ESTIMATING WHITE-TAILED DEER ABUNDANCE USING NON-INVASIVE DNA COLLECTION AND SPATIALLY EXPLICIT CAPTURE RECAPTURE MODELS

Jerry Nelson[a], Shannon M. Knapp[a], Thomas E. Owens[a], Woodrow L. Myers[a], Jerry Cline[b], Charles Henderson[c]

A fundamental requirement for managing hunted big game populations is to estimate the population size either before or after the harvest period. Densities expressed for representative habitat types or indices that are validated for population size are often used as surrogates for point estimates of populations. Lacking those metrics, harvest coupled with harvest effort is often used to track trends in big game populations.

We attempted to estimate white-tailed deer abundance by collecting scat and identifying individual animals using DNA from those samples and then employed spatially explicit capture-recapture (SECR) models to estimate deer population size and density for the study site.

STUDY AREA

We collected white-tailed deer scat on the Little Pend Oreille National Wildlife Refuge (LPO; 48° N, 117° W) in Stevens County Washington. The LPO is 168.2 km^2. Our sampling area was initially established as a 36 km^2 square located in the central-east portion of the refuge (Fig. 1).

The LPO lies within the Okanogan Highlands Physiographic Province of northeast Washington (Franklin and Dyrness 1973). The Okanogan Highlands Province extends from the Okanogan River east to the Idaho border. Soils on the LPO are mostly sandy loams deposited by glacial activity (USFWS 2000).

The dominant land cover is coniferous forest. The next largest land cover types are shrub and brush land and to a lesser extent grassland. Common plant associations of dry forests found at lower elevations within the study area include ponderosa pine (*Pinus ponderosa*)-Idaho fescue (*Festuca idahoensis*), ponderosa pine-snowberry (*Symphoricarpus albus*), and Douglas-fir (*Pseudotsuga menziesii*)-ponderosa pine, and Douglas-fir series (Daubenmire and Daubenmire 1984). Grand fir (*Abies grandis*), western hemlock (*Tsuga heterophylla*), western red cedar (*Thuja plicata*), subalpine fir (*Abies lasiocarpa*), and whitebark pine (*Pinus albacaulis*) dominate the over-story with increasing elevations within the wet forests (Daubenmire and Daubenmire 1984, Williams et al. 1995).

[a]Washington Department of Fish and Wildlife
[b]U.S. Fish and Wildlife Service
[c]Montana Cooperative Wildlife Research Unit, University of Montana

The climate is influenced by westerly maritime air flows from the Pacific Ocean to the west which create a moderating influence on temperatures while more extreme temperatures are produced from continental air flows from the east and northeast (Williams et al. 1995). The area is characterized by cool, wet winters and warm, dry summers with most precipitation falling during winter and spring. The precipitation range for the LPO is 38.1 to 63.5 cm. Temperatures range from 9° to 30° C in summer and -12° to 0° C in winter (USFWS 2001). Elevations ranged from 798 m to slightly over 1,443 m across the study area.

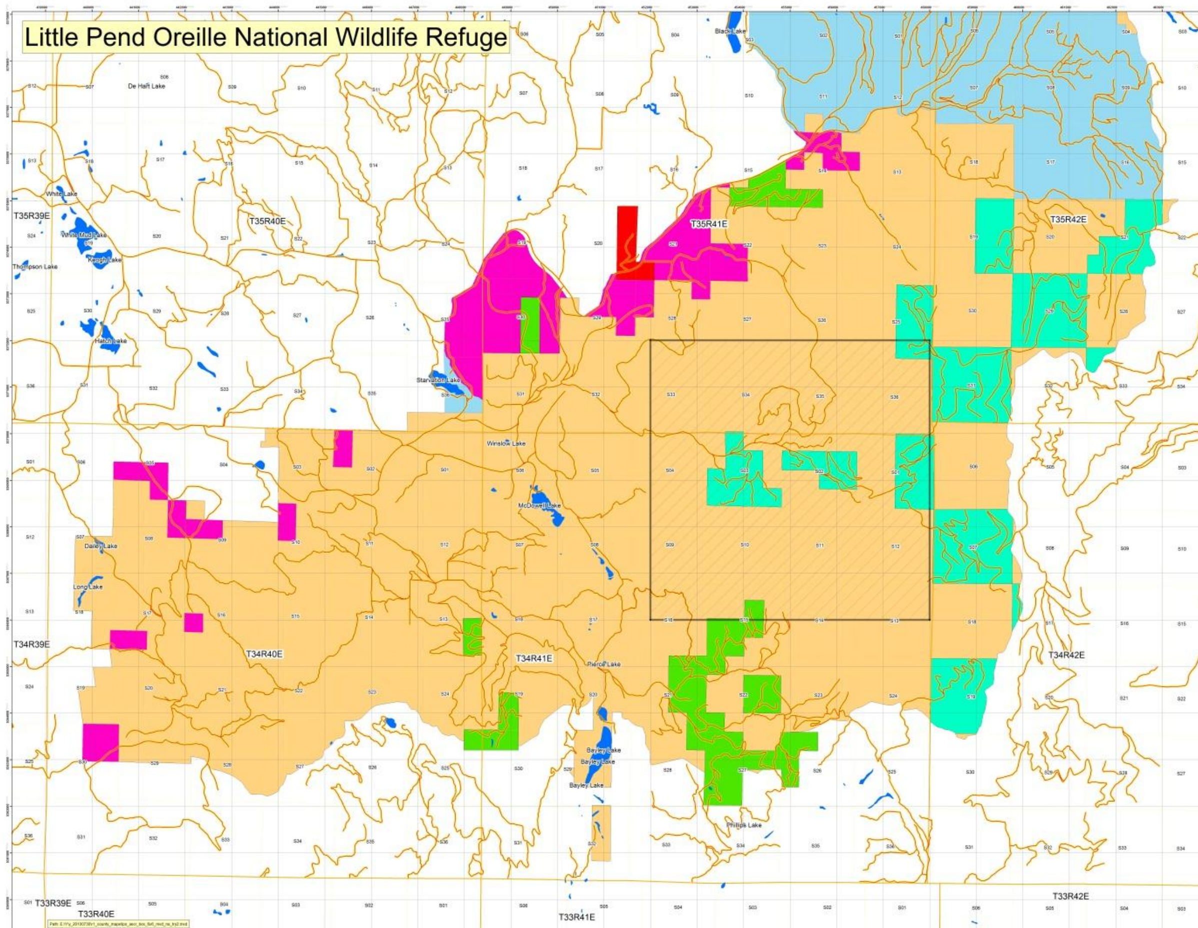

Figure 1. Little Pend Oreille National Wildlife Refuge and 36 km² sampling area within the refuge boundary.

METHODS

Sample Collection

We used scat detection dogs to locate deer pellets in a 6x6 km ***sampling grid*** (Fig. 2). Sampling grid size was determined based on a number of factors. If the sampling grid was too large, the number of samples collected would likely be cost prohibitive to genotype. If the sampling grid was too small it would encompass a true population that was too small to effectively estimate and the estimates would have unacceptable coefficients of variation (CV). The low number of deer would influence the number of samples, the number of samples successfully genotyped, and the number of

recaptures. Also, the approach that we used is more effective and the result in precision more acceptable if a majority of the animals' home ranges are found within the sample space. Using our knowledge of the available work space (LPO), home ranges for deer in the area, and some simulations of sampling "captures" and "recaptures", we established a sample grid size of 36 km^2.

