model values from VerificationSECR.Rmd
fullModel<-c(14,15,14,13,14)
names(fullModel)<-c("Model A", "Model B", "Model C", "Model D", "Model E")

#'A box-whisker plot function to streamline the process for each model.
BearBWplot<-function(model="Model A"){
  ggplot(filter(BearEst, Model==model), aes(x=Subtype, y=densEstimate))+
    geom_boxplot() +
    ylab("Density Estimate (Bears per Sq Mile)")+
    ggtitle(model) +
    geom_hline(yintercept=fullModel[model], col="red")
  }

#'Treating all models the same, how does the subtype affect estimate
ggplot(BearEst, aes(x=Subtype, y=densEstimate))+
  geom_boxplot() +
  ylab("Density Estimate (Bears per Sq Mile)")+
  ggtitle("All Models")

#'Constructing a bwplot to see the difference between the different subtypes for each model
BearBWplot("Model A")
BearBWplot("Model B")
BearBWplot("Model C")
BearBWplot("Model D")
BearBWplot("Model E")

#'Look at the residuals between the full model and the means of the subtypes.
BearResid<-function(model="Model A"){
  resids<-mosaic::mean(densEstimate~Subtype, data=filter(BearEst, Model==model))-fullModel[model]
  barplot(resids, ylim=c(-1,1))
}

BearResid("Model A")
BearResid("Model B")
BearResid("Model C")
BearResid("Model D")
BearResid("Model E")

#'Another useful look at the data: ANOVA to see if the estimates are significantly
#'different from one another
bearmod<-lm(densEstimate~Subtype, data=BearEst)
Anova(bearmod)

```

```

#'Now by model - Interesting, they are only significantly different in A, C, E (as of
#'1/22/16) and those are the three that have behavior as a parameter for g0!
Anova(lm(densEstimate~Subtype, data=filter(BearEst, Model=="Model A")))
Anova(lm(densEstimate~Subtype, data=filter(BearEst, Model=="Model B")))
Anova(lm(densEstimate~Subtype, data=filter(BearEst, Model=="Model C")))
Anova(lm(densEstimate~Subtype, data=filter(BearEst, Model=="Model D")))
Anova(lm(densEstimate~Subtype, data=filter(BearEst, Model=="Model E")))

#'Spinning into md document
#'  spin("EstimateSummary.R")

```

## IX. SizeSummary.R

Size summary data that was also presented on Feb 9 2016 in Mankato. First, this script enumerates the number of models that have been completed for each size x subtype combination, then performs a summary on a lm between density estimate and size, for models D and E, for subtypes SimpleRandom and Spread.one. Lastly, the relationship between sd and sample size is examined in a graph.

```

sizesum<-read.csv("../data/SizeData/FinalBearEst.csv")
library(mosaic)
library(ggplot2)
colnames(sizesum)<-c("SubsampleID", "densEstimate", "lcl", "ucl", "Subtype", "Model", "Size")
tally(Subtype~Size + Model, data=sizesum)

#less significant slope for simple random
summary(lm(densEstimate~Size, data=filter(sizesum, Model=="Model D", Subtype=="SimpleRandom")))
xyplot(densEstimate~Size, data=filter(sizesum, Model=="Model D", Subtype=="SimpleRandom"), type="l")
mdD<-sd(densEstimate~Size, data=filter(sizesum, Model=="Model D", Subtype=="SimpleRandom"))
plot(mdD~names(mdD))

summary(lm(densEstimate~Size, data=filter(sizesum, Model=="Model E", Subtype=="SimpleRandom")))
xyplot(densEstimate~Size, data=filter(sizesum, Model=="Model E", Subtype=="SimpleRandom"), type="l")
mdE<-sd(densEstimate~Size, data=filter(sizesum, Model=="Model E", Subtype=="SimpleRandom"))
plot(mdE~names(mdE))

#more significant slope for spread.one
summary(lm(densEstimate~Size, data=filter(sizesum, Model=="Model D", Subtype=="Spread.one")))
xyplot(densEstimate~Size, data=filter(sizesum, Model=="Model D", Subtype=="Spread.one"), type="l")
mdD<-sd(densEstimate~Size, data=filter(sizesum, Model=="Model D", Subtype=="Spread.one"))
plot(mdD~names(mdD))

summary(lm(densEstimate~Size, data=filter(sizesum, Model=="Model E", Subtype=="Spread.one")))
xyplot(densEstimate~Size, data=filter(sizesum, Model=="Model E", Subtype=="Spread.one"), type="l")
mdE<-sd(densEstimate~Size, data=filter(sizesum, Model=="Model E", Subtype=="Spread.one"))
plot(mdE~names(mdE))

```

