

Population estimates for the 2012 Cabinet-Yaak grizzly bear DNA mark-recapture study

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1. Introduction

This report details population and density estimates for the 2012 Cabinet-Yaak DNA inventory project. It mainly focuses on mark-recapture estimation methods and results. Other sampling details are given in other reports. It is assumed these results will be incorporated into a larger report on survey results.

2. Methods

2.1. General field methods

The Cabinet-Yaak project used a multi-data source approach to estimate grizzly bears within a 9,875 kilometer squared study area. During this project, 5 sessions of hair snag corral sampling, and 7 sessions of rub tree sampling were conducted systematically within the study grid. In addition, opportunistic recording of bears known to be on the study area during the time DNA sampling was also conducted.

2.2. Estimation methods

A multi data source mark-recapture methodology was used to jointly analyze the 3 data sources (Boulanger et al. 2008a, Kendall et al. 2008, Kendall et al. 2009) to estimate population size. The methodology closely followed (Kendall et al. 2009) where the hair snag and rub tree data sets were modeled individually to define optimal models for each data source. The Huggins closed capture model (Huggins 1991) and heterogeneity mixture models (Pledger 2000) in program MARK (White and Burnham 1999) were used for the stand-alone analyses. Once individual analyses were completed, they were then combined into the joint model with the opportunistic samples. Opportunistic samples were modeled as a single session and therefore individual analyses were not required. In general sex of bears were modeled as a group with the pooled estimate as the summation of male and female estimates. The standard errors of pooled estimates were obtained as the summation of the variance-covariance matrix for sex or area-specific estimates. Log-based confidence intervals that incorporated the minimal number of bears detected ($Mt+1$) were estimated using the formulas of (White et al. 2002). Simulated annealing was used to check model convergence for all of the MARK analyses.

2.3. Estimation of density and average population size

The Cabinet-Yaak sampling grid encompassed the majority of grizzly bear habitat and therefore it was likely that the population was closed to movement on all borders except the northern Canadian border. In addition, the population of bears in the study area was composed of native bears and augmented bears. Augmented bears were known to have larger, less centralized home ranges and had potential to move from the study area during

sampling. Therefore, it was possible that closure violation was violated for the northern border and by augmentation bears.

We used the Ivan density estimator (Ivan 2011, Ivan et al. 2013a;b) in program MARK (White and Burnham 1999) to estimate density and average number of bears on the sampling grid. The density estimation module uses information from DNA bears and bears that were collared to estimate density. The general approach of this estimator can be thought of in terms of how an estimate is derived using mark-recapture methods. The general estimator of population size using mark-recapture methods is the count of individual detected (M_{t+1}) divided by the capture probability of individuals across all sampling occasions (p^*) (Huggins 1991). ($\hat{N} = M_{t+1}/p^*$). Another way this can be expressed is the summation of individuals each divided by p^* ($\hat{N} = \sum_{i=1}^{M_{t+1}} (\frac{1}{p^*})$). For example, if 5 unique bears are detected on the sampling grid and the overall detection rate is 0.5 then the population size estimate would be 5/0.5 or 10 bears. This could also be obtained by adding each bear divided by 0.5 to get 10. ($1/0.5+1/0.5+1/0.5+1/0.5+1/0.5=10$). The key assumption with this equation is that each bear is spending all of the time during DNA sampling on the grid so that each bear counts fully towards (the 1 in the numerator for each bear) the population estimate. If closure violation is occurring, then a bear may be only spending a smaller proportion of time on the sampling grid leading to a positive bias in estimates. The MARK module basically uses estimates of residency estimated by the proportion of points that radioed bears were on the sampling grid to correct DNA estimates. It does this by substituting the 1 in the above equation with an estimate of residency (symbolized as \tilde{p}). So, \tilde{p} replaces the 1 in the previous equation to estimate the average number of bears on the sampling grid at one time (N_{ave}) ($\hat{N}_{ave} = \sum_{i=1}^{M_{t+1}} (\frac{\tilde{p}}{p^*})$). In this equation, the bears actual time on the grid is not assumed to be 1, but its residency. For example, say the 5 unique bears detected only spent 80 of their time on the grid (i.e. 80 percent of the collar points were on the grid). In this case, the closure corrected estimate of population size would be 8. This would be estimated as ($0.8/0.5+0.8/0.5+0.8/0.5+0.8/0.5+0.8/0.5=8$) (Ivan 2011). Estimates of density were then obtained by dividing N_{ave} by the area of the sampling grid ($9,875 \text{ km}^2$).

Residency of radioed or DNA bears often is a function of the distance of the bears from the sampling grid edge. (Boulanger and McLellan 2001). Bears that occur near the edge are more likely to be off the grid than bears in the middle. We therefore estimated the distance of radioed and DNA bears from the entire grid edge and the northern edge of the sampling grid. Only radioed collared bear points that fell within the DNA sampling grid were used to estimate mean locations and distance from edge to ensure equivalency of DNA and radio collared bears. By using distance from edge as a covariate, the assumption of similar distributions of DNA and radio collared bears was relaxed, making this assumption more reasonable. In addition, models of residency for male and female bears, as well as augmented and native bears were considered.

Data from radio collared bears was available for years previous to the actual DNA project. This data was used for the analysis by adding the radio collared bears as a unique group in MARK. This group was used to only estimate \tilde{p} under the assumption of similar residency of grizzly bears prior to the DNA project and during the project. As described next, various covariates such as mean distance from grid edge and whether a bear was an augmentation bear was used to further model variation in residency. The Ivan estimator for \tilde{p} is a logistic

regression model of a binary response (Ivan 2011, Ivan et al. 2013a;b). For initial stand-alone modelling of residency, SAS proc GENMOD (Stokes et al. 1997, SAS Institute 2000) was used to determine optimal residency models. The events/trials response variable input was used where the response was number of points on grid and the number of trials was the total number of daily locations for a bear within the time of sampling for a given year. In many cases, individual bears were radioed for more than one year and therefore the radio collar data set contained multiple bear-year records for individual bears. To avoid issues of pseudoreplication, we pooled individual records for multiple years into a single record by estimating the mean number of locations on the grid, mean total locations, and mean distances from edge for each bear in the radio collared data set. This approach avoided potential bias in variance estimates given that the Ivan estimator does not have a method for modelling repeated measures data.

2.4. Covariates for detection probability and residency models

Covariates were used to define groups for the analysis and model variation in detection probabilities and bear residency. In most cases covariates were binary to allow specific modeling based on geographic location of detection (Cab or Yaak), previous live capture (pcap) (Boulanger et al. 2008b), whether a bear had been transplanted from another area (aug), or whether a bear had a collar for research but was not an augment bear (res). In addition, distance from nearest grid edge and northern edge was used to model detection probability or residency variation. Distance from edges were calculated using mean detection locations of DNA bears in hair snags, rub trees, or opportunistic samples, and mean collar locations within the sampling grid for the radio collared bears samples.

Table 1: Individual covariates used for mark-recapture analysis

Name	Values	Description
sex	M or F	sex of bear
Cab	0 or 1	Bear detected in Cabinets
Yaak	0 or 1	Bear detected in Yaak
pcap	0 or 1	Bear previously live captured
aug	0 or 1	Bear augmented (moved) from other area
res	0 or 1	Research bear (not augmented)
dN	continuous	Distance of mean location to North edge of grid
dAll	continuous	Distance of mean location to closest edge of grid

In addition, temporal covariates, such as rub tree effort were used to describe temporal variation in detection probabilities. Rub tree effort was the number of rub tree days (number of rub trees times the number of days that rub trees were available) that rub trees were available to bears for each sampling session.

3. Results

Forty two bears were detected on the Cabinet Yaak sampling grid. Of these 20 were female, 21 were male and 1 bear of unknown sex was detected as part of a family group (Sibling of 729a) using radio telemetry. Because the analyses required bears of known sex, this bear was not included in the mark-recapture analyses (Table 2).

Table 2: Number of bears detected by each sampling type. Note that bears could be detected in more than one type so the total does not add up to the total number of unique bears detected.

Sex	Hair snag	Rub tree	Opportunistic
male	17	15	5
female	11	13	7
total	28	28	12

In terms of rub tree and hair snag sampling, 3 bears were not detected using either method, and 10 bears were detected using only rub trees whereas 10 bears were only detected using hair snags (Table 3).

Table 3: Frequencies of unique bears detected by hair snag, rub tree methods.

Data type	Rub tree	
Hair snag	not detected	detected
<u>Females</u>		
not detected	3	6
detected	4	7
<u>Males</u>		
not detected	0	4
detected	6	11
<u>Pooled</u>		
not detected	3	10
detected	10	18

3.1. Hair snag-only analysis

Hair snag sampling detected 11 and 7 unique males and females (Table 4). Detections were initially high in session 1 then declined through session 3 but then increased in sessions 4 and 5. The number of newly caught bears decreased after the initial session except for 4 males detected in session 5. Detection frequencies, the number of sessions individual bears were detected, suggested that most bears were only detected once with no bear detected in more than 3 sessions.

Table 4: Summary statistics for hair snag only sampling.

Session	1	2	3	4	5	Total
<u>Females</u>						
Animals caught	6	2	1	5	4	
Total caught	0	6	7	8	10	11
Newly caught	6	1	1	2	1	
Frequencies	6	3	2	0	0	
<u>Males</u>						
Animals caught	6	2	1	7	6	
Total caught	0	6	7	8	12	17
Newly caught	6	1	1	4	5	
Frequencies	13	3	1	0	0	

Plots of detections suggested similar declines in the number of detections and overall trends in detections for males and females (Figure 1).

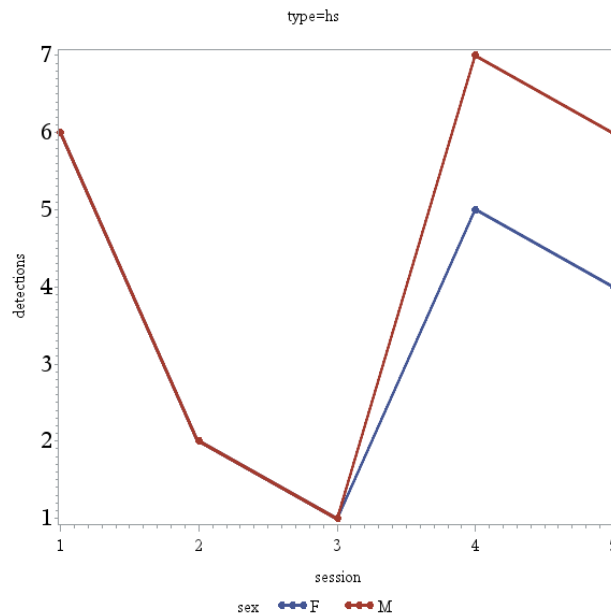


Figure 1: Number of unique bears detected by session for hair snag sampling.