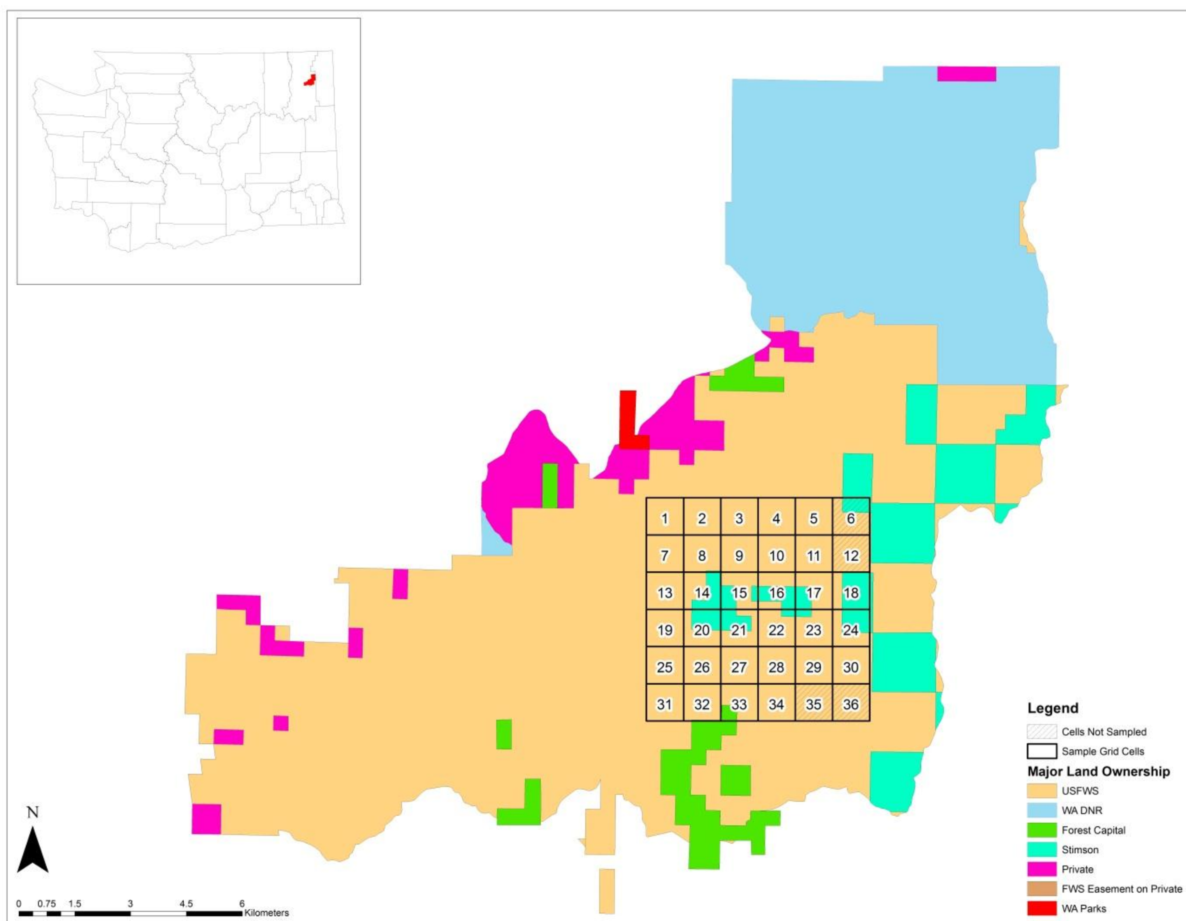

Figure 2. Location of 6x6 sampling grid in relation to the boundaries and ownership of the Little Pend Oreille National Wildlife Refuge.

Each sampling team consisted of a dog, dog handler, and navigator. Only fresh pellet groups were sampled. Freshness was determined by color, moisture, and professional assessment by teams with extensive experience in scat collection for these purposes. As the project progressed, the dogs were not rewarded when they located scat that was too old to sample. Given enough time the dogs may have been trained to focus on only fresh samples but the duration of this project did not allow for that additional training.

Two teams sampled 32 of the 36, 1x1 km squares. Effort varied with density of pellet groups and desired intensity of sampling effort for comparison in analysis. In each 1x1 km square a team consistently sampled every 3rd, 5th, or 7th fresh pellet group, respectively.

At the beginning of the project, sampling grid cell #13 was uniquely sampled with an intermittent effort approach. Teams would collect every fresh scat encountered when working the dogs and collect no samples when moving a predetermined distance to the next sampling start point within the cell. Start and stop times and track logs were recorded to quantify effort.

In addition, 4 squares in the center of the 6x6 sampling grid were more intensively sampled than the others. On separate dates these four cells (9, 10, 15, and 16) were double sampled. Every fresh pellet group detected in the second sampling event was sampled. Cells 6, 12, 35, and 36 were not sampled to accommodate the intensive, second sampling effort. These varying levels of effort were incorporated in model development and analysis. Samples were sent to USDA Forest Service, Rocky Mountain Research Station, Wildlife Genetics Lab in Missoula, MT for DNA analysis.

Model Development

After samples were collected and DNA analysis completed model development was initiated. We buffered the 6x6 km sampling grid by 5 km, creating a 16x16 km full sample space of 256 km^2 ($\mathcal{S}$). We overlaid a number of post-hoc ***trap grids*** over the sampling grid with square cells of 1 km, 0.5, km, 0.25 km, 0.2 km, and 0.125 km on a side. Each trap grid was aligned with the sampling grid so that all traps were fully contained in a single sampling grid cell. A trap was considered to be located at the center of the trap cell; thus, the "capture" location of any scat was assigned to be the center of the trap cell in which it was found. For our purposes, an encounter represents a sample that was successfully genotyped to individual. Encounter data was organized into an encounter history matrix where the value in row *i* and column *j* (y_{ij}) was set to 1 if individual *i* was encountered in trap *j* and was set to zero otherwise. Note that if multiple scat samples for a single individual were encountered within the same trap this would count as a single encounter for that individual; thus, the number of encounters for each individual may vary among trap grid sizes.

We followed the approach of Thompson et al. (2012) and Russell et al. (2012) in modeling encounter probabilities as a function of distance, gender, and search effort. The probability of encounter of individual *i* at trap *j* was modeled as

$$p_{ij} = \Pr\left(y_{ij} = 1\right) = 1 - \exp\left(-\lambda_{0,ij} g_{ij}\right) \tag{1}$$

where $\lambda_{0,ij}$ is the expected number of encounters for individual *i* at trap *j* if that individual's activity center is located at trap *j* (this can be thought of as a baseline encounter rate) and g_{ij} models the effect of distance of the activity center for individual *i* from trap *j* on encounter probability. Specifically,

$$\ln\left(\lambda_{0,ij}\right) = \beta_{0,i} + \beta_{\text{effort}} \ln\left(\text{effort}_j\right) \tag{2}$$

and

$$g_{ij} = \exp\left(\frac{-d_{ij}^2}{\sigma_i^2}\right) \tag{3}$$

where $\beta_{0,i}$ was either constant $\left(\beta_{0,i} \equiv \beta_0\right)$ or varied by gender (i.e., $\beta_{0,i} = \beta_{0,\text{male}}$ if individual *i* is male and $\beta_{0,i} = \beta_{0,\text{female}}$ if individual *i* is female), depending on the model; d_{ij}^2 is the squared Euclidian distance between the activity center of individual *i* and trap *j*; and σ_i is a scaling parameter which was either constant $\left(\sigma_i \equiv \sigma\right)$ or varied by gender (i.e., $\sigma_i = \sigma_{\text{male}}$ if individual *i* is male and $\sigma_i = \sigma_{\text{female}}$ if individual *i* is female), depending on the model.

We used dog track GPS points and sampling intensity to quantify effort (Fig. 3).