```

#Output for slide - four linear models showing the effect of size of the sample on the density
par(mfrow=c(2,2))

d1<-ggplot(data=filter(sizesum, Model=="Model D", Subtype=="Spread.one"), aes(x=Size, y=dens))
  geom_point() +
  geom_smooth(method=lm, se=TRUE, col="red", size=1) +
  ggtitle("Model D - Spread") +
  ylab("DensEstimate")+
  xlab("Size") +
  theme(plot.title = element_text(size=22))

d2<-ggplot(data=filter(sizesum, Model=="Model D", Subtype=="SimpleRandom"), aes(x=Size, y=dens))
  geom_point() +
  geom_smooth(method=lm, se=TRUE, col="red", size=1) +
  ggtitle("Model D - Simple Random") +
  ylab("DensEstimate")+
  xlab("Size") +
  theme(plot.title = element_text(size=22))

e1<-ggplot(data=filter(sizesum, Model=="Model E", Subtype=="Spread.one"), aes(x=Size, y=dens))
  geom_point() +
  geom_smooth(method=lm, se=TRUE, col="red", size=1) +
  ggtitle("Model E - Spread") +
  ylab("DensEstimate")+
  xlab("Size") +
  theme(plot.title = element_text(size=22))

e2<-ggplot(data=filter(sizesum, Model=="Model E", Subtype=="SimpleRandom"), aes(x=Size, y=dens))
  geom_point() +
  geom_smooth(method=lm, se=TRUE, col="red", size=1) +
  ggtitle("Model E - Simple Random") +
  ylab("DensEstimate")+
  xlab("Size") +
  theme(plot.title = element_text(size=22))

library(cowplot)
plot_grid(d1, d2, e1, e2, ncol = 2, nrow = 2)

```

## Appendix

### X. Example SECR Simulation

Here is an example of a single iteration of a SECR subsampling simulation. Note that this just the code from the inside of BearSubParallelSECR, with some minor tweaks to save time in the knitting of this document. Before each function, the input is shown, and after each function, the resultant output.

First, set some objects that would have been the arguments for BearSubParallelSECR.

```

subtype<-"SimpleRandom"
size<-450
iterNo<-999

#' This is where BearSubParallelSECR starts
source('~/Google Drive/spatialMR/Rscripts/BearParallelModelFit.R')

## Warning: package 'secr' was built under R version 3.2.3

source('~/Google Drive/spatialMR/Rscripts/BearSubsample.R')
source('~/Google Drive/spatialMR/Rscripts/BearSumFunc.R')

#' Loading necessary libraries.

library(dplyr)
library(secr)
library(secrdesign)
library(scrbook)
library(mosaic)

# Read in raw data on samples and individuals tab (saved as .csv files)
ind<-read.csv("../data/Individuals2.csv")
samps<-read.csv("../data/samplesCorrected.csv")

# Note: on July 23, David sent a file with corrections made to a few observations that were
# or had period="6?". This program uses the corrected "samples" tab from that spreadsheet.
# main difference from the DataExploration.R file.
#

head(ind) ## data frame organized by individuals genotyped

##   Individual Sex no_Samples Loci    CXX20      G1D      G10M     MSUT2      MU50
## 1           56   F        65    24 123.137 176.186 214.218 205.207 134.136
## 2          1435   F        1    24 123.123 172.186 208.214 205.209 132.136
## 3          2213   F       117    24 135.139 174.184 206.216 197.205 120.132
## 4          3002   F        26    24 135.145 174.186 206.206 197.205 120.140
## 5          3101   M        1    24 123.123 172.182 208.214 197.205 120.132
## 6          3103   F        1    24 123.123 172.180 208.214 197.209 120.132
##   G10X     G10P REN144.A06      G1A      G10C      D1A      G10J      G10L
## 1 133.147 163.163    129.129 194.194 209.215 157.179 207.211 137.159
## 2 147.149 163.163    125.129 194.196 215.215 167.179 187.211 137.141
## 3 141.145 153.157    121.121 198.198 205.213 157.163 187.203 137.137
## 4 141.151 153.155    119.121 196.198 205.213 163.165 203.205 137.149
## 5 141.147 151.163    119.129 194.194 215.215 175.179 187.191 137.153

```