Huggins model selection initially focused on modeling the temporal variation in detections. Two hypotheses were possible. First, trap habituation could have caused a decline in redetection rates since the sites were not moved for sessions 1 to 3, followed by an increase in detections in session 4 when sites were moved and a potential reduced redetections in session 5 when sites were not moved. Second, the sites in site 1 may have become less appealing as snow melted leading to selection to higher elevation sites which would have caused an increase in detections in sessions 4 and 5 when sites were moved to higher areas. Finally random variation in detection could have caused the observed patterns.

For the trap habituation hypothesis, it would be expected that detection rates (p) would be higher than redetections (c) in sessions 2 and 3 (signified by t_{23}). If redetection rates were similar for all sessions where sites were not moved then it would be expected that c would be equal for sessions 2,3 and 5 (signified by t_{235}). None of the trap habituation models (Table 5: models 12 and 14) were supported compared to a model with unique detections (equal to redetections) for all sessions (model 8) or a model with unique detection rates for sessions 2 and 3 (Model 2).

As a second step, models were fit to describe potential heterogeneity variation including the use of sex as a covariate (Models 1, 3 etc), previous capture as a covariate (Model 1), augmentation (Model 5), geographic area (Model 6) and undefined mixture heterogeneity (Models 10, 16 and 17).

Of the models considered, a model with sex-specific detection rates and detection rates varying as a function of previous capture, and with unique detections for sessions 2 and 3 was most supported. Other models with varying combinations of covariates in the most supported model were also supported as indicated by ΔAIC_c of less than 2.

Table 5: Hair snag only Huggins model selection results. Detection probabilities are symbolized by p and redetection probabilities as c . Mixture model probabilities of mixture are symbolized by π and 2 mixture detection probabilities as $\theta_{1\&2}$. Session-specific variation in detection rates is symbolized by a t with applicable sessions listed as subscripts. Akaike Information Criteria (AIC_c), the difference in AIC_c values between the i th model and the model with the lowest AIC_c value (ΔAIC_c), Akaike weights (w_i), number of parameters (K) are presented and deviance are presented.

No	Detection probability	AIC_c	ΔAIC_c	w_i	K	Deviance
1	$p(\text{sex}+\text{prevcap}+t_{23})$	140.67	0.00	0.201	4	132.4
2	$p(t_{23})$	140.79	0.12	0.189	2	136.7
3	$p(\text{sex}+t_{23})$	140.95	0.28	0.174	3	134.8
4	$p(\text{sex}+\text{prevcap}+t_{23})$	141.13	0.46	0.159	3	135.0
5	$p(\text{sex}+\text{augment}+t_{23})$	141.81	1.15	0.113	4	133.5
6	$p(\text{Caab/Yaak}+t_{23})$	142.88	2.21	0.067	3	136.7
7	$\text{sex}*(t_{23})$	143.07	2.40	0.060	4	134.8
8	$\text{sessions}(t)$	146.09	5.42	0.013	5	135.6
9	$\text{sex}+\text{sessions}(t)$	146.35	5.68	0.012	6	133.7
10	$\pi(\text{sex}) \theta_{1\&2}(\text{sex}+t_{23})$	146.76	6.09	0.010	6	134.1
11	$p(.)$	152.96	12.30	0.000	1	150.9
12	$p(t_{123}, t_{45}) c(t_{23})$	153.12	12.45	0.000	4	144.8
13	$p(\text{sex})$	153.18	12.51	0.000	2	149.1
14	$p(t_{123}, t_{45}) c(t_{23}, t_5)$	153.50	12.83	0.000	5	143.1
15	$p(.) c(.)$	154.84	14.17	0.000	2	150.8
16	$\pi(\text{sex}) \theta_{1\&2} (+\text{sex})$	159.15	18.49	0.000	5	148.7
17	$\pi(\text{sex}) \theta_{1\&2} (*\text{sex})$	161.35	20.68	0.000	6	148.7

Estimates of detection probabilities suggested higher detection rates (>0.2) for all sessions except 2 and 3 where rates were low (Table 6).

Table 6: Model averaged estimates of detection probabilities for male and female bears from models in Table 5. Redetection rates, or mixture model rates were not estimated given low support for these model types.

Session	Estimate	SE	LCI	UCI
<u>Females</u>				
1	0.319	0.106	0.152	0.550
2	0.090	0.050	0.029	0.247
3	0.089	0.050	0.028	0.244
4	0.319	0.106	0.152	0.550
5	0.317	0.105	0.152	0.547
<u>Males</u>				
1	0.217	0.085	0.095	0.425
2	0.056	0.033	0.017	0.170
3	0.055	0.033	0.016	0.167
4	0.218	0.085	0.094	0.426
5	0.216	0.083	0.095	0.419

Model averaged estimates of superpopulation size were marginal in terms of precision (CV>20%) with the pooled estimate being close to the target level of precision of 20% (or lower) (Table 7).

Table 7: Model averaged estimates of superpopulation size for the HS only analysis.

Parameter	M_{t+1}	\hat{N}	SE	LCI	UCI	CV
Females	11	15	3.93	12	31	25.4%
Males	17	31	10.94	20	71	35.6%
total	28	46	11.72	31	80	25.4%

3.2. Rub tree-only analysis

Twenty eight bears were detected during 7 rub tree sampling sessions. Thirteen females were detected with many of the new detections occurring in the latter sessions of sampling (Table 8). Earlier sampling sessions had few detections of females which is similar to other rub-tree projects conducted in the NCDE. Detection frequencies of females were heterogeneous with the majority of females being detected once but single bears being detected in up to 5 sessions. Male detections were more even across sessions with the most detections in earlier and latter sessions. The number of newly caught males decreased with session. Male detection frequencies were also heterogeneous with males being in up to 5 different sessions.

Rub tree effort increased with sampling session. The duration of rub tree exposure was equal to approximately 14 days for each sampling sessions. In some cases, duration was lower or higher than the 14 days of a session, however, the majority of durations for rub trees were within 2-3 days of the optimal 14 day length as indicated by the 5th and 95th percentiles of the distribution of durations for each session.

Table 8: Summary statistics for rub tree only analysis. Statistics are given for male and female bears. In addition rub tree sampling effort by session is listed.

Statistic	Session							total
	1	2	3	4	5	6	7	
<u>Females</u>								
Animals caught	2	0	2	5	4	4	6	13
Total caught	0	2	2	4	8	10	11	
Newly caught	2	0	2	4	2	1	2	
Frequencies	9	1	1	1	1	0	0	
<u>Males</u>								
Animals caught	7	6	2	4	3	5	6	15
Total caught	0	7	9	10	11	12	12	
Newly caught	7	2	1	1	1	0	3	
Frequencies	7	3	2	1	2	0	0	
<u>Sampling effort</u>								
number of trees	1086	1188	1263	1298	1322	1317	1333	
Rub tree days	15,212	16,712	17,832	18,355	18,621	18,693	19,011	
Mean duration	14.0	14.1	14.1	14.1	14.1	14.2	14.3	
S.D.	1.8	2.0	2.5	2.6	1.4	2.9	3.0	
min duration	2	2	3	1	3	1	1	
max duration	22	29	43	56	40	54	70	
5 th percentile	12	12	12	14	14	12	13	
95 th percentile	16	15	15	14	14	15	14	

A graph of detections with session further illustrates that female detections increased with sessions whereas male detections were more variable with session (Figure 2)

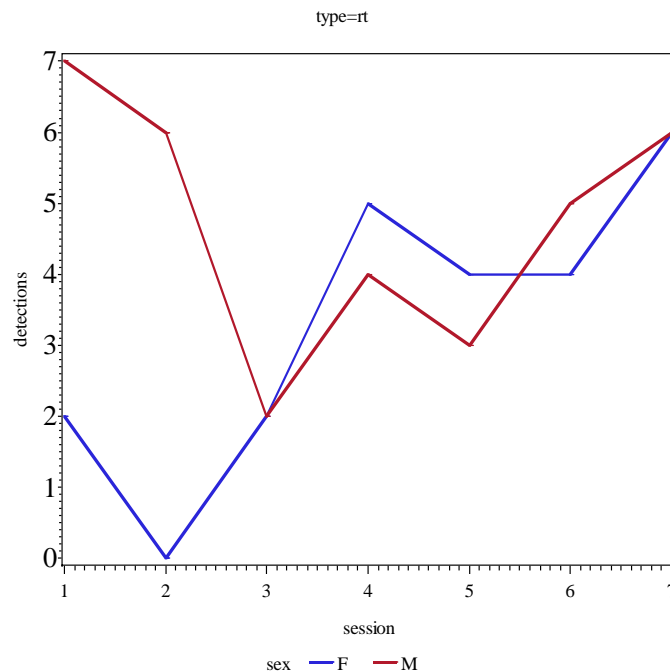


Figure 2: Detections of bears by session and sex for rub tree data.

Model development initially focused on developing a parsimonious model of temporal variation in detection rates for male and female bears. Models with session and sex-specific detection rates (Table 9: Models 18 and 19), detections varying as a function of rub tree effort (days) (Models 16 and 17) were initially proposed. However, these models had less support than a model with constant detection probabilities (Model 14). Models that considered both temporal trends in detection by sex (symbolized by T ; Models 7, 8, and 11) were introduced, with models that had sex-specific trends (symbolized by T_F) being most supported (of trend models). A model that had similar detection rates for females for sessions 1, 2 and 3 (symbolized by t_{123F}) and equal detection rates for other sessions for male and female bears was most supported of the non-mixture temporal trend models (Model 4).

Once a baseline temporal trend model was established, undefined heterogeneity mixture models were considered. In many cases, mixture models were unstable leading to high standard errors on either the beta terms or the derived population estimates which was presumably due to the sparse data set. For example, models with sex-specific probabilities of mixture (π) resulted in excessively high estimates with large standard errors. These models were not considered further, however, sex-specific mixture probabilities was considered further in the joint model analysis under the assumption that the mixture models may be more stable in a joint data analysis. Of the models that were stable, a model that had pooled sex probabilities of mixture (π) but unique point estimates of mixture probabilities for sex and unique detection rates for females in sessions 1-3 was most supported (Table 9, model 1).