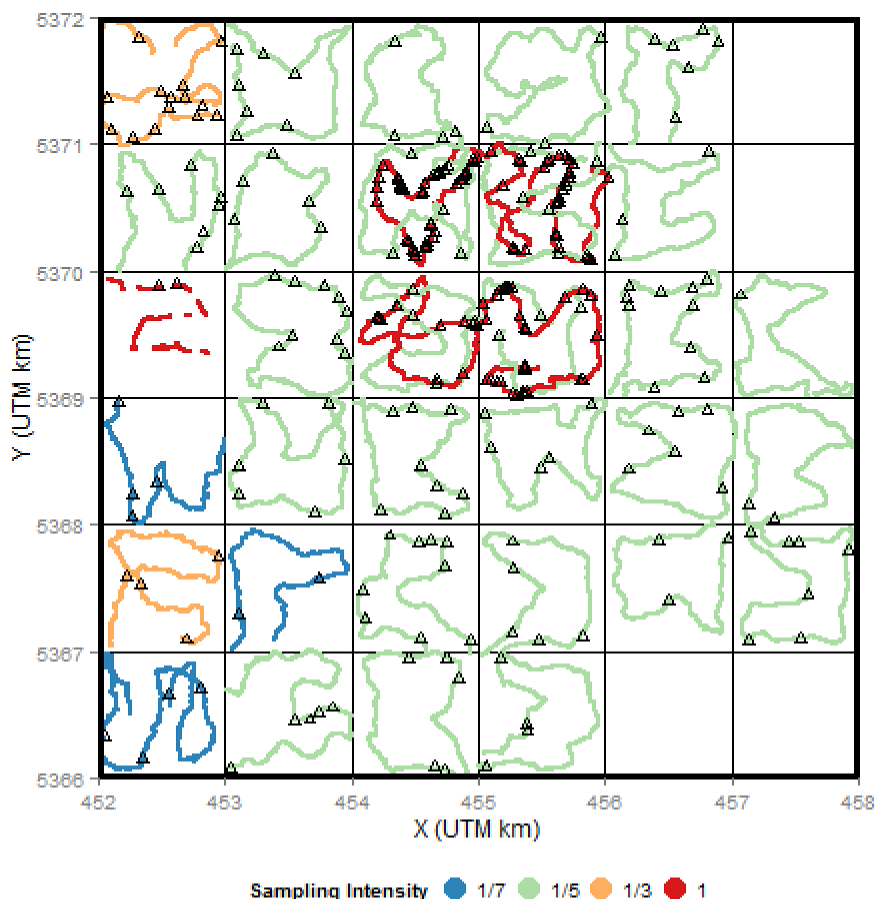

Figure 3. Detection dog track logs showing sampling intensity. Colors of the track logs indicate how often detected scat were sampled (i.e., every 7th fresh scat detected [blue]; every 5th fresh scat detected [green]; every 3rd fresh scat detected [orange]; or every fresh scat detected [red]) and the locations of scat samples that were identified to unique deer and used in the analysis.

Because GPS points for the individual dog tracks were recorded at inconsistent intervals. There was a need to standardize based on dog track data. We interpolated a continuous curve for the dog tracks using points from the track log to generate a line for each grid cell's dog track via ArcGIS's Data Management Tools / Features / Points to a Line tool (ESRI, Redding, CA). Points were then generated along each line, 1 meter apart, using ArcGIS's "Construct Points" tool available within ArcGIS Editor. Each dog-track point was weighted by the intensity with which scats were sampled along that track; for example, if every 5th fresh scat was collected along that dog-track, each point was given a weight of 1/5 and if every fresh scat was collected along that dog-track, each dog-track point was given a weight of 1. Table 1 lists the sampling intensities used for each dog-track by sampling grid cell and date (for those cells sampled on >1 date). The weighted dog-track points within a trap cell were then summed to give the effort for that trap (Figs. 4, 5, and 6).

Table 1. Sampling intensity for 36 sample grid cells. The 4 cells that were sampled twice are followed in parentheses by the day of the month they were sampled [e.g., cell (day)].

Sampling Intensity	***Cell Number***
Every Fresh Pellet Group Detected	9 (31); 10 (31); 13; 15 (30); 16 (30)
Every Third Fresh Pellet Group Detected 1/3	1; 25
Every Fifth Fresh Pellet Group Detected 1/5	2; 3; 4; 5; 7; 8; 9 (23); 10 (22); 11; 14; 15 (16); 16 (16); 17; 18; 20; 21; 22; 23; 24; 27; 28; 29; 30; 32; 33; 34
Every Seventh Fresh Pellet Group Detected 1/7	19; 26; 31
Not sampled	6; 12; 35; 36

There was a GPS failure during sampling of sampling grid cell #1. Therefore, scat samples collected during the time of the GPS failure were excluded from the analysis. Samples excluded were Pellets E002, E003, E004, and E005. Of these only E005 was genotyped to individual (individual 12-WDFW-1).

At the beginning of this pilot study, the field crews tried different protocols to address the high density of available samples that might be collected. One of these protocols involved sampling effort being a function of active searching by the dogs. For sampling grid cell #13, the dogs intermittently were "on-effort", during which they would collect every fresh scat encountered, or "off-effort" during which time the dogs were leashed and no scat was collected. The start and stop times for "on-effort" were recorded. In calculating effort, only the dog-track points during "on-effort" intervals were included and these were given a weight of 1. Although we were still able to effectively use the samples collected in the final analysis, after sampling was completed in cell #13 this approach was deemed less than optimum and the field crews changed to the sampling intensity protocols listed above. Due to loss of field notes, some of the start-stop times were lost, so any dog-track points without start-stop times had to be excluded. Therefore, we also had to exclude any pellets collected prior to the first known start time. This required the exclusion of Pellets E032, E033, E034, E035, E036, E037, E038, E039, E040, E041, E042, E043, and E044. Of these, 5 were genotyped to individual: E032 = 12-WDFW-9, E036 = 12-WDFW-10, E037 = 12-WDFW-11, E038 = 12-WDFW-12, and E043 = 12-WDFW-13.

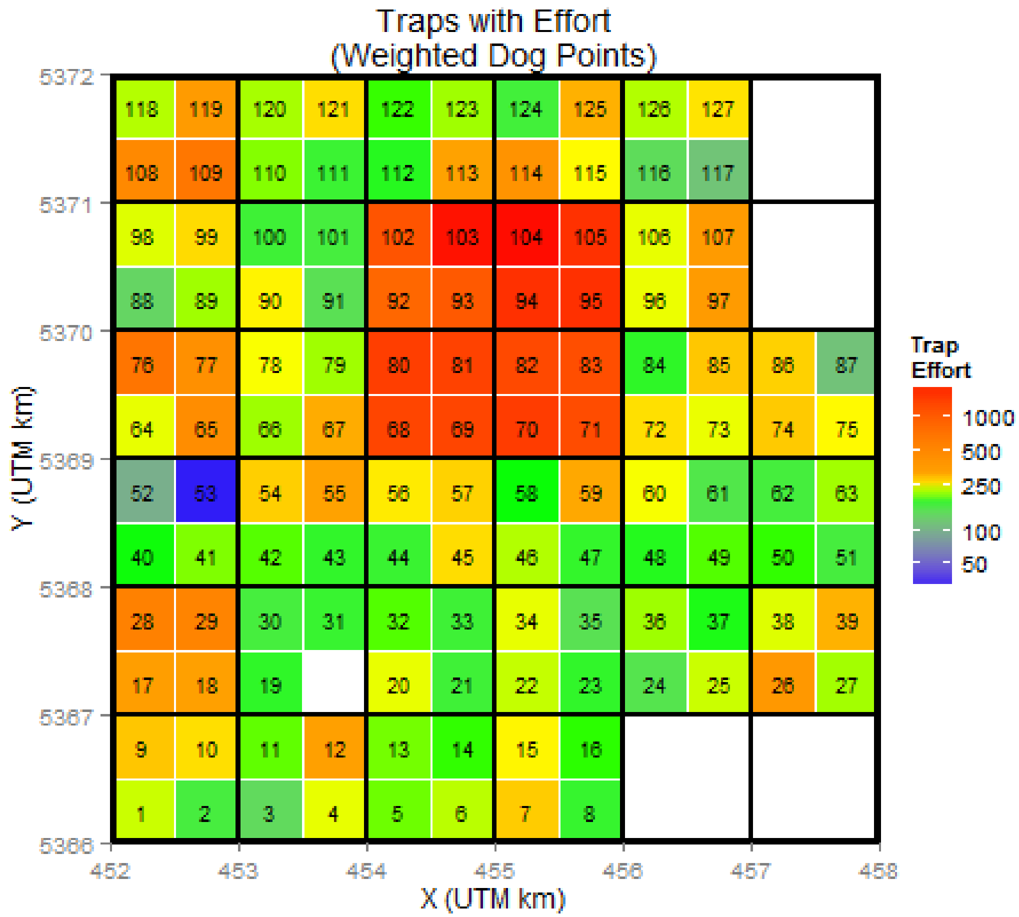

Figure 4. Post-hoc, 500 m trap grid with effort (weighted dog points) for each trap.