```

## 6 141.149 157.163    119.125 194.198 213.215 167.179 187.187 141.153
##      CPH9  CXX110     D123     MU26     G10U     MU59 REN145.P07     G10B
## 1 143.149 155.159 141.145 183.185 179.181 233.237    157.157 156.158
## 2 143.149 155.159 143.145 185.199 175.179 233.243    157.167 156.158
## 3 143.149 137.159 145.155 185.195 179.181 231.241    157.159 156.160
## 4 143.149 137.153 155.155 185.185 177.181 231.237    157.157 158.160
## 5 149.151 157.159 141.145 185.185 175.179 233.239    159.167 156.164
## 6 143.149 157.159 141.145 185.185 173.179 239.243    159.167 156.156
##      MU23     G10H Sex.1
## 1 203.207 239.241      F
## 2 187.203 241.253      F
## 3 189.203 241.253      F
## 4 189.199 241.253      F
## 5 187.205 241.241      M
## 6 203.203 241.253      F

```

```
head(samps) ## data frame organized by samples
```

```

##      Sample Lab.ID Class Individual Bundle.No. Period Event.ID Priority
## 1 120-1-1    885 sample        0056      130      1 120-01       4
## 2 380-120-03   732 sample        0056      380      1 120-03       3
## 3 120-1-6   1004 sample        0056      254      1 120-06       4
## 4 380-120-07   731 sample        0056      380      1 120-07       2
## 5 20-120-09     20 sample        0056      20       1 120-09       2
## 6 20-120-10     87 sample        0056      20       1 120-10       3
##      Selected Bear.No. X X.G X.U Left U.L      Comments X.1 Loci      CXX20
## 1           1 NA NA     30     A L 1st envelope NA     7 123.137
## 2           1 NA NA     10     A L                   NA     7 123.137
## 3           2 NA NA     10     A L 1st envelope NA     7 123.137
## 4           1 NA NA     10     A L                   NA     7 123.137
## 5           3 NA NA     30     A L 1st envelope NA    15 123.137
## 6           1 NA NA     10     A U                   NA    12 123.137
##      G1D     G10M MSUT2     MU50     G10X      G10P REN144.A06      G1A G10C
## 1 176.186 214.218 205.207 134.136 133.147                   NA      NA      NA
## 2 176.186 214.218 205.207 134.136 133.147                   NA      NA      NA
## 3 176.186 214.218 205.207 134.136 133.147                   NA      NA      NA
## 4 176.186 214.218 205.207 134.136 133.147                   NA      NA      NA
## 5 176.186 214.218 205.207 134.136 133.147      129.129 194.194      NA
## 6 176.186 214.218 205.207 134.136 133.147      163.163      NA      NA      NA
##      D1A     G10J G10L CPH9 CXX110     D123     MU26     G10U     MU59 REN145.P07
## 1     NA                   NA     NA     NA     NA     NA                   NA
## 2     NA                   NA     NA     NA     NA     NA                   NA
## 3     NA                   NA     NA     NA     NA     NA                   NA
## 4     NA                   NA     NA     NA     NA     NA                   NA
## 5 157.179 207.211 137.159     NA     NA 141.145     NA     NA                   NA
## 6     NA 207.211 137.159     NA     NA     NA     NA 233.237      NA
##      G10B     MU23     G10H     Sex

```

```

## 1 NA NA 250.25
## 2 NA NA 250.25
## 3 NA NA 250.25
## 4 NA NA 250.25
## 5 NA 203.207 239.241 250.25
## 6 NA NA 239.241 250.25

```

Take samples and add site id, filter for just successful samples, do a little cleanup.