Table 9. Model selection results for the rub-tree only analysis. Detection probabilities are symbolized by p and redetection probabilities as c . Mixture models probabilities of mixture are symbolized by π and 2 mixture detection probabilities as $\theta_{1\&2}$. Session-specific variation in detection rates is symbolized by a t with applicable sessions listed as subscripts. Linear trends are symbolized by T . See Table 1 for information on covariates. Akaike Information Criteria (AIC_c), the difference in AIC_c values between the i th model and the model with the lowest AIC_c value (ΔAIC_c), Akaike weights (w_i), number of parameters (K) are presented and deviance are presented.

No	Model	AIC_c	ΔAIC_c	w_i	K	Deviance
1	$\pi(.)\theta_{1\&2} ((*sex)+t_{123F})$	216.2	0.00	0.676	6	203.7
2	$\pi(.)\theta_{1\&2} (sex)+T_F$	218.1	1.89	0.263	6	205.6
3	$\pi(.)\theta_{1\&2} (*sex)$	223.9	7.71	0.014	5	213.6
4	$p(sex+t_{123F})$	224.2	8.03	0.012	3	218.1
5	$\pi(.)\theta_{1\&2} (*sex+rteffort)$	225.6	9.42	0.006	6	213.2
6	$p(sex+T_F)$	225.7	9.54	0.006	3	219.6
7	$p(sex+t_{123F}+T_{1234})$	226.1	9.95	0.005	4	217.9
8	$p(sex+ t_{123F} +T_{4567})$	226.1	9.95	0.005	4	217.9
9	$p(sex*rteffort+t_{123F})$	227.0	10.80	0.003	5	216.7
10	$p(sex*rteffort)$	227.0	10.84	0.003	4	218.8
11	$p(sex*T*rteffort)$	227.7	11.47	0.002	6	215.2
12	$p(sex*rteffort*season)$	227.9	11.75	0.002	6	215.5
13	$p(sex*rteffort)+cab/yaak$	228.7	12.50	0.001	5	218.4
14	$p(.)$	229.8	13.62	0.001	1	227.8
15	$p(sex)$	230.5	14.29	0.001	2	226.4
16	$p(rteffort)$	231.5	15.30	0.000	2	227.4
17	$p(sex+rteffort)$	232.2	15.98	0.000	3	226.0
18	$p(sex*t)$	235.8	19.58	0.000	13	207.8
19	$p(sex+t)$	236.3	20.10	0.000	8	219.5

Model averaged estimates of detection probabilities revealed a high degree of heterogeneity for both males and females as indicated by large differences between the two detection probability estimates for each mixture distribution. The mean detection probabilities (mean= $\pi * \theta_1 + (1 - \pi) * \theta_2$) for males and females (from the 2 distributions) were 0.2 for males and between 0.18-0.23 for females as derived from the estimates in Table 10.

Table 10: Model averaged mixture model detection probabilities for the rub-tree only analysis

Sex	Parameter	session	Estimate	SE	LCI	UCI
both	π		0.14	0.08	0.04	0.39
females	θ_1	1	0.28	0.14	0.09	0.61
	θ_2	1	0.01	0.02	0.00	0.11
	θ_1	4	0.66	0.17	0.30	0.90
	θ_2	4	0.07	0.06	0.01	0.32
males	θ_1	all	0.59	0.16	0.28	0.84
	θ_2	all	0.13	0.12	0.02	0.55

Estimates of superpopulation were imprecise for all models and apparently precise if only non-mixture models were considered (Table 11). It is hard to interpret the mixture model estimates given the low precision, and it is likely the non-mixture model estimates of superpopulation and variance are negatively biased due to heterogeneity variation.

Table 11: Model averaged estimates of superpopulation for the rub tree only analysis. Estimates from all models (mixture and non-mixture) and non-mixture models are given

Sex	M _{t+1}	\hat{N}	SE	CI		cv
All models						
Females	13	30	17.43	16	102	57.4%
Males	15	22	10.82	16	76	48.7%
Total	28	53	18.72	35	121	35.6%
Non-mixture models						
Females	13	16	2.62	14	26	16.4%
Males	15	17	1.59	15	23	9.6%
Total	28	33	3.07	29	43	9.4%

3.3. Telemetry

The telemetry data set consisted of 34 records of 11 females and 10 males. Many bears had repeated yearly measurements. Initially the full data set was used for summaries and then an analysis was conducted on a data set that only included 1 record per individual bear.

Inspection of the residency data (proportion of points on the sampling grid) as a function of distance from northern edge and all edges revealed differences by both sex and whether a bear was a native bear or an augmented (transplant) bear. Relationships were evaluated using estimates of distance from edge using all points (on and off the grid) and points only on the grid. Estimates that used all the points were most likely a better reflection of true spatial location of the bear on the sampling grid, however, these estimates were not equitable to the estimates from DNA bears that could only be sampled on the sampling grid. However, if closure was minimal then it was likely that the difference would be minimal.

For females, residency was close to 1 at distances greater than 10 kilometers from the north or all edges for management and research bears (Figure 3). Augmented bears showed fewer patterns in residency as a function of distance from edge.

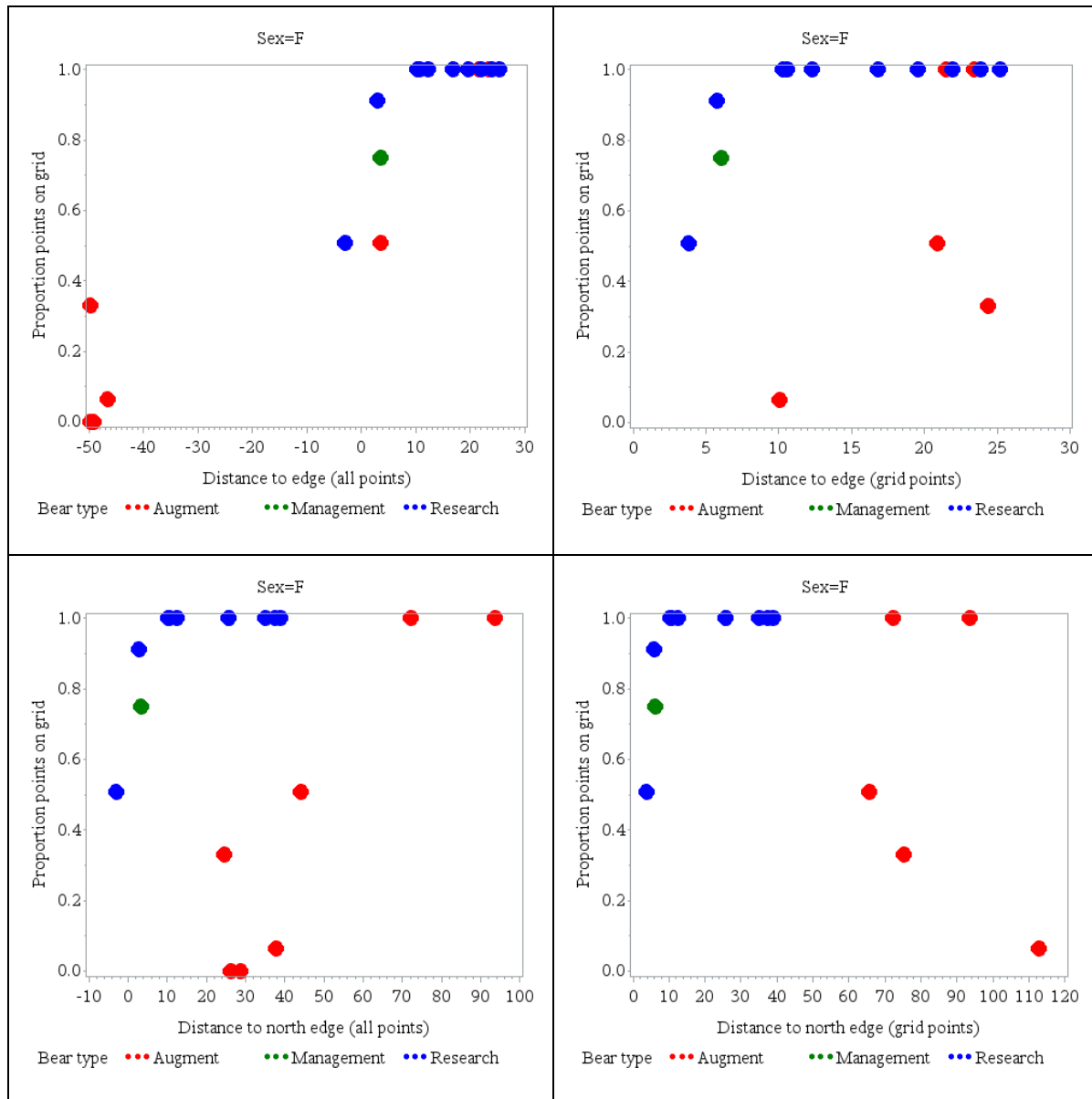


Figure 3: Summary of female radio telemetry bear distances from all edges and the north edge of the sampling grid for mean detection locations using all the telemetry points (left) and only points on the sampling grid (right). For the all telemetry point summaries, distances from edge are shown as negative if the mean detection location was outside of the grid area.

For males, few bears had data points that were closer than 10 kilometers from the grid edge and all research or management bears showed residency of greater than 0.8 (Figure 4). Two data points from augmented bears displayed lower residency compared to management or research bears.