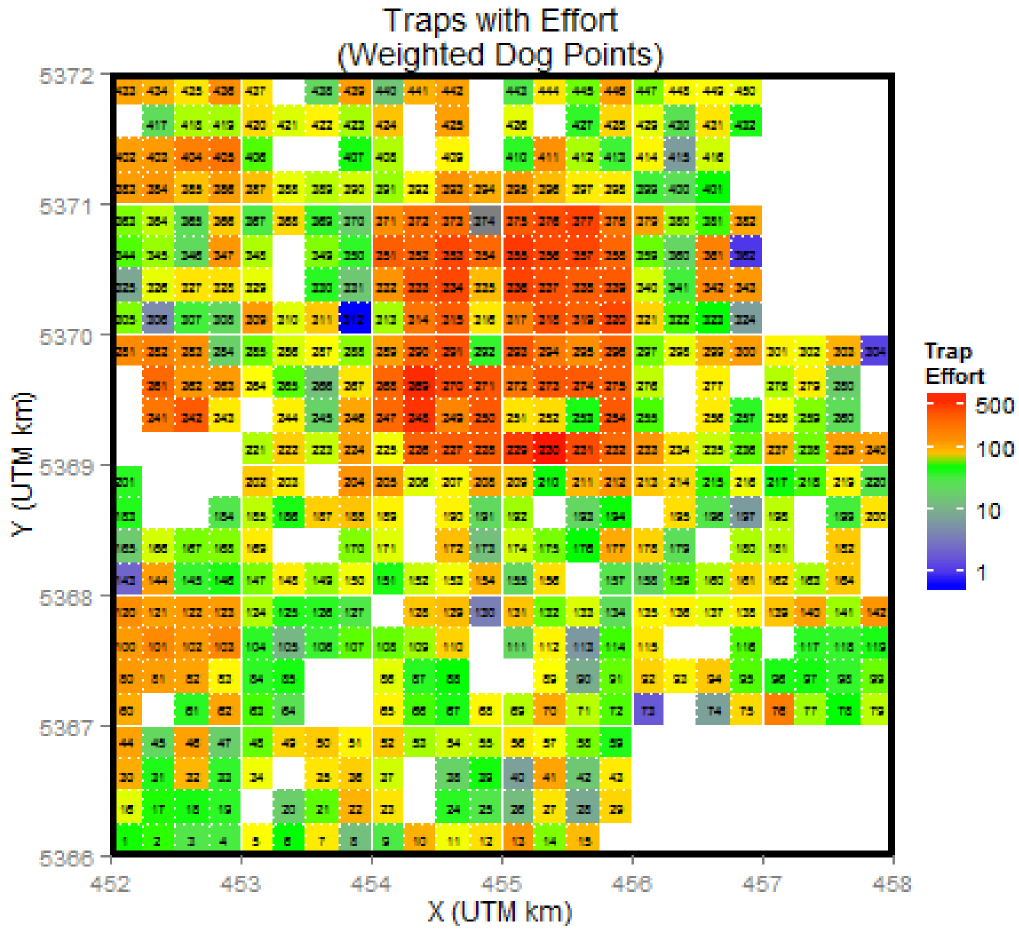

Figure 5. Post-hoc, 250 m trap grid with effort (weighted dog points) for each trap.

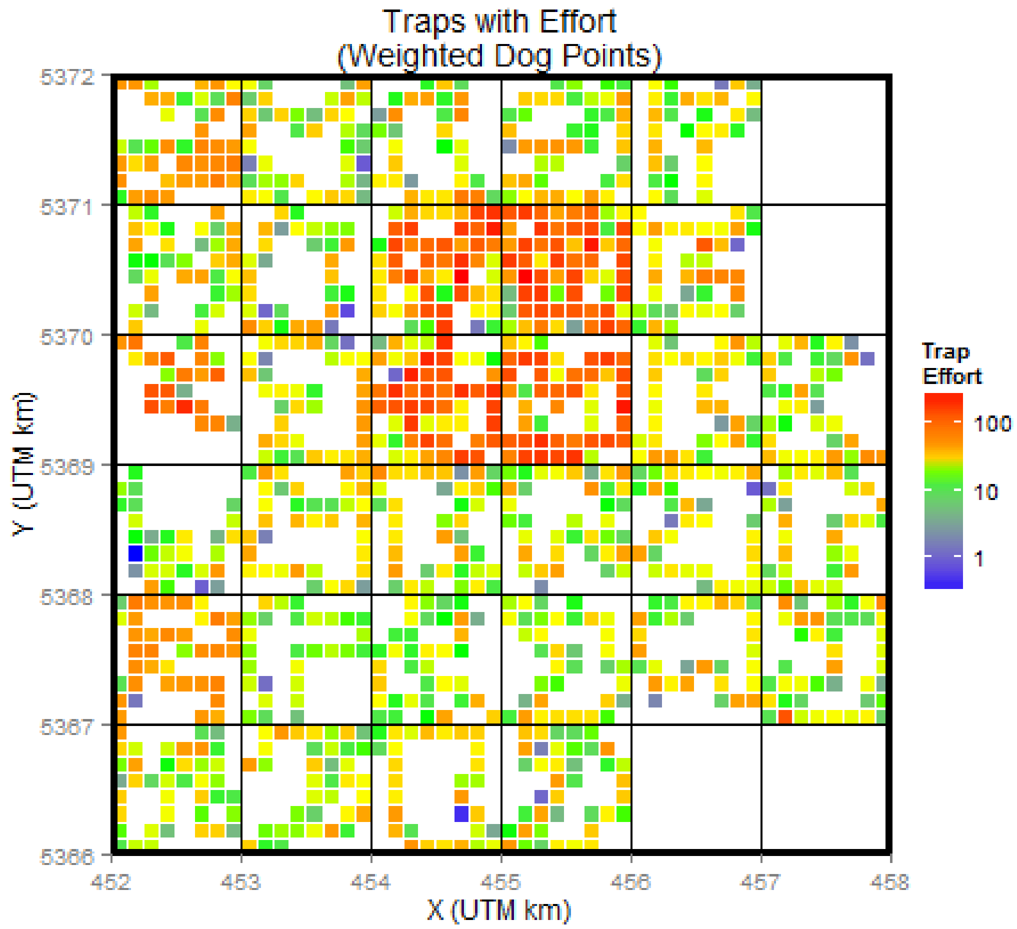

Figure 6. Post-hoc, 125 m trap grid with effort (weighted dog points) for each trap.

The number of traps included in the analysis ranged from 32 (trap grid size 1-km) to 1193 (trap grid size 0.125-km) (Table 2).

Table 2. The number of traps capturing some number of unique deer. The number of traps available was dependent on the post-hoc, trap grid size that was superimposed on the sampling grid. The number of traps for the core subset is represented by one trap grid size.

Trap Grid Size (km)	0 deer	1 deer	2 deer	3 deer	4 deer	5 deer	6 deer	7 deer	8 deer	9 deer	10 deer	11 deer	12 deer	Total # of Traps
0.125	978	184	22	7	1	1								1193
0.2	442	155	24	6	7									634
0.25	277	134	24	6	6	2	1							450
0.5	28	52	23	10	8	1	2	1	0	1	1			127
1	0	1	4	6	7	2	5	2	2	0	0	1	2	32
0.25 (core subset)	22	16	12	6	5	2	1							64

Traps with 0 effort (0 dog-track points) were excluded from the analysis. In addition to the scats excluded above, 2 scats were excluded in the analyses with trap grid size 0.125 due to having 0 dog-track points recorded in the trap cells where these samples were collected. This indicates the trap grid sizes of ≤0.125 km were too fine for the level of precision of effort. For trap grid sizes ≥0.2 km, a total of 288 scat samples were included in the analysis (this includes only those genotyped to individual) representing 104 different individual deer (72 females, 28 males, 4 unknown gender). At trap grid size 0.125-km, 286 scat samples were included in the analysis representing 104 different individual deer (Table 3).

Table 3. The number of unique deer encountered in some number of all the traps available. The number of traps available was dependent on the post-hoc, trap grid size that was superimposed on the sampling grid (Table 2). The number of unique deer for the core subset is represented by one trap grid size.

Trap Grid Size (km)	1 trap	2 traps	3 traps	4 traps	5 traps	6 traps	7 traps	8 traps	9 traps	10 traps	11 traps	12 traps	13 traps	Total # of Unique Deer
0.125	54	18	11	6	4	4	1	0	2	2	2			104
0.2	55	17	13	6	4	3	0	0	2	3	1			104
0.25	54	20	9	10	3	1	2	2	2	1				104
0.5	59	18	15	5	3	2	1	1						104
1	71	16	12	4	1									104
0.25 (core subset)	9	6	3	4	2	0	2	3						29

We tested a total of four models, denoted Le, Les, Le_Ss, and LesSs (Table 4). All 4 models included an effect of effort on $\lambda_{0,ij}$. The models varied by whether or not they included an effect of gender on $\lambda_{0,ij}$ and/or on σ_i.

