

# Estimates of population size and density of black bears from the 2014 South Jasper National Park DNA mark-recapture inventory



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## 1. Abstract

This is a report of a spatially explicit mark-recapture estimation of black bears in south Jasper National Park based on DNA sampling that occurred during the summer of 2014. The field sampling for this project was completed in conjunction with a grizzly bear DNA mark recapture project for south Jasper National Park and Alberta Bear Management Area 3 (Stenhouse et al 2015). For this project, a 7 x 7 km grid design was used. Grid cells were only sampled if the centroid intersected bear habitat (defined as areas below 2000 meters elevation that were not rock or ice). Hair snag corrals were installed in each sampled cell, but some cells were also sampled with associated rub trees. Detection data were categorized into 5 sampling sessions that occurred from late May to mid-August. Overall, 93 bears (45 females, 48 males) were detected during the DNA inventory project in the south Jasper National Park area. Most bears were detected at 1 to 3 unique sites during the survey. Analyses were conducted separately for males and females due to likely differences in movements and detection rates. Males and females displayed distinct detection rates with respect to rub trees and hair snags. Males displayed different movement patterns for hair snags and rub trees, and movement of males changed after initial detection. Females displayed a constant scale of movement. Estimates of expected population size were 77.7 (CI=57.4-105.2) for females and 51.5 (CI=39.8-66.6) for males. The estimate for males and females combined was 129.7 (CI=105.2-160) with a resulting habitat area based density estimate of 29.73 (CI=24.1-36.7) bears per 1,000 km<sup>2</sup>. Note that this estimate is based on a sampling scheme (habitat area of 4,335 km<sup>2</sup>, and a 7 x 7 km sampling grid) that was designed for