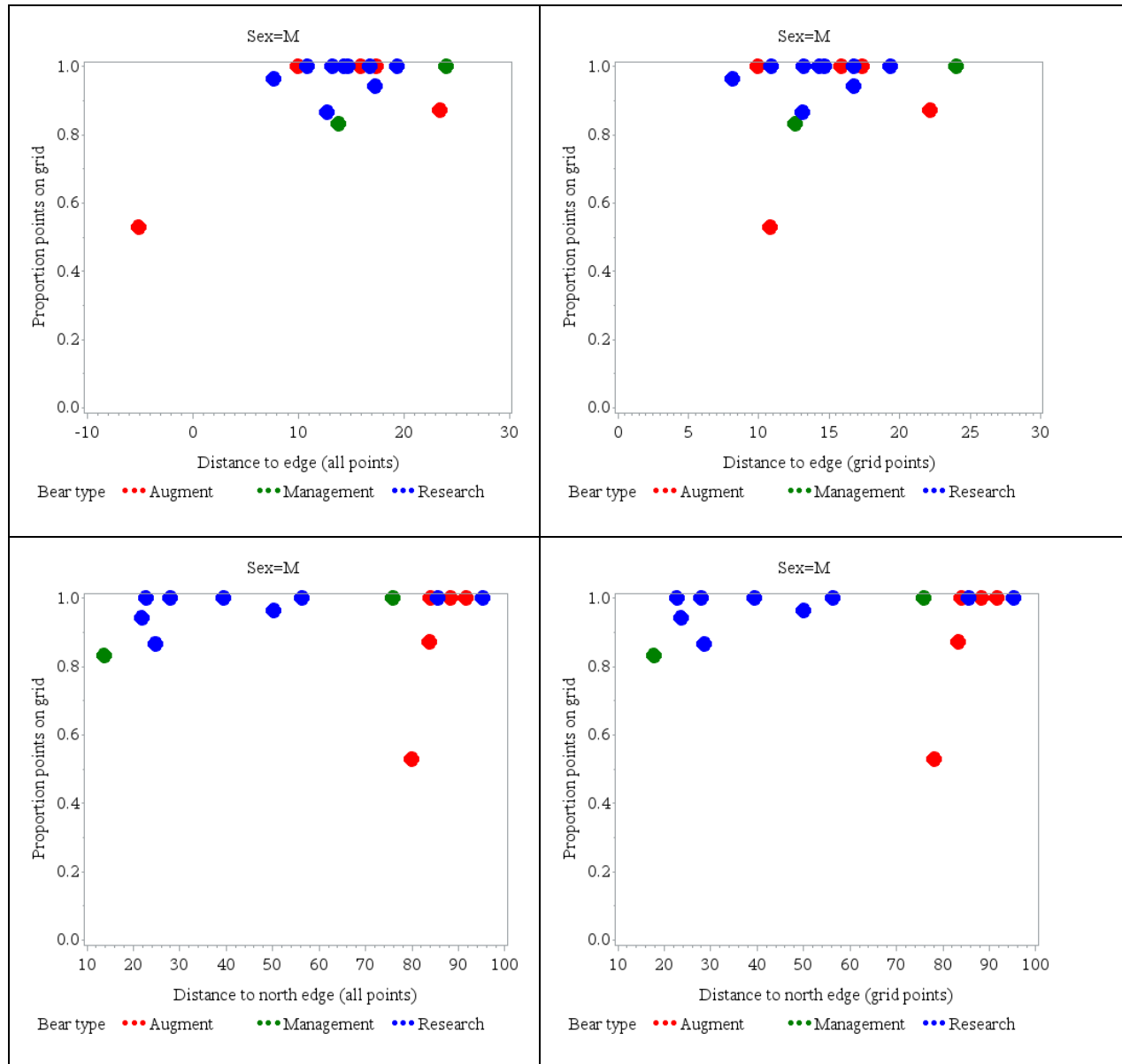


Figure 4: Summary of male radio telemetry bear distances from all edges and the north edge of the sampling grid for mean detection locations using all the telemetry points (left) and only points on the sampling grid (right). For the all telemetry point summaries, distances from edge are shown as negative if the mean detection location was outside of the grid area.

For logistic regression analysis, the mean distance from edge and residency for bears was used for bears that had multiple yearly records. This reduced the data set to 11 females and 10 males. This data set was more acceptable to the Ivan estimator since it did not contain repeated yearly measurements of the same bear. A secondary analysis with the full data set was also conducted (using the repeated measures option in SAS proc GENMOD) to assess the sensitivity of results to reduction in data set size.

For the analysis, the distance from edge calculated using only grid points was used since this data set was equitable with the DNA data set where bears could only be detected on the grid edge. Research bears were pooled with management bears for this analysis since both bear types were bears native to the Cabinet/Yaak. Augment bears were treated as a separate class.

Model selection was focused on fitting sex-specific and specific curves for augmented bears. Initial models with research and augment bears pooled used distance from northern edge as a covariate (Table 12: Models 5-6). Subsequent models that considered augmented and research bears separately suggested sex-specific curves with residency of research bears being associated with distance from northern edge whereas augmented bear residency was most associated with distance from all grid edges (Table 12, Model 1). This general result was intuitive given the low residency values of augmented bears even when bears occurred within the middle areas of the sampling grid.

Table 12: Model selection results for the telemetry stand-alone analysis. One record per bear was used for this analysis. Distance from edge that used only grid points were used for the analysis. dN is distance from the northern edge whereas dAll is distance from all edges. . Akaike Information Criteria (AICc), the difference in AICc values between the i th model and the model with the lowest AICc value (ΔAIC_c), Akaike weights (w_i), number of parameters (K) are presented and log-likelihood are presented

No	Model	AICc	ΔAIC_c	w_i	K	Log-likelihood
1	sex RES: sex*dN AUG: sex*dAll	136.219	0.00	1.00	6	-58.879
2	sex RES: sex*dN AUG: dAll	144.709	8.49	0.00	5	-65.212
3	sex RES: sex*d AUG: sex*dAll	148.375	12.16	0.00	6	-64.957
4	sex RES: sex*dN AUG: sex*dN	282.893	146.67	0.00	5	-134.3
5	sex sex*dN	357.434	221.22	0.00	4	-173.38
6	sex sex*dAll	522.615	386.40	0.00	4	-255.97
7	dN	552.891	416.67	0.00	2	-274.09
8	dAll	655.762	519.54	0.00	2	-325.53
9	sex	560.674	424.46	0.00	2	-277.98

Plots of model 1 predictions suggested that residency for research females was close to 1 at distances greater than 5 kilometer to the northern border whereas augmented females residency did not get close to 1 until distances of greater than 20 kilometers from all borders (Figure 5).

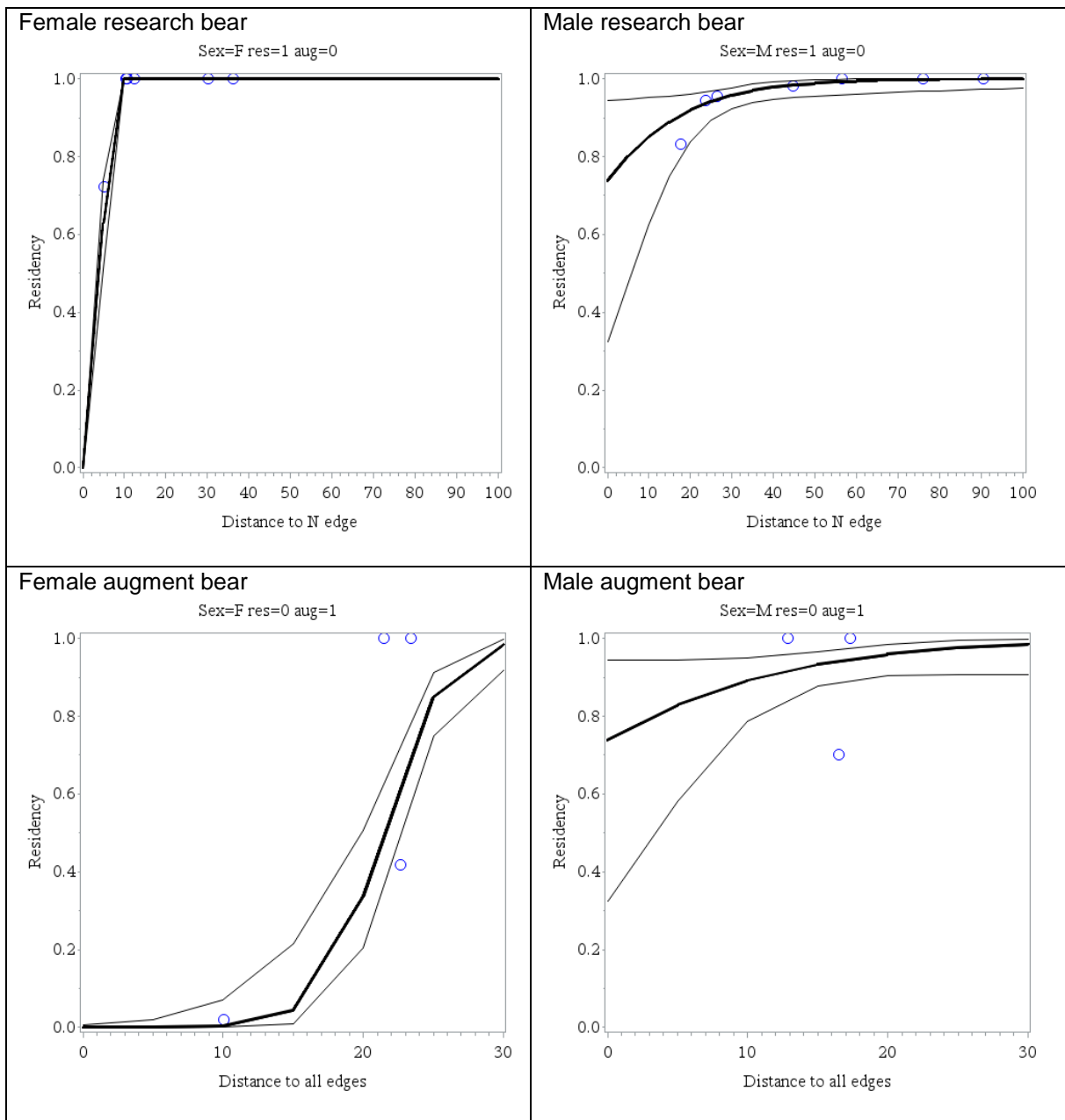


Figure 5: Predicted and observed residency of male and female telemetry bears as a function of sex and whether the bear was a research or a augment bear. Predictions are from Model 1 in Table 12.

The same analysis was conducted for the full data set (with repeated observations for bears) with similar model selection results. The predictions from model 1 for the full data set are shown in Figure 6. From this it can be concluded that reduction of the data set to only include single observations of bears did not substantially impact model selection results or model predictions.