Table 4. Description and formulation of 4 models explored.

Label	***Description***	***Formula for*** $\lambda_{0,ij} g_{ij}$
Le	λ_0 varies by trap-effort. No effect of sex on λ_0 or σ	$\exp\left\{\beta_0 + \beta_{\text{effort}}\left[\ln\left(\text{effort}_j\right)\right] - \frac{d_{ij}^2}{\sigma^2}\right\}$
Les	λ_0 varies by trap-effort and sex. No effect of sex on σ	Males: $\exp\left\{\beta_{0,\text{male}} + \beta_{\text{effort}}\left[\ln\left(\text{effort}_j\right)\right] - \frac{d_{ij}^2}{\sigma^2}\right\}$ Females: $\exp\left\{\beta_{0,\text{female}} + \beta_{\text{effort}}\left[\ln\left(\text{effort}_j\right)\right] - \frac{d_{ij}^2}{\sigma^2}\right\}$
Le_Ss	λ_0 varies by trap-effort. No effect of sex on λ_0 σ varies by sex.	Males: $\exp\left\{\beta_0 + \beta_{\text{effort}}\left[\ln\left(\text{effort}_j\right)\right] - \frac{d_{ij}^2}{\sigma_{\text{male}}^2}\right\}$ Females: $\exp\left\{\beta_0 + \beta_{\text{effort}}\left[\ln\left(\text{effort}_j\right)\right] - \frac{d_{ij}^2}{\sigma_{\text{female}}^2}\right\}$
LesSs	λ_0 varies by trap-effort and sex. σ varies by sex.	Males: $\exp\left\{\beta_{0,\text{male}} + \beta_{\text{effort}}\left[\ln\left(\text{effort}_j\right)\right] - \frac{d_{ij}^2}{\sigma_{\text{male}}^2}\right\}$ Females: $\exp\left\{\beta_{0,\text{female}} + \beta_{\text{effort}}\left[\ln\left(\text{effort}_j\right)\right] - \frac{d_{ij}^2}{\sigma_{\text{female}}^2}\right\}$

We conducted a Bayesian analysis of the models using data augmentation (Royle and Dorazio 2008, Royle and Young 2008). We augmented the encounter history matrix with enough rows of zeros to bring the total number of rows (M) to 1536, putting an upper limit of density at 6 deer/km^2 over the full 256-km^2 sample space ($\mathcal{S}$). A latent variable z_i is used to determine whether individual i is a true member of the population N (z_i = 1) or not (z_i = 0), where z_i is modeled as a Bernoulli random variable with parameter ψ. Examination of the posterior distributions of the population size and density over $\mathcal{S}$ indicated M was set sufficiently large in all models.

For models that included a sex-effect on λ_0 and/or σ and additional variable, $I_{d,i}$ was used, where $I_{d,i}$ = 1 if individual i was a female and $I_{d,i}$ = 0 if individual i was a male. For individuals that were encountered and for which the sex could be determined genetically, the true value of $I_{d,i}$ was used. For individuals not encountered (including individuals that were real but not encountered, encountered and genotyped to individual but not genetically sexed, and individuals that were part of the data augmentation), $I_{d,i}$ is a latent variable, modeled as a Bernoulli random variable with parameter ψ_{doe}.

All analyses were run in R versions 2.15.1, 2.15.2, 3.0.0, and 3.0.1 (R Core Team 2013) using package R2jags (Su and Yajima 2012).

Priors

We used the following priors for all analyses for which the parameter was included.

- Parameters on λ_0
  - β_0 or $\beta_{0,\text{male}}$ and $\beta_{0,\text{female}}$ ~ Uniform[-10, 10]
  - β_{effort} ~ Uniform[-5, 5]
- σ or σ_{male} and σ_{female} ~ Uniform[0,5]
- Activity centers for each individual were continuous uniform over the entire 256-km^2 sample space, $\mathcal{S}$ (the 6-by-6 km sampling grid plus the 5-km surrounding buffer)
  - *x*-coordinate ~ Uniform[452-5, 458+5]
  - *y*-coordinate ~ Uniform[5366-5, 5372+5]
- ψ ~ Uniform[0,1]
- ψ_{doe} ~ Uniform[0,1]

For each analysis, we ran three independent Markov Chains for 8,000 total iterations. We used a burn-in period of 1,000 iterations and thinned chains to every 10$^{\text{th}}$ iteration.

Model Selection

We assessed whether a sex-effect was necessary in each λ_0 and σ by visual comparison of the posterior distributions of those parameters between males and females for the models that included sex-specific estimates of those parameters (Figs. 7 and 8). The initial assessment was made when results were only available from each of the models using a trap grid size of 0.5 km. There was a strong separation between the sex-specific posterior distributions in the intercept parameter of λ_0 (i.e., $\beta_{0,\text{male}}$ vs. $\beta_{0,\text{female}}$) in model Les, but not in model LesSs, for which sex was also included in σ. However, there was strong separation in the posterior distributions of σ_{male} and σ_{female} for both models Le_Ss and LesSs (that is, regardless of whether sex was included in the parameterization of λ_0). Therefore, we determined the most parsimonious model was Le_Ss.

All four models were run using trap grid sizes of 1-km, 0.5-km, and 0.25-km, but only model Le_Ss was used at finer levels of trap grid size, due to time and computational limitations.