```

#' Look at event IDs & Periods. Use strsplit to determine the site associated with each sample.
events<-unlist(strsplit(as.character(samps$Event.ID), "-"))
samps$site<-as.numeric(sapply(strsplit(as.character(samps$Event.ID), "-"), `[, 1]))
suppressWarnings(samps$cid<-as.numeric(sapply(strsplit(as.character(samps$Event.ID), "-"), `[, 1)))
table(samps$site)

```

```

##
##   1   2   3   4   5   7   8   9   10  11  12  13  14  15  16  17  18  19
## 11  18   2  14  15   2  10   1  27  21   1   1  28  29  28   8  18   1
## 20  21  22  23  24  25  26  27  28  29  32  33  34  35  36  38  39  40
##  7  20  29  13   9   7  33  25  17  13   4  25  34  18  26   6   8   1
## 41  42  45  46  48  49  50  51  52  53  54  55  56  57  59  60  61  62
## 12  16  18  35   9   6  23   4   8   8   1  21  22   7  10  30   4  29
## 63  64  66  67  69  70  71  72  73  74  75  77  78  80  81  82  83  84
##  1  11  12  20  17   1  26  20  12   9  26  11   7   1   4   2  21   6
## 85  86  87  88  89  90  91  92  93  94  95  96  98  99 100 101 102 103
## 11  20  17  12  20  20  16  17  10   7   5  21  14  15  24  10   7  18
## 104 105 106 107 108 109 113 114 115 116 117 118 119 120 121
## 10  12  22   4  12   9   9  23   5   1   6   2   8  38   18

```

```

#' Focus only on observations that were sampled successfully.
sampobs<-filter(samps, Class=="sample")

#' Fix the 6? entries, turn this variable into a numeric variable
sampobs$Period[sampobs$Period=="6?"]<-"6"

#' For now, drop observations that are missing Period. Eventually, however, we will want to
sampobs<-filter(sampobs, Period!="")
head(sampobs)

```

	Sample	Lab.ID	Class	Individual	Bundle.No.	Period	Event.ID	Priority
## 1	120-1-1	885	sample	0056	130	1	120-01	4
## 2	380-120-03	732	sample	0056	380	1	120-03	3
## 3	120-1-6	1004	sample	0056	254	1	120-06	4
## 4	380-120-07	731	sample	0056	380	1	120-07	2
## 5	20-120-09	20	sample	0056	20	1	120-09	2
## 6	20-120-10	87	sample	0056	20	1	120-10	3

```

##   Selected Bear.No. X X.G X.U Left U.L      Comments X.1 Loci    CXX20
## 1       1     NA NA     30     A     L 1st envelope  NA    7 123.137
## 2       1     NA NA    10     NA     A     L             NA    7 123.137
## 3       2     NA NA    10     NA     A     L 1st envelope  NA    7 123.137
## 4       1     NA NA    10     NA     A     L             NA    7 123.137
## 5       3     NA NA     30     A     L 1st envelope  NA   15 123.137
## 6       1     NA NA    10     NA     A     U             NA   12 123.137
##       G1D     G10M    MSUT2    MU50     G10X     G10P REN144.A06     G1A   G10C
## 1 176.186 214.218 205.207 134.136 133.147                 NA     NA   NA
## 2 176.186 214.218 205.207 134.136 133.147                 NA     NA   NA
## 3 176.186 214.218 205.207 134.136 133.147                 NA     NA   NA
## 4 176.186 214.218 205.207 134.136 133.147                 NA     NA   NA
## 5 176.186 214.218 205.207 134.136 133.147           129.129 194.194  NA
## 6 176.186 214.218 205.207 134.136 133.147 163.163     NA     NA   NA
##       D1A     G10J    G10L   CPH9 CXX110     D123   MU26   G10U     MU59 REN145.P07
## 1     NA                   NA     NA     NA     NA     NA             NA
## 2     NA                   NA     NA     NA     NA     NA             NA
## 3     NA                   NA     NA     NA     NA     NA             NA
## 4     NA                   NA     NA     NA     NA     NA             NA
## 5 157.179 207.211 137.159     NA     NA 141.145     NA     NA             NA
## 6     NA 207.211 137.159     NA     NA     NA     NA     NA 233.237             NA
##       G10B    MU23     G10H     Sex site cid
## 1     NA     NA     NA 250.25   120     1
## 2     NA     NA     NA 250.25   120     3
## 3     NA     NA     NA 250.25   120     6
## 4     NA     NA     NA 250.25   120     7
## 5     NA 203.207 239.241 250.25   120     9
## 6     NA     NA 239.241 250.25   120    10

```

Take in sampobs (1019 samples), output a subsample with the chosen subtype, and the size specified.