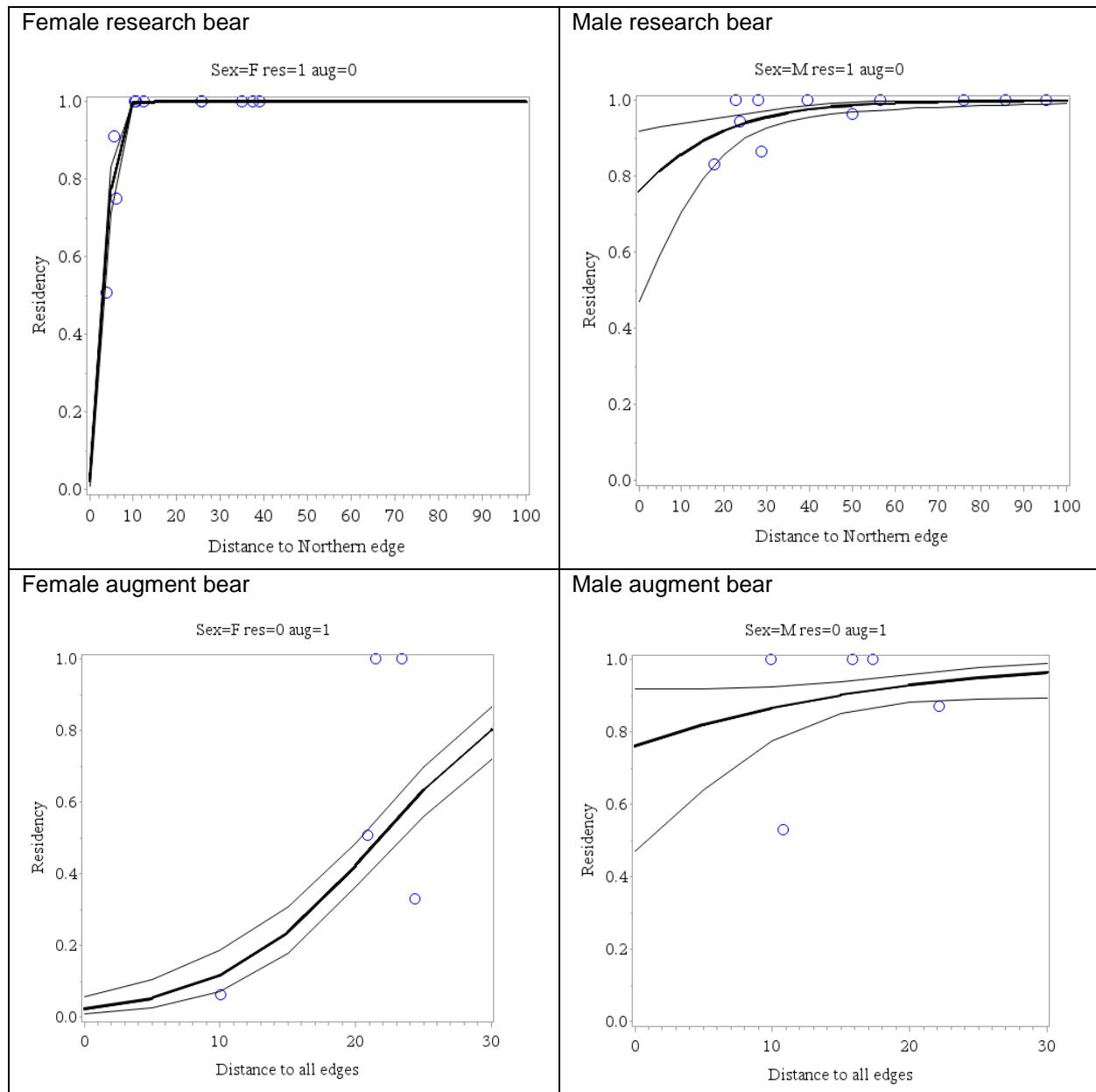


Figure 6: Predicted and observed residency of male and female telemetry bears as a function of sex and whether the bear was a research or a augment bear. The full data set with repeated observations of bears was used for this analysis. Predictions are from Model 1 in Table 12.

The sample size of augmented bears in the telemetry and DNA analysis was low and therefore it was possible that sex-specific augmented bear residency curves may be less supported in the joint analysis model. Therefore specific modelling of augmented bears was revisited in the joint model analysis.

3.4. Joint model analysis

The joint model analysis combined the most supported hair snag (Table 5), rub tree (Table 9) and telemetry (Table 12) models to provide density estimates that utilized all data sources. The main model selection that was pursued for this analysis was fitting of a sex or non-sex specific opportunistic data source model and modelling the detection probability of all DNA bears as a function of distance from grid edge. The distance from grid edge analysis was guided by the results of the telemetry residency analysis that suggested that native bear residency was most related to distance from the northern border whereas augment bear residency was more related to distance from all borders. Plots of the distributions of distance from the northern border for DNA bears showed that no female bears were detected within 9 kilometers of the northern edge compared to males that were detected closer to the northern border (Figure 7). Distance from edge models from simple covariate to threshold models (Kendall et al. 2009) were considered. Threshold models were considered with thresholds at 10 kilometers and beyond given the lack of bears (especially females) detected at distances less than 10 kilometers.

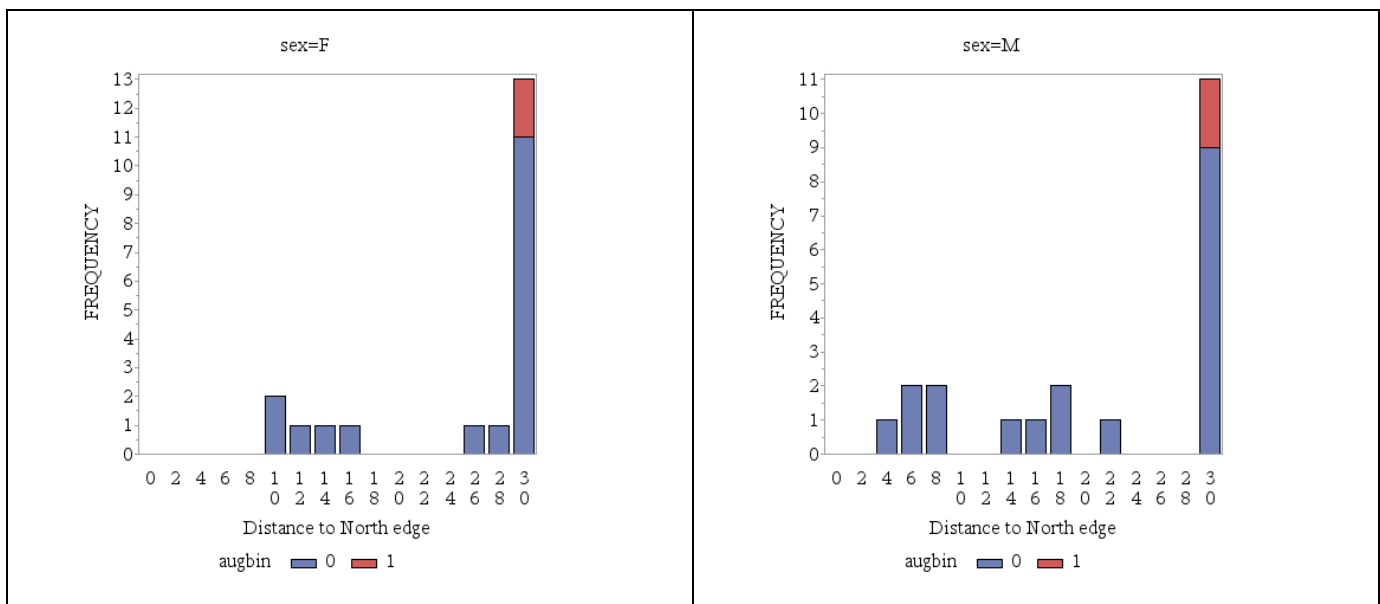


Figure 7: Distance of DNA bears (augbin=0) from the northern grid edge by sex of bear and whether a bear was an augmented bear (augbin=1). The midpoint of each category is shown. The 30 category contains bears with distance from the northern border of 29 or more kilometers.

For this analysis male and female bears for the Cabinet and Yaak were entered as separate groups in MARK to allow sex-specific estimates for both the Cabinet and the Yaak. In most analyses the Cabinet and Yaak data were pooled given that previous hair-snag and rub tree analyses suggested minimal differences in detection

rates between the two areas. Area-specific detection probabilities for each data source (HS, RT, and OP) were tested again as a final step in the model selection analysis to further test the assumption that the geographic area (Cabinet or Yaak) did not influence detection probabilities for each of the data sources. The rationale behind the retesting of the effect of geographic area on data source-specific detection rates was that the power to detect differences in detection rates would be higher when all data sources were considered in a joint model (compared to the stand-alone analyses).

For model selection, the most supported model for each data source was used. For the rub tree model, sex-specific mixture probabilities were used as long as the mixture model provided stable estimates for the joint model analysis. Sex-specific mixtures ensured the most robust estimates from the rub tree mixture model. For the opportunistic models, a model with pooled sex detection probabilities was more supported (Table 13: model 8) than sex-specific detection probabilities (Model 12). For distances to edge, as with the telemetry analysis, a model with distance to north border for DNA bears (Model 14) was more supported than a model with detection probabilities as a function of all borders (Model 19). A model that attempted to model sex-specific detection probabilities for augmented bears as a function of distance from edge did not converge (due to low sample sizes of augmented bears in the analysis) and therefore sexes were pooled for the augment detection rates.

Threshold models were then run for non-augmented bears at intervals of 5 kilometers with various distances for male and female bears. The most supported model (Model 4) pooled detection curves as a function of distance of 15 kilometers from the north border for male and female bears.

One potential issue with the base model was that augmented bears comprised a relatively small proportion of the actual DNA data set (2 males and 2 females). In addition, the number of augmented bears in the radio collar data set was low and therefore it was potentially questionable whether the joint analysis could support sex-specific residency curves or augment-bear specific detection curves. A set of models was run which reduced the models to not include sex-specific residency curves or augment bear specific detection probability curves. Of the models considered, a model with pooled sex augment bear residency curves and augment-bear detection probabilities at constant levels was most supported (Table 13, Model 3). However, models with augment-specific detection curves and sex-specific augment bear residency curves were still supported by the data as indicated by delta AICc values of less than 2.