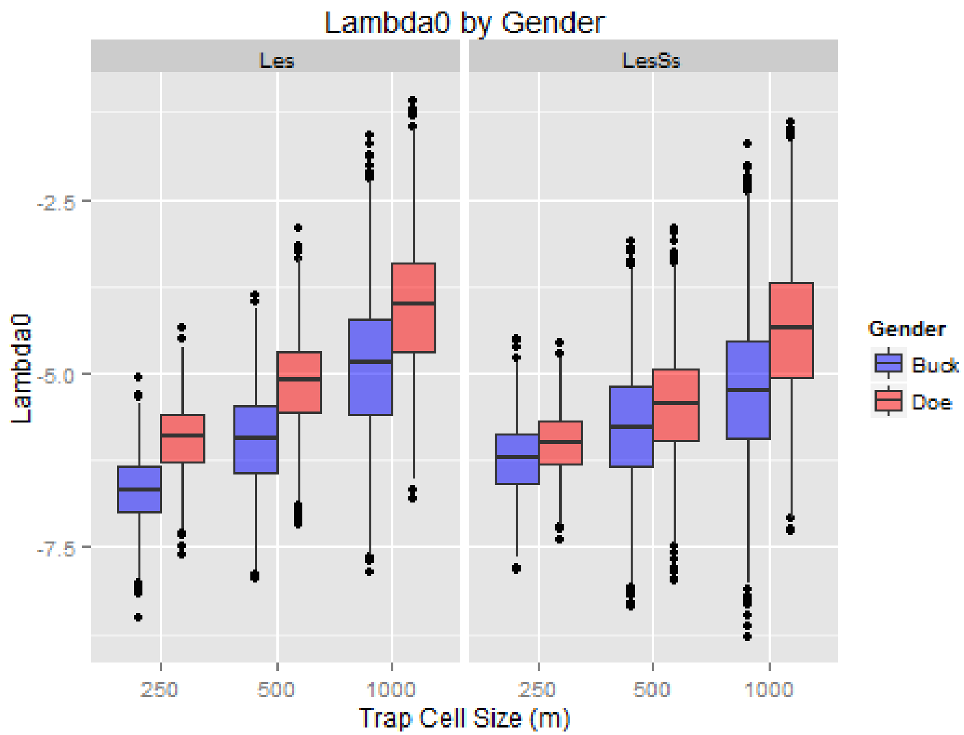

Figure 7. Posterior Distributions of LAM0.SEX

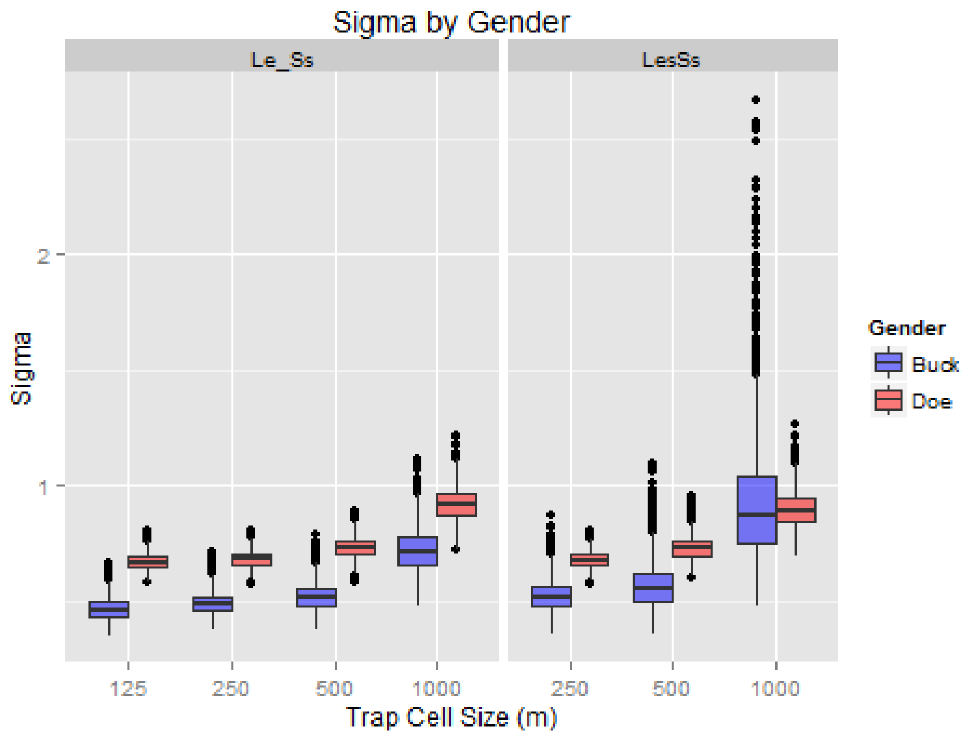

Figure 8. Posterior Distributions of SIGMA.SEX.

Double Sampling

To assess the efficacy of using a smaller sampling area, we also conducted an analysis assuming only sampling grid cells 9, 10, 15, and 16 were sampled (these are the 4 cells that were each sampled twice: the first time with every 5th scat collected, the second time with every scat collected). We will refer to these 4 cells as the "core" area. Although the core area was only 1/8th of the total sampled area (4 of 32 1-km^2 cells), because these 4 cells were intensively sampled (Figs. 3 and 5, Table 1) this subset included a total of 137 scats from 29 different individuals (21 does, 4 bucks, and 4 of unknown gender). For this analysis, we only used model Le_Ss and only used the trap grid size of 0.25 km, for a total of 64 traps. We did also attempt to conduct the analysis using a trap grid size of 0.5 km; however, this is only 16 traps and we found the posterior distribution for at least one parameter (β_0) was flat and resembled its prior distributions, indicating there was insufficient data at this scale.

As with the analysis of the full data set, we used a 5-km buffer on the 2-km by 2-km core sampling area, resulting in a sample space ($\mathcal{S}$) of 144 km^2. We used the same priors as with the analyses of the full data set, with the following exceptions. First, the prior on β_0 was Uniform [-20, 10], instead of Uniform [-10, 10]. Second, we augmented the encounter history matrix with enough rows of zeros so that the upper limit of density in the full 144-km^2 was 8 deer/km^2 (as opposed to 6 deer/km^2 in the analyses of the full data set). Initially these priors were set to the same values as in the analyses of the full data set; however, examination of the posterior distributions suggested that these limits needed to be expanded as the original values appeared to be limiting the parameter space.

We compared the estimates obtained from the analysis of the subset data to those obtained from the analysis of the full data set using the same model (Le_Ss) and trap grid size (0.25 km). We calculated the number of individuals in the core area for each iteration in the analysis of the full data set, resulting in a full posterior distribution of N in the core area from the full data set. Dividing the population estimate (N) by the area (4 km^2) for each iteration yields the posterior distribution of density.

RESULTS

In August of 2012, 546 scat samples were collected (Fig. 9). Of those, 294 samples were successfully genotyped. The probability of identity (PID), the chance of calling two samples the same when they are from 2 different deer, was 1.63×10^{-8}, or 1 chance in 61,199,510 for this type of misidentification. The probability of identifying samples from two siblings as the same deer (Psib) was 5.89×10^{-4}. Of the 294 samples that were genotyped, 107 unique deer were identified (Figs. 10 and 11). Of those individual deer identified, 57 were sampled once, 20 were sampled twice, and 30 were sampled 3 or more times. One hundred three (103) of the 107 unique deer were also assigned a gender. Of those 28 were male and 75 were female. For individuals encountered more than once, we calculated the maximum distance between all pairs of encounter locations. Across individual deer, this distance ranged from 0.08 to 3.17 km (median 0.63 km).

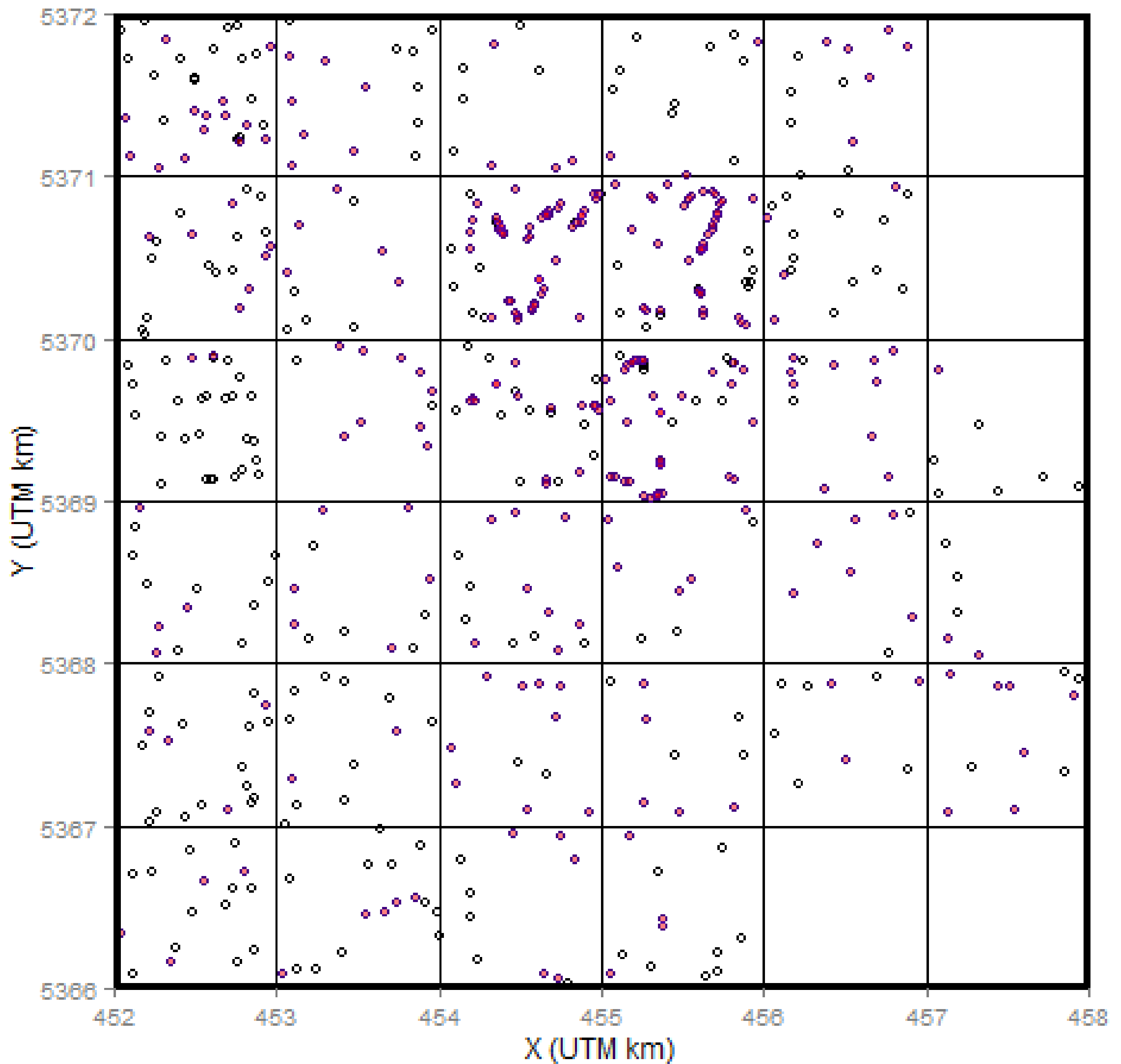

Figure 9. Locations of all scat groups sampled including those that were not successfully genotyped and those excluded from analysis (e.g., because of unknown effort as with SG cells 1 and 13). Colored locations represent samples used in the analysis and white locations represent all other samples.