```

#' Subsampling of the sampobs data.
sampobs2 <- BearSubsample(sampobs, subtype, size)
nrow(sampobs2) == size;size

## [1] TRUE

## [1] 450

head(sampobs2)

```

```

##          Sample Lab.ID Class Individual Bundle.No. Period Event.ID
## 903 219-92-02    436 sample   67-114-04     219     4   92-02
## 154 328-14-02    634 sample      2213     328     6   14-02
## 855 64-8-01       64 sample   56-28-01      64     2   8-01
## 533 206-115-03   414 sample  171-105-09     206     3 115-03

```

```

## 8      120-1-12    965 sample        0056      214      1 120-12
## 284  387-83-05    744 sample  12-106-02      387      2 83-05
##   Priority Selected Bear.No. X X.G X.U Left U.L     Comments X.1 Loci
## 903      1         1     NA NA  10  NA    A   L           NA   7
## 154      1         1     NA NA  10  NA    B   L           NA   7
## 855      1         1     NA NA  10  NA    A   L 1st envelope NA  12
## 533      1         1     NA NA       30  C   L           NA   7
## 8        4         1     NA NA  10  NA    A   L 1st envelope NA   7
## 284      1         1     NA NA       30  A   U 1st envelope NA   7
##          CXX20      G1D      G10M    MSUT2      MU50      G10X      G10P REN144.A06 G1A
## 903 137.139 176.182 210.214 195.197 120.120 129.153           NA  NA
## 154 135.139 174.184 206.216 197.205 120.132 141.145           NA  NA
## 855 143.143 172.186 210.218 199.205 132.140 141.147 153.155           NA  NA
## 533 139.139 178.182 206.214 195.207 120.122 141.153           NA  NA
## 8    123.137 176.186 214.218 205.207 134.136 133.147           NA  NA
## 284 135.139 184.184 206.212 181.201 120.130 153.153           NA  NA
##          G10C D1A      G10J      G10L CPH9 CXX110 D123 MU26 G10U      MU59 REN145.P07
## 903  NA  NA           NA  NA  NA  NA  NA  NA           NA
## 154  NA  NA           NA  NA  NA  NA  NA  NA           NA
## 855  NA  NA 189.205 135.137  NA  NA  NA  NA  NA 245.245           NA
## 533  NA  NA           NA  NA  NA  NA  NA  NA           NA
## 8    NA  NA           NA  NA  NA  NA  NA  NA           NA
## 284  NA  NA           NA  NA  NA  NA  NA  NA           NA
##          G10B MU23      G10H      Sex site cid orig.ids
## 903  NA  NA     NA 204.25   92   2    903
## 154  NA  NA     NA 250.25   14   2    154
## 855  NA  NA 241.251 204.25    8   1    855
## 533  NA  NA     NA 204.25  115   3    533
## 8    NA  NA     NA 250.25  120  12     8
## 284  NA  NA     NA 204.25   83   5    284

```

Normally, we would save the subsample Lab.ID's in the correct folder, but we'll skip this step because we won't actually be running the SECR model fitting in this example. Set file pathways to contain the temporary files needed to fit the secr model (sample data, tempSampobs.csv, and prox data, erroneously named tempCapHist.csv)

```

#' NEW 1/14/16 - saving the subsample labID for later use in huggins models,
#' that way the same subsample can be reused.
# if (size==450){
#   write.table(matrix(sampobs2$Lab.ID, 1, size), file = "../data/SubsamplingData/SubsampleLabID.csv")
# }
# if (size!=450){
#   write.table(matrix(sampobs2$Lab.ID, 1, size), file = "../data/SizeData/SubsampleLabID.csv")
# }
#' Now, turn Period into a numeric variable
#sampobs2$Period<-droplevels(sampobs2$Period)
sampobs2$Period<-as.numeric(sampobs2$Period)
table(sampobs2$Period)

```

```

##      1   2   3   4   5   6
##  34  96  76 102  86  56

#' Drop several of the columns that we will not need.
sampobs3<-sampobs2[,c(1:9, 16,18,42:44)]