As a last step, models were introduced that tested whether there were differences in overall detection rates between the Cabinet and Yaak sub-grids for each of the data sources. Models that assumed different RT detection probabilities (Models 1 and 2) for the Cabinets and Yaak were more supported than models with specific Cabinet Yaak detection probabilities for hair snags (Model 10) or opportunistic samples (Model 5). A model with sex-specific detection probabilities for rub trees for the Cabinet and Yaak was most supported (Model 1)

The support of temporal covariates for HS and RT were verified by the low support of model without these covariates(model 21). The support for rub tree mixture models was verified by the low support of a model

without mixtures for rub trees (model 20). The support for a residency model with residency defined by distance from edges was verified by the low support of a model with no covariates for residency (model 22).

Table 13: Model selection results for HS, RT, and telemetry joint mark-recapture model. For distance to edge models, aug indicated augment bears, res indicated native bears and CY indicates separate parameters for the Cabinet and Yaak sub-grids. Threshold models are indicated by subscript distances and sex (M or F). Akaike Information Criteria (AIC_c), the difference in AIC_c values between the i th model and the model with the lowest AIC_c value (ΔAIC_c), Akaike weights (w_i), number of parameters (K) are presented and deviance are presented.

No	HS/RT/Telem model	Opp	Dist to edge (DNA bears)	AIC_c	ΔAIC_c	w_i	K	Deviance
1	Base (AUG: dAll) +RT(CY(sex))		res: dN:MF15	1109.7	0.00	0.169	20	1068.7
2	Base (AUG: dAll) + RT(CY)		res: dN:MF15	1110.8	1.02	0.102	19	1071.8
3	Base (AUG: dAll)	.	res: dN:MF15	1110.8	1.04	0.101	18	1073.9
4	Base	.	res:dN: MF15	1110.9	1.13	0.096	19	1071.9
5	Base (AUG: dAll)	CY	res: dN:MF15	1111.2	1.45	0.082	19	1072.2
6	Base (AUG: dAll)	.	aug:dALL res:dN: MF15	1111.2	1.48	0.081	19	1072.3
7	Base	.	aug:dALL res:dN: MF15	1111.3	1.57	0.077	20	1070.3
8	Base	.		1111.6	1.86	0.067	18	1074.7
9	Base	.	aug:dALL res:DN M15, F10	1112.6	2.86	0.040	21	1069.4
10	Base (AUG: dAll) + HS(CY)		res: dN:MF15	1112.9	3.14	0.035	19	1073.9
11	Base	.	aug:dALL res:dN: MF20	1113.3	3.51	0.029	20	1072.2
12	Base	sex		1113.3	3.55	0.029	19	1074.3
13	Base		aug:dALL res: dN: M20, F10	1113.8	4.02	0.023	21	1070.6
14	Base	.	aug:dALL res:sex*dN	1114.5	4.73	0.016	21	1071.3
15	Base	.	aug:dALL res dN:M25, F15	1114.5	4.80	0.015	21	1071.4
16	Base	.	aug:dALL res:dN	1114.7	4.94	0.014	20	1073.6
17	Base	.	aug:dALL res: dN M30, F20	1115.4	5.67	0.010	21	1072.2
18	Base	.	aug:dALL res:sex* log(dN)	1115.5	5.77	0.009	21	1072.3
19	Base	.	aug:dALL res:sex*dall	1117.3	7.55	0.004	21	1074.1
20	Base (no RT mix model)			1125.2	15.48	0.000	14	1096.7
21	Base (no t covariates)	.		1130.5	20.72	0.000	15	1099.9
22	Base (constant ptilde)			1512.9	403.15	0.000	13	1486.4

^ABase model was HS: $p(\text{sex} + \text{prevcap} + t_{23})$ RT $\pi(\text{sex}) \theta_{1\&2} ((\text{sex}) + t_{123F})$ Telemetry (\tilde{p}) (sex + RES: sex*dN AUG: sex*dAll). See Tables 5, 9, and 12 for details on each of the individual data source models. Any differences from the base model are noted in the HS/RT/Telem model column.

Estimates of detection probability and residency from the most supported model for non-augmented bears are shown in Figure 8. Estimates of residency (\tilde{p}) reflect the stand-alone logistic regression results with both male and female residency being close to 1 after 20 kilometers. Detection probabilities reflect the threshold model results with lower detection rates up to 15 kilometers from the northern edge for both males and females.

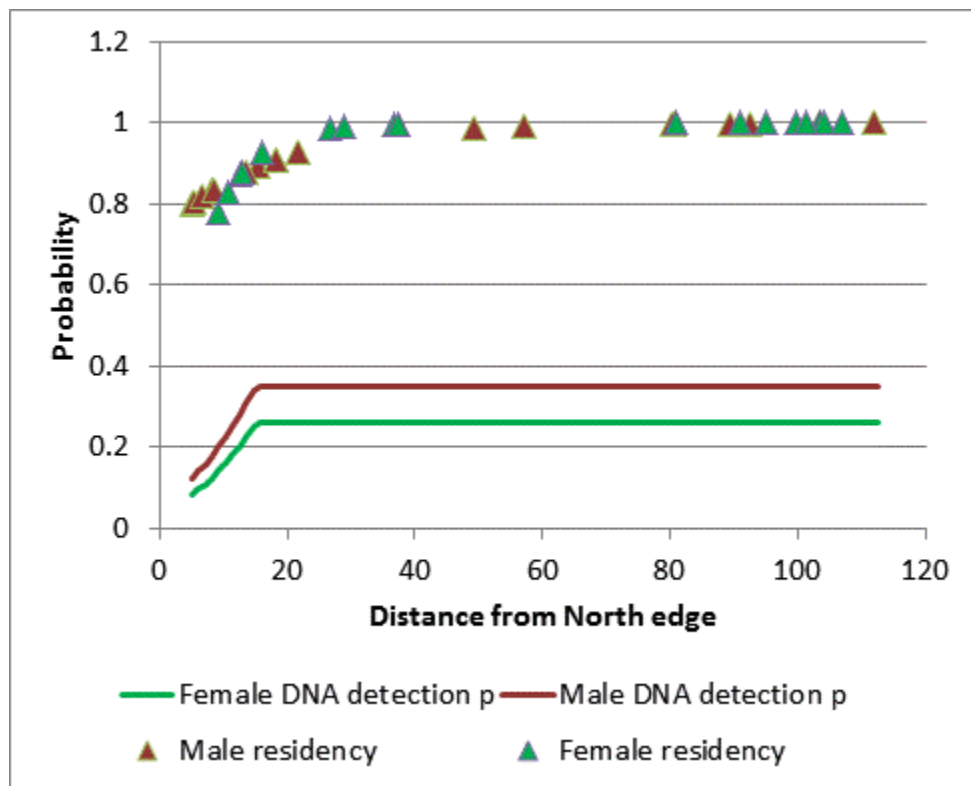


Figure 8: Estimates of residency and detection probability from Model 1 (Table 13) for non-augmented bears detected in DNA sampling. Detection probability estimates are for hair snag session 4. The actual height of the detection probability lines will vary with session and data type. The residency points are based on actual distance data points for DNA bears.

Estimates of detection probability from the joint analysis suggested reasonable detection probabilities across all the data sources (Table 14). When considered across sessions the cumulative coverage (p^*) was high especially for rub trees where 7 sampling sessions were conducted (compared to 5 sessions for hair snags). Male rub tree detection probabilities were slightly higher for the Yaak whereas female detection probabilities were slightly lower. The cumulative detection rates across all data sources (i.e. 7 sessions RT, 5 sessions HS and 1 session OP) was above 0.9 for all sex and area combinations further suggesting that a very high proportion of the population of bears in each of the study area was detected due to the high level of sampling effort (13 sessions of sampling). The large number of sessions in this context basically compensated for low detection rates from any of the single data sources.

Table 14: Model average estimates of average detection probabilities and cumulative detection probability (p^*) across all sampling sessions for models in Table 13. Cabinet and Yaak estimates are given for rub trees.

Hair snag estimates were virtually identical for the Cabinet and Yaak. Ranges of estimates are given for parameters that displayed per session variation (except all data sources)

Data type	Area	sex	Average detection (p)	p^*
Rub trees	Cabinet	F	0.24 (0.11-0.33)	0.86
		M	0.25	0.87
	Yaak	F	0.23(0.11-0.32)	0.86
		M	0.28	0.90
Hair snag	Cabinet/Yaak	F	0.15 (0.05-0.21)	0.57
		M	0.20 (0.075-0.28)	0.68
Opportunistic	Cabinet/Yaak	F	0.26	0.26
		M	0.24	0.24
All data sources	Cabinet	F	0.21	0.96
		M	0.23	0.97
	Yaak	F	0.20	0.95
		M	0.25	0.98

Estimates of density and average population size from the joint model analysis were precise with coefficients of variation below 15% even for sex or area specific estimates (Table 15). Sex-specific estimates for the Cabinet or Yaak were less precise, but CV's were still below 20%. The precision of model averaged estimates was surprising, however, in general all the models listed in Table 13 gave similar density estimates (Appendix 1) leading to minimal variation in estimates due to model estimate variation. The estimate of average numbers of grizzly bears on the grid was 44.2 which was only 2 bears higher than the number of marked bears in the area during sampling (including 1 unknown sex bear not used in the analysis).

Confidence limits for the average number of bears on the sampling grid were estimated assuming a symmetric confidence limit and an asymmetric confidence limit with the lower bound being determined by the minimum number of bears detected on the sampling grid (M_{t+1}). In theory, if closure violation is high, it is possible that there would be less than the minimal number of bears detected on the grid during the course of sampling and therefore use of M_{t+1} as a lower bound on the confidence limit would lead to a biased interval. However, in the case of the Cabinet and Yaak, closure violation was minimal and therefore the use of M_{t+1} as a lower bound probably does not cause excessive bias in the confidence limit. Use of this limit assumes that there were always M_{t+1} bears present on the grid during sampling.

Table 15: Estimates of density (bears per 1000 km²), average population on the sampling grid, and superpopulation from the joint model analysis. Estimates of density for the Cabinet and Yaak are based on grid areas of 5800 km² and 4075 km² respectively. Confidence limits assuming symmetry and that all detected bears were always on the sampling grid (M_{t+1} CI) are given.