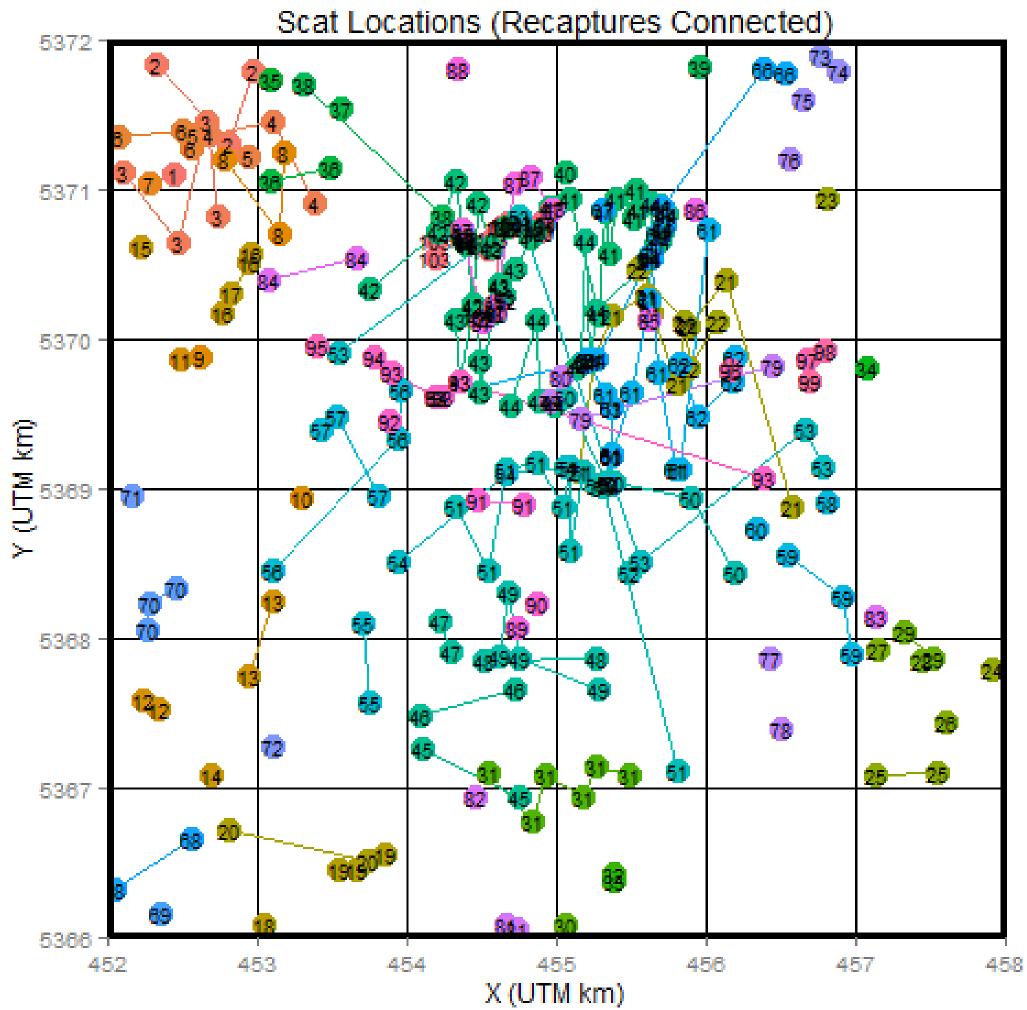

Figure 10. Scat sample locations that were identified to individual deer. The numbers represent individual deer. Similarly colored dots do not necessarily represent the same deer. Initial and subsequent encounters for individuals are connected by like-colored lines.

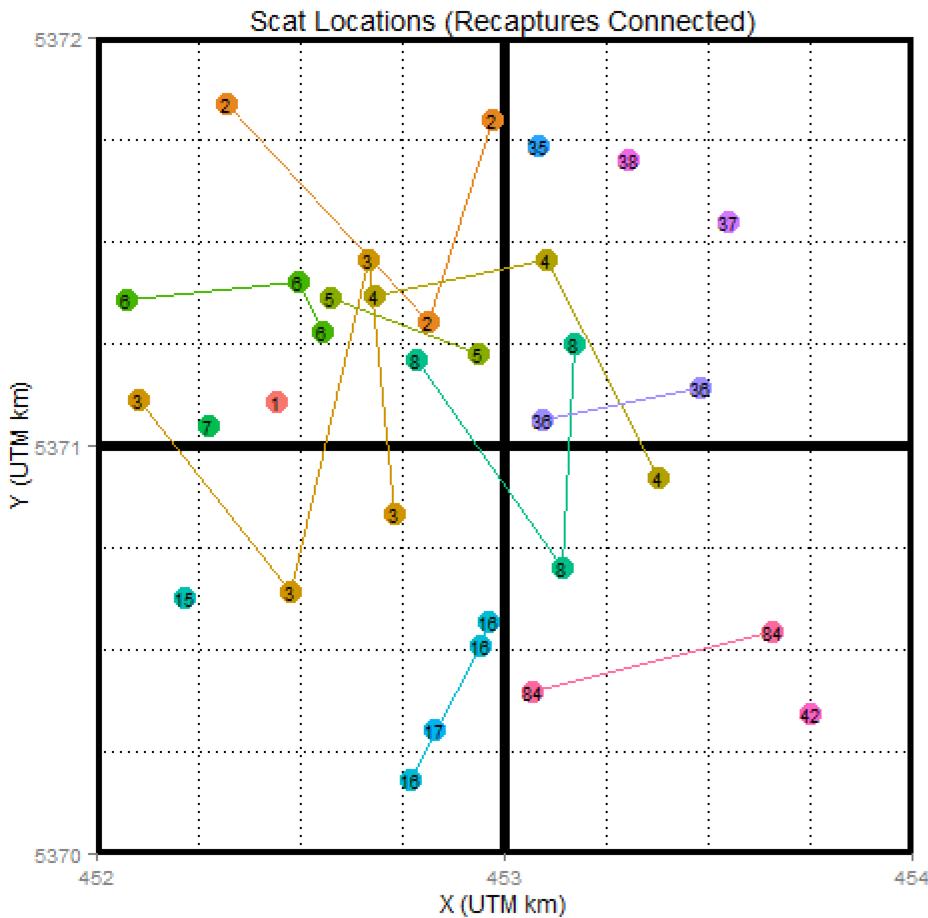

Figure 11. Scat sample locations for sampling cells 1, 2, 7, and 8 that were identified to individual deer. The numbers represent individual deer. Similarly colored dots do not necessarily represent the same deer. Initial and subsequent encounters for individuals are connected by like colored lines. Post-hoc trap grid size is 250 m.

The August population estimate (mean of the posterior distribution) for the 32 km^2 study area was approximately 120 deer depending on post-hoc trap grid size, and the density estimate was 3.75 deer/km^2. Table 4 shows how population and density estimates vary by trap grid size.

Table 4. Model Le_Ss posterior distribution summary statistics for the August population size (N) and deer/km^2 (Density) by size of post-hoc trap grid.