#' Setting csv pathways, Write this file out
if (size==450){
  pathcsv1<-paste("../data/SubsamplingData/", subtype, "/TempSampobs.csv", sep = "")
  pathcsv2<-paste("../data/SubsamplingData/", subtype, "/TempCaphist.csv", sep = "")
  write.csv(sampobs3, file=pathcsv1, row.names=FALSE)
}

if (size!=450){
  pathcsv1<-paste("../data/SizeData/", subtype, "/TempSampobs.csv", sep = "")
  pathcsv2<-paste("../data/SizeData/", subtype, "/TempCaphist.csv", sep = "")
  write.csv(sampobs3, file=pathcsv1, row.names=FALSE)
}

```

Takes in the sample observations (same as above) and output a prox data frame for BearParallelModelFit.

```

#' Apply the capture history transformation necessary for secr models
BearSumFunc(data=pathcsv1, summary = FALSE, output=pathcsv2)
head(read.csv(pathcsv2))

```

```

##      BearMR X0056 X4 X81 F
## 1 BearMR  0056  3  92 F
## 2 BearMR  0056  4  93 F
## 3 BearMR  0056  2  96 F
## 4 BearMR  0056  6 102 F
## 5 BearMR  0056  4 103 F
## 6 BearMR  0056  5 103 F

```

Finally, actually run the model using the prox data output from above and the trapgrid that is used for every simulation. These are saved, as seen above, in FinalBearEst.csv and in Model folders as objects. Note that I am not actually running the model here, just for ease of knitting this document. Here is an examples of the csv line saved using model output.

```

#' Run the model fitting and storage function.
#BearParallelModelFit(subtype = subtype, iteration=iterNo, size= size)
test<-read.csv("../data/SubsamplingData/FinalBearEst.csv") [30,]
colnames(test)<-c("SubsampleID", "densEstimate","lcl", "ucl", "subtype", "Model")
test

```

```

##      SubsampleID densEstimate      lcl      ucl    subtype Model
## 30              6     12.27586 8.945905 16.84534 Spread.two Model D

```

And here is an example of the actual model object that is saved after each model fitting.

```
readRDS("../data/SubsamplingData/SimpleRandom/Model A/secr104.rds")
```

```

##
## secr.fit(capthist = bearCH, model = modelEval, buffer = 10, CL = TRUE,
##           trace = FALSE)
## secr 2.10.2, 20:05:38 28 Jan 2016
##
## Detector type      proximity
## Detector number    121
## Average spacing    1.078547 m
## x-range            -10.24721 8.170471 m
## y-range            -10.32148 9.661065 m
##
## N animals          : 38
## N detections       : 310
## N occasions        : 6
## Mask area          : 0.1224767 ha
##
## Model              : g0~b + t + Sex sigma~Sex
## Fixed (real)       : none
## Detection fn       : halfnormal
## N parameters       : 10
## Log likelihood     : -1203.684
## AIC                : 2427.368
## AICc               : 2435.516
##
## Beta parameters (coefficients)
##             beta   SE.beta      lcl      ucl
## g0      -2.5405523 0.29033486 -3.10959814 -1.97150639
## g0.bTRUE 0.2040771 0.27502061 -0.33495343 0.74310756
## g0.t2   1.1651293 0.32054537  0.53687195 1.79338669
## g0.t3   0.9836750 0.36035138  0.27739923 1.68995068
## g0.t4   1.3624337 0.37795625  0.62165301 2.10321429
## g0.t5   1.0988556 0.38774081  0.33889758 1.85881364
## g0.t6   0.6827297 0.39761983 -0.09659084 1.46205026
## g0.SexM -0.5222601 0.21702365 -0.94761867 -0.09690161
## sigma    0.9518281 0.06070928  0.83284006 1.07081607
## sigma.SexM 0.5751746 0.08457258  0.40941543 0.74093384
##
## Variance-covariance matrix of beta parameters
##             g0      g0.bTRUE      g0.t2      g0.t3
## g0 0.084294332 -0.0103724219 -5.048276e-02 -0.0481124288

```