Density					Ave \hat{N}		Symmetric CI		M_{t+1} CI		
Sex	\hat{D}	SE	LCI	UCI	Estimate	SE	LCI	UCI	LCI	UCI	CV
<u>Cabinet</u>											
Female	1.85	0.35	1.17	2.53	10.8	2.01	6.8	14.7	10.0	22.9	18.7%
Male	1.93	0.28	1.39	2.48	11.2	1.62	8.0	14.4	10.2	18.8	14.5%
Total	3.79	0.48	2.84	4.73	22.0	2.80	16.5	27.5	20.2	35.5	12.8%
<u>Yaak</u>											
Female	2.69	0.44	1.84	3.54	11.0	1.77	7.5	14.4	10.1	20.4	16.2%
Male	2.77	0.42	1.93	3.60	11.3	1.73	7.9	14.7	11.0	23.0	15.4%
Total	5.46	0.62	4.25	6.66	22.3	2.51	17.3	27.2	22.0	38.8	11.3%
<u>Cabinet + Yaak</u>											
Female	2.20	0.30	1.62	2.78	21.7	2.92	15.9	27.4	20.2	36.9	13.5%
Male	2.28	0.27	1.75	2.80	22.5	2.64	17.3	27.7	21.1	36.5	11.8%
Total	4.48	0.40	3.69	5.26	44.2	3.94	36.5	51.9	42.2	65.1	8.9%

3.5. Estimation of superpopulation

It was possible to derive superpopulation estimates from the Ivan estimator by fixing residency (\tilde{p}) to 1 which essentially turns the Ivan density model into a Huggins closed model. The same set of model run for the joint telemetry estimator were run for this analysis and estimates were model averaged with similar model selection results (Table 16).

Table 16: Model selection results for HS and RT Huggins model. For distance to edge models, aug indicated augment bears, res indicated native bears and CY indicates separate parameters for the Cabinet and Yaak sub-grids. Threshold models are indicated by subscript distances and sex (M or F). Akaike Information Criteria (AIC_c), the difference in AIC_c values between the i th model and the model with the lowest AIC_c value (ΔAIC_c), Akaike weights (w_i), number of parameters (K) are presented and deviance are presented.

No	HS/RT model	Opp	Dist to edge (DNA bears)	AIC_c	ΔAIC_c	w_i	K	Deviance
1	Base +RT(CY(*sex))		res: dN:MF15	505.52	0.00	0.205	15	474.9
2	Base + RT(CY)		res: dN:MF15	506.56	1.05	0.121	14	478.0
3	Base	.	res: dN:MF15	506.61	1.10	0.118	13	480.2
4	Base	CY	res: dN:MF15	506.99	1.48	0.098	14	478.5
5	Base	.	aug:dALL res:dN: MF15	507.03	1.51	0.096	14	478.5
6	Base	.		507.37	1.85	0.081	12	483.0
8	Base	.	aug:dALL res:DN M15, F10	508.28	2.76	0.051	15	477.7
9	Base + HS(CY)		res: dN:MF15	508.68	3.16	0.042	14	480.1
10	Base	.	aug:dALL res:dN: MF20	508.96	3.44	0.037	14	480.4
11	Base	sex		509.04	3.52	0.035	13	482.6
12	Base		aug:dALL res: dN: M20, F10	509.44	3.92	0.029	15	478.8
13	Base	.	aug:dALL res:sex*dN	510.15	4.63	0.020	15	479.5
14	Base	.	aug:dALL res dN:M25, F15	510.22	4.70	0.020	15	479.6
15	Base	.	aug:dALL res:dN	510.39	4.88	0.018	14	481.9
16	Base	.	aug:dALL res: dN M30, F20	511.09	5.57	0.013	15	480.5
17	Base	.	aug:dALL res:sex* log(dN)	511.19	5.67	0.012	15	480.6
18	Base	.	aug:dALL res:sex*dall	512.97	7.45	0.005	15	482.4
19	Base (no RT mix model)			521.12	15.60	0.000	8	504.9
20	Base (no t covariates)	.		526.33	20.81	0.000	9	508.1

^ABase model was HS: $p(\text{sex} + \text{prevcap} + t_{23})$ RT $\pi(\text{sex}) \theta_{1\&2} ((\text{*sex}) + t_{123F})$. See Tables 5 and 9 for details on each of the individual data source models. Any differences from the base model are noted in the HS/RT model column.

This resulted in an estimate of 48 bears on the grid and surrounding area with sex and area specific estimates for the Cabinet and Yaak (Table 17). Population estimates are given with decimal points but can be rounded off to integer form when appropriate. The full grid estimate is similar to the HS only estimate (Table 7: N=46, CI=31-80, CV=25.4%) and rub-tree only estimate (Table 11 N=53, CI=35-121, CV=35.6%) but it is much more precise.

Table 17: Model averaged estimates of superpopulation from the Huggins estimator models in Table 16.

Area/sex	M_{t+1}	\hat{N}	SE	LCI	UCI	CV
<u>Cabinet</u>						
Female	10	12.3	2.26	10.4	21.6	18.4%
Male	10	11.5	1.67	10.3	18.7	14.5%
Total	20	23.8	3.01	20.9	34.9	12.7%
<u>Yaak</u>						
Female	10	11.9	1.79	10.4	19.1	15.1%
Male	11	12.4	1.64	11.2	19.7	13.2%
Total	22 ^a	24.2	2.49	22.4	35.0	10.3%
<u>Cabinet+Yaak</u>						
Female	20	24.1	3.05	21.1	35.0	12.6%
Male	21	23.9	2.45	21.7	33.3	10.3%
Total	42	48.0	4.11	43.8	62.2	8.6%

^aThe confidence limit was calculated assuming a minimum number of alive bears of 22 (including 1 additional bear of unknown sex known to be on the grid but not included in the sex-specific analysis).

3.5.1. Exploratory superpopulation estimates with unknown sex and unknown status bears included

We also conducted exploratory analyses that included 3 bears that were not conclusively detected on the 2012 sampling grid (Ca713M, GB 724, and N323M) to assess estimate sensitivity to inclusion of these bears using the pooled Huggins estimator. These bears were set as detected in the opportunistic sample to therefore allow their inclusion in the analysis. We also ran the analyses with the unknown sex bear (Sibling of 729a) ran as a male and female bear. Distances to the grid edge were unknown for the 3 unknown status bears. To mitigate this issue, mean distances from edge were assigned to these bears based upon the mean values for bears in the Cabinets or the Yaak (dependant on what area they were last observed). This basically allowed these bears to be in the analysis but minimized the actual effect of their distances on the distance from edge model coefficients.

The joint estimator superpopulation models (Table 16) were run and estimates were model averaged (Table 18). The pooled estimate for Cabinet-Yaak increased to 54 bears when the unknown bears were included.

Table 18: Superpopulation Estimates with 2 bears of unknown status, and 1 bear of unknown sex included.

These are model averaged estimates from the models listed in Table 16. M_{t+1} is the unique number of individuals detected in DNA and opportunistic sampling.

Region	Sex	M_{t+1}	\hat{N}	SE	CI		CV
<u>Unknown sex bear is male</u>							
Cabinet	Females	10	12.1	2.16	10.4	21.1	17.8%
	Males	12	15.2	2.76	12.8	25.8	18.1%
	Total	22	27.4	3.84	23.5	40.9	14.0%
Yaak	Females	10	11.6	1.64	10.3	18.4	14.1%
	Males	13	15.2	2.07	13.5	23.5	13.6%
	Total	23	26.9	2.74	24.1	36.5	10.2%
Total	Females	20	23.8	2.81	21.0	33.9	11.8%
	Males	25	30.4	3.67	26.6	43.1	12.0%
	Total	45	54.2	4.93	48.5	69.6	9.1%
<u>Unknown sex bear is female</u>							
Cabinet	Females	10	12.5	2.38	10.5	22.1	19.2%
	Males	12	14.9	2.62	12.7	25.1	17.5%
	Total	22	27.4	3.88	23.5	41.1	14.2%
Yaak	Females	11	13.1	1.94	11.5	20.8	14.8%
	Males	12	13.8	1.85	12.3	21.5	13.4%
	Total	23	26.9	2.76	24.1	36.6	10.2%
Total	Females	21	25.6	3.20	22.3	36.8	12.5%
	Males	24	28.7	3.37	25.3	40.6	11.7%
	Total	45	54.3	4.97	48.5	69.8	9.1%

3.5.2. Estimates of regions-specific superpopulation with pooled Huggins estimator

We ran the data with sessions pooled for each data type through the Huggins estimator (without the Ivan telemetry density estimator) to cross check the joint model estimates. This approach pooled all the session data for each data type which reduced heterogeneity variation but also decreases precision through the loss of replicate sampling sessions. However, it does provide a way to produce a simpler estimate of superpopulation and a way to cross-check the joint model estimates. We mirrored the model selection of the joint model selection (Model 1, Table 13) with detection rates being associated with a threshold distance from the northern edge for the native (non-Augment bears) and with sex-specific detection rates for rub trees in the Cabinets and Yaak. We also entered the Cabinet and Yaak as groups to allow specific superpopulation estimates for each area.

Table 19: Huggins closed joint pooled session model selection. For distance to edge models, res indicated native bears and CY indicates separate parameters for the Cabinet and Yaak sub-grids. Akaike Information Criteria (AIC_c), the difference in AIC_c values between the i th model and the model with the lowest AIC_c value (ΔAIC_c), Akaike weights (w_i), number of parameters (K) are presented and log-likelihood are presented. CY refers to separate parameters for the Cabinet and Yaak subgrids.

Model	AIC_c	ΔAIC_c	w_i	K	Deviance
RT(sex+CY) HS(sex) OS(.)	149.72	0.00	0.232	6	137.0
RT(sex+CY) HS(sex) OS(.) +res: dN:MF15	150.31	0.59	0.173	7	135.3
RT(sex*CY) HS(sex) OS(.)	150.41	0.69	0.164	7	135.4
RT(sex) HS(sex) OS(.)	150.73	1.01	0.140	5	140.2
RT(CY*sex) HS(sex) OS(.) +res: dN:MF15	150.83	1.11	0.133	8	133.6
RT(sex) HS(sex) OS(.) +res: dN:MF15	151.34	1.63	0.103	6	138.6
sex*type	152.73	3.01	0.052	6	140.0
sex*type*region	158.12	8.40	0.003	12	131.3

This resulted in an overall estimate of 47.8 bears which was 0.2 bears less than the joint model analysis. Precision was slightly lower for the pooled model analysis especially for the sex and regions estimates. This difference was most likely due to the fact that the pooled model analysis was less efficient at modelling heterogeneity variation. Region specific estimates suggested relatively equal numbers of bears in the Cabinet and the Yaak. Precision was marginal for female estimates and acceptable for male estimates.