Trap Grid Size (m)	N					Density			
	mean	95% Credible Interval				mean	95% Credible Interval		
1000	122.5	101.0	-	149.0		3.8	3.2	-	4.7
500	121.2	102.5	-	144.0		3.8	3.2	-	4.5
250	118.0	101.0	-	139.0		3.7	3.2	-	4.3
200	119.0	102.0	-	139.0		3.7	3.2	-	4.3
125	120.7	104.0	-	142.0		3.8	3.3	-	4.4

Using only the data collected in the 4 km^2 core area, the estimated August population size in the core area was 14.4 deer with a 95% Credible Interval (CrI) of 10 to 19 deer. Using the full data set the estimated August population size for the same area was 15.9 deer with a 95% CrI of 12 to 20.5 deer. In order to compare the precision of estimates across scales (the core area based on the subset of data and the full 32 km^2 sampled area), we compared densities.

Figure 12 shows the posterior distributions of density obtained from the subset of data (core 4 km^2) as well as those obtained from the full data set for both the 4 km^2 core area and the full 32 km^2 sample area. Both distributions are shown because the density may differ between the core area and the full sample area (i.e., the core area may have a higher or lower density than the full sample area on average). To enable a more direct comparison of the precision of the estimates from the two datasets and at the two scales, we also centered density (subtracted the mean of the posterior distribution) so that all three distributions would be centered on zero (Figure 13).

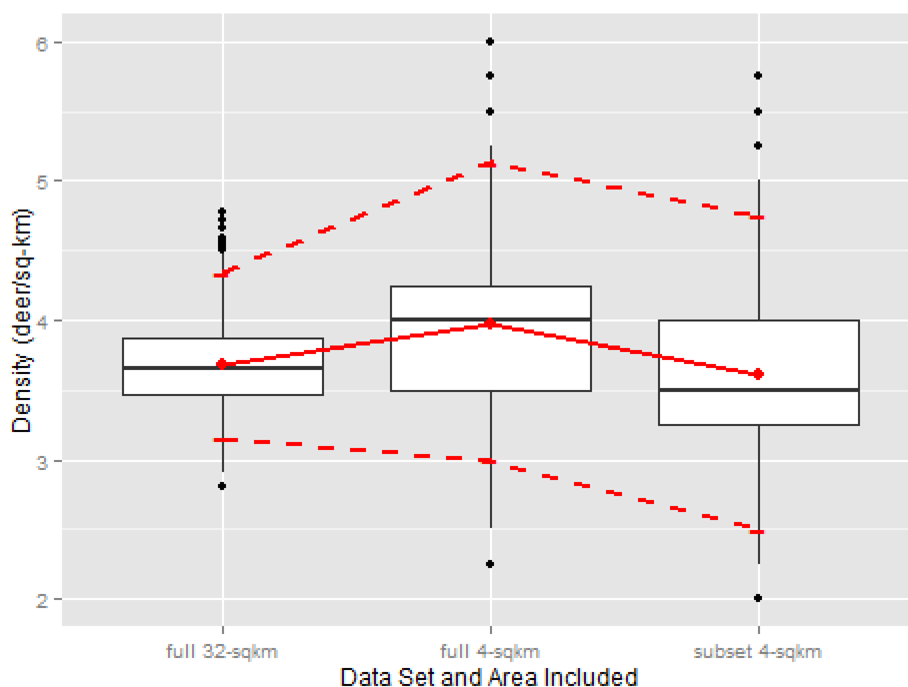

Figure 12. Posterior distributions of deer density for the full sampling area and 4 km^2 core area using the full data set and the core area data set. Black solid line in box is the median. Upper and lower limits of the box are the upper and lower quartiles. Red solid line is the mean. Red dotted lines are the 95% CrI.

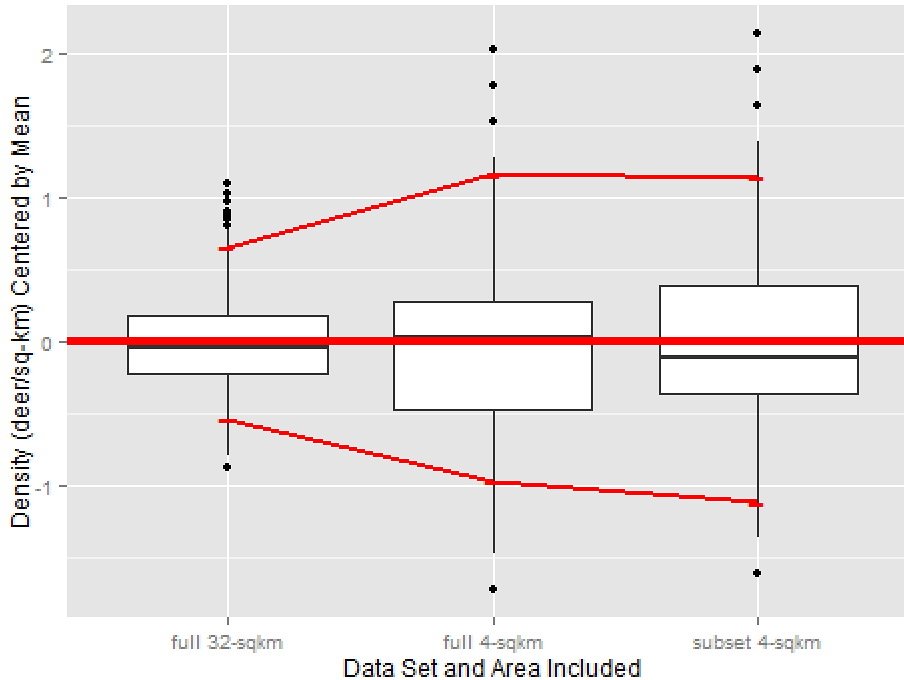

Figure 13. Centered posterior distributions of deer density for the full sampling area and 4 km^2 core area using the full data set and the core area data set. Black solid line in box is the median. Upper and lower limits of the box are the upper and lower quartiles. Red solid line is the mean. Red dotted lines are the 95% CrI.

DISCUSSION AND MANAGEMENT IMPLICATIONS

Capture-recapture techniques using unstructured spatial sampling to collect non-invasive DNA samples from animal scat have been effectively used for low density, wide-ranging predators (Russell et al. 2012, Thompson et al. 2012). We determined that similar approaches can be successfully used for commonly occurring ungulates with seasonal, small home ranges such as white-tailed deer. We selected late summer to collect samples. Recent radio telemetry data from white-tailed deer in this location suggest there are no transitional or migratory movements taking place at this time of the year. The same estimation strategy could be employed after deer have settled into their winter range locations. Based on telemetry data, using the same site in winter would reflect substantially higher densities of deer as the LPO is winter range for white-tailed deer. It would be prudent to avoid sampling during times of the year when transitional or migratory movements are taking place.

For relatively higher density ungulates, accommodations must be made in sampling protocols to avoid being overwhelmed with samples. Collecting every 3rd or 5th or 7th sample proved to be an effective protocol modification to address the abundance of available scat. When using scat detection dogs, a high density of potential samples can also overwhelm the search behavior of the dogs. There is the possibility that training can reinforce the dog's focus on fresher samples but the duration of this project did not allow for that.

One of the challenges for sampling low density animals in this fashion is getting enough recaptures for the technique to be effective. Even with a genotyping rate of 55%, and of those genotyped

samples 36% being identified to individual, we did not encounter the problem of not achieving enough recaptures.

Our results suggest that sampling more intensively but on a smaller geographic scale would provide similar estimates of density however the tradeoff is reduced precision. There is the possibility that one could design a survey protocol that would use small, randomly selected plots spread over a much larger landscape and then use those density estimates as an index of deer abundance on the larger area, however the precision of those estimates would be substantially compromised.

Overall, the SECR approach, using non-invasively collected DNA from scat, meets or exceeds the efficacy of other abundance estimating techniques that the Department is currently using for deer. The additional benefits to the SECR utilizing non-invasive DNA approach, especially when using scat detection dogs, is that it doesn't require staff to use aircraft and it can be used in areas where aircraft surveys aren't effective.

Currently the major drawback to using this approach for deer is the cost. The majority of those costs come from extracting DNA from scat samples and genotyping. Using the Selkirk white-tailed deer zone (GMUs 105-124) as an example, there are over 11,000 km^2 of deer habitat in the Selkirk zone (WDFW 2010). If we were to sample 1% of that deer habitat using the same cost rates incurred for this project, it would require approximately 8x the amount of funds typically used by the entire Region for both deer and elk aerial surveys combined. Although this is a very effective method to estimate abundance of common species like white-tailed deer, unless the laboratory costs for individual DNA identification can somehow be reduced, the approach is cost-prohibitive.

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