```

## g0.bTRUE -0.010372422 0.0756363363 -4.175924e-02 -0.0603111481
## g0.t2 -0.050482756 -0.0417592404 1.027493e-01 0.0907332061
## g0.t3 -0.048112429 -0.0603111481 9.073321e-02 0.1298531158
## g0.t4 -0.046003546 -0.0707336318 9.651985e-02 0.1138666332
## g0.t5 -0.045428109 -0.0730439446 9.779063e-02 0.1157049606
## g0.t6 -0.047190793 -0.0739744850 9.822330e-02 0.1163708096
## g0.SexM -0.032021469 0.0071982794 -5.053287e-03 -0.0066402786
## sigma -0.006201258 -0.0013457914 3.993988e-04 0.0007653391
## sigma.SexM 0.006447876 0.0005965166 -9.270164e-05 -0.0003509171
##           g0.t4      g0.t5      g0.t6      g0.SexM
## g0 -0.0460035460 -0.0454281092 -0.0471907933 -0.032021469
## g0.bTRUE -0.0707336318 -0.0730439446 -0.0739744850 0.007198279
## g0.t2 0.0965198532 0.0977906285 0.0982232973 -0.005053287
## g0.t3 0.1138666332 0.1157049606 0.1163708096 -0.006640279
## g0.t4 0.1428509278 0.1258375599 0.1265791445 -0.008250145
## g0.t5 0.1258375599 0.1503429390 0.1288268960 -0.009013009
## g0.t6 0.1265791445 0.1288268960 0.1581015317 -0.006778850
## g0.SexM -0.0082501450 -0.0090130094 -0.0067788502 0.047099263
## sigma 0.0008238526 0.0008053862 0.0013321246 0.006566707
## sigma.SexM -0.0003615833 -0.0002382688 -0.0007088851 -0.009316653
##           sigma      sigma.SexM
## g0 -0.0062012583 6.447876e-03
## g0.bTRUE -0.0013457914 5.965166e-04
## g0.t2 0.0003993988 -9.270164e-05
## g0.t3 0.0007653391 -3.509171e-04
## g0.t4 0.0008238526 -3.615833e-04
## g0.t5 0.0008053862 -2.382688e-04
## g0.t6 0.0013321246 -7.088851e-04
## g0.SexM 0.0065667075 -9.316653e-03
## sigma 0.0036856166 -3.670457e-03
## sigma.SexM -0.0036704574 7.152521e-03
##
## Fitted (real) parameters evaluated at base levels of covariates
##   link estimate SE.estimate      lcl      ucl
## g0    logit 0.07306376 0.01966306 0.04271307 0.1222272
## sigma  log 2.59044083 0.15740881 2.29984117 2.9177596

print(paste(subtype,iterNo, "done!"))

## [1] "SimpleRandom 999 done!"

```

## XI. Other Scripts and Functions

- a) BearModelFit.R and BearSubSECR.R

These are outdated versions of BearParallelModelFit.R and BearSubParallelSECR.R. As the names

suggest, the newer versions of these functions employ parallel processing as a means to cut down on processing time.

b) `Synthesisv2.R`, `Synthesisv3.R`, and `PilotFitSummary.Rmd`

These are the first attempts of running all three of the functions one after the other, and can be thought of as precursors to `BearSubParallelSECR.R`. As such, they are also outdated.

c) `VerificationSECR.rmd` and `VerificationSECR_corrected.Rmd`

Originally meant to verify the model results that John produced for his progress report, this rmd file creates the ‘full model’ estimates using all 1019 samples for the 5 models I chose to analyze. The folder of the same name houses the csv with these estimates, as well as the RDS files of the model output for later use.

d) `Data Exploration.R` and `Data ExplorationUpdated.R`

These were written by John, and they analyze the original sample data. Much of this was incorporated into the very beginning of `BearSubParallelSECR.R` in order to make sure there were no discrepancies between how John and I aggregated the samples.

e) `Data Summary.R`

This script is as it sounds, is a summary of the bear data, mostly verified what Dave reported in the original bear study. Much of it is looking at the differences in individuals propensity to revisit traps and other individual heterogeneity.

f) `huggins.R` and `HuggyBear.R`

Huggins analysis of the bear data for the purpose of comparing estimates between closed pop models and secr. Much of `HuggyBear.R` was incorporated into `BearHugginsParallel`, with the only major difference being that the latter is a function that saves its model output and takes in subsamples.

g) `SecrAll1.R` and `SecrAll2.R`

These scripts run various SECR models for the purpose of inclusion in the progress report sent to Dave.