Table 20: Superpopulation estimates from the Cabinet and Yaak pooled Huggins analysis. M_{t+1} is the unique number of individuals detected in DNA and opportunistic sampling.

Sex	M_{t+1}	\hat{N}	SE	CI		CV
<u>Cabinet</u>						
Males	10	11.0	1.3	10	17	11.7%
Females	10	13.4	3.2	11	26	23.8%
Total	20	24.4	3.6	21	38	14.8%
<u>Yaak</u>						
Males	11	11.5	0.8	11	16	7.1%
Females	10	12.0	2.0	10	20	16.6%
Total	22	23.4	2.2	22	34	9.4%
<u>Total (Cab+Yaak)</u>	42	47.8	4.5	44	64	9.5%

^AOne unknown sex bear was in the Yaak during the analysis. This was not included in the analysis but was considered when estimating the confidence limits for the Yaak pooled sex estimate.

4. Discussion

In point form:

- This analysis demonstrates the utility of joint models with data sets from small populations. Each of the stand-alone data source estimates were imprecise with CV's > 20%. However, when combined the joint estimate CV was 9%. Sex-specific estimates for the Yaak and Cabinet with reasonable precision were also generated using this approach. This is similar to a study of (Gervasi et al. 2012) which used multiple data sources to get precise estimates of a similar sized population of bears in Italy.
- The similarity of the average N and superpopulation estimate is not too surprising given that the residency model suggested that the only open border was the northern border and residency was reasonably high after 10-15 kilometers from the border (Figures 5 and 8). If this is considered in unison with the distribution of non-augment bears (Figure 7) then it becomes clear that the majority of bears had residency values of 1.
- Detection probabilities for each data source were relatively high (Table 14) when evaluated across all the data sources which resulted in minimal differences in estimates regardless of underlying detection probability model as noted by the similarity of estimates from all the models in Appendix 1. Basically, sampling was highly effective given that 13 sessions of sampling were conducted (when all data sources are put together). As a result, the vast majority of bears were detected. In fact, if p^* is calculated across all data sources it ends up being 0.95-0.96 for females and 0.97-0.98 for males (Table 14).
- Spatially explicit methods should be considered for this analysis. They could account better for uneven rub tree coverage and the irregular augmented bear home ranges/residency (especially if telemetry data is also used to model sigma). Theoretically, spatially explicit methods can account for uneven distributions (Efford and Fewster 2012), however, modelling the boundaries of the grid and density gradients at the edge of the grid may be challenging (Royle et al. 2013). It will be interesting to see how estimates compare to those in this paper.

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6. Appendix 1—Model averaged density and average population size estimates for Cabinet and Yaak from models listed in Table 13

6.1. Cabinet males

<u>Cabinet Males</u>						
No	HS/RT/Telem model	Opp	Distedge DNA	Weight	Density	ave N
1	Base (AUG: dAll) + RT(C/Y{sex})		res: dN:MF15	0.169	2.03	11.78
2	Base (AUG: dAll) + RT(C/Y)		res: dN:MF15	0.102	1.98	11.49
3	Base (AUG: dAll)	.	res: dN:MF15	0.101	1.93	11.17
4	Base	.	res:dN: MF15	0.096	1.93	11.17
5	Base (AUG: dAll)	C/Y	res: dN:MF15	0.082	1.95	11.32
6	Base (AUG: dAll)	.	aug:dALL res:dN: MF15	0.081	1.88	10.93
7	Base	.	aug:dALL res:dN: MF15	0.077	1.88	10.92
8	Base	.		0.067	1.86	10.76
9	Base	.	aug:dALL res:DN M15, F10	0.040	1.88	10.88
10	Base (AUG: dAll) + HS(C/Y)		res: dN:MF15	0.035	1.93	11.18
11	Base	.	aug:dALL res:dN: MF20	0.029	1.85	10.74
12	Base	sex		0.029	1.87	10.84
13	Base		aug:dALL res: dN: M20, F10	0.023	1.85	10.72
14	Base	.	aug:dALL res:sex*dN	0.016	2.06	11.95
15	Base	.	aug:dALL res dN:M25, F15	0.015	1.85	10.74
16	Base	.	aug:dALL res:dN	0.014	1.92	11.11
17	Base	.	aug:dALL res: dN M30, F20	0.010	1.88	10.92
18	Base	.	aug:dALL res:sex* log(dN)	0.009	1.94	11.23
19	Base	.	aug:dALL res:sex*dall	0.004	1.87	10.85
20	Base (no RT mix model)			0.000	1.77	10.25
21	Base (no t covariates)			0.000	1.87	10.82
Weighted average					1.93	11.21
Unconditional SE					0.40	1.62

6.2. Yaak Males

Yaak Males

No	HS/RT/Telem model	Opp	Distedge DNA	Weight	Density	ave N
1	Base (AUG: dAll) + RT(C/Y(sex))		res: dN:MF15	0.169	2.71	11.03
2	Base (AUG: dAll) + RT(C/Y)		res: dN:MF15	0.102	2.77	11.27
3	Base (AUG: dAll)	.	res: dN:MF15	0.101	2.85	11.60
4	Base	.	res:dN: MF15	0.096	2.65	10.81
5	Base (AUG: dAll)	C/Y	res: dN:MF15	0.082	2.81	11.47
6	Base (AUG: dAll)	.	aug:dALL res:dN: MF15	0.081	3.05	12.45
7	Base	.	aug:dALL res:dN: MF15	0.077	2.84	11.56
8	Base	.		0.067	2.59	10.56
9	Base	.	aug:dALL res:DN M15, F10	0.040	2.89	11.77
10	Base (AUG: dAll) + HS(C/Y)		res: dN:MF15	0.035	2.84	11.59
11	Base	.	aug:dALL res:dN: MF20	0.029	2.72	11.09
12	Base	sex		0.029	2.61	10.64
13	Base		aug:dALL res: dN: M20, F10	0.023	2.81	11.46
14	Base	.	aug:dALL res:sex*dN	0.016	2.51	10.25
15	Base	.	aug:dALL res dN:M25, F15	0.015	2.70	10.99
16	Base	.	aug:dALL res:dN	0.014	2.53	10.32
17	Base	.	aug:dALL res: dN M30, F20	0.010	2.63	10.72
18	Base	.	aug:dALL res:sex* log(dN)	0.009	2.59	10.55
19	Base	.	aug:dALL res:sex*dall	0.004	2.59	10.57
20	Base (no RT mix model)			0.000	2.46	10.03
21	Base (no t covariates)			0.000	2.59	10.57
Weighted average					2.77	11.27
Unconditional SE					0.42	1.73

6.3. Cabinet Females

<u>Cabinet Females</u>						
No	HS/RT/Telem model	Opp	Distedge DNA	Weight	Density	ave N
1	Base (AUG: dAll) + RT(C/Y(sex))		res: dN:MF15	0.169	1.85	10.72
2	Base (AUG: dAll) + RT(C/Y)		res: dN:MF15	0.102	1.95	11.31
3	Base (AUG: dAll)	.	res: dN:MF15	0.101	1.88	10.92
4	Base	.	res:dN: MF15	0.096	1.88	10.90
5	Base (AUG: dAll)	C/Y	res: dN:MF15	0.082	1.93	11.19
6	Base (AUG: dAll)	.	aug:dALL res:dN: MF15	0.081	1.79	10.38
7	Base	.	aug:dALL res:dN: MF15	0.077	1.79	10.36
8	Base	.		0.067	1.82	10.56
9	Base	.	aug:dALL res:DN M15, F10	0.040	1.80	10.43
10	Base (AUG: dAll) + HS(C/Y)		res: dN:MF15	0.035	1.89	10.94
11	Base	.	aug:dALL res:dN: MF20	0.029	1.78	10.35
12	Base	sex		0.029	1.79	10.41
13	Base		aug:dALL res: dN: M20, F10	0.023	1.81	10.47
14	Base	.	aug:dALL res:sex*dN	0.016	1.80	10.44
15	Base	.	aug:dALL res dN:M25, F15	0.015	1.79	10.39
16	Base	.	aug:dALL res:dN	0.014	1.92	11.11
17	Base	.	aug:dALL res: dN M30, F20	0.010	1.78	10.34
18	Base	.	aug:dALL res:sex* log(dN)	0.009	1.79	10.39
19	Base	.	aug:dALL res:sex*dall	0.004	1.82	10.56
20	Base (no RT mix model)			0.000	1.70	9.87
21	Base (no t covariates)			0.000	1.86	10.81
Weighted average					1.85	10.75
Unconditional SE					0.49	2.01

6.4. Yaak females

Yaak Females

Model no	HS/RT/Telem model	Opp	Distedge DNA	Weight	Density	ave N
1	Base (AUG: dAll) +RT(C/Y(sex))		res: dN:MF15	0.169	2.73	11.13
2	Base (AUG: dAll) + RT(C/Y)		res: dN:MF15	0.102	2.57	10.49
3	Base (AUG: dAll)	.	res: dN:MF15	0.101	2.68	10.93
4	Base	.	res:dN: MF15	0.096	2.69	10.95
5	Base (AUG: dAll)	C/Y	res: dN:MF15	0.082	2.62	10.69
6	Base (AUG: dAll)	.	aug:dALL res:dN: MF15	0.081	2.78	11.33
7	Base	.	aug:dALL res:dN: MF15	0.077	2.79	11.36
8	Base	.		0.067	2.73	11.13
9	Base	.	aug:dALL res:DN M15, F10	0.040	2.61	10.62
10	Base (AUG: dAll) + HS(C/Y)		res: dN:MF15	0.035	2.68	10.91
11	Base	.	aug:dALL res:dN: MF20	0.029	2.79	11.37
12	Base	sex		0.029	2.69	10.94
13	Base		aug:dALL res: dN: M20, F10	0.023	2.61	10.62
14	Base	.	aug:dALL res:sex*dN	0.016	2.69	10.96
15	Base	.	aug:dALL res dN:M25, F15	0.015	2.64	10.76
16	Base	.	aug:dALL res:dN	0.014	2.63	10.70
17	Base	.	aug:dALL res: dN M30, F20	0.010	2.67	10.88
18	Base	.	aug:dALL res:sex* log(dN)	0.009	2.66	10.83
19	Base	.	aug:dALL res:sex*dall	0.004	2.65	10.79
20	Base (no RT mix model)			0.000	2.52	10.27
21	Base (no t covariates)			0.000	2.71	11.06
Weighted average					2.69	10.97
Unconditional SE					0.44	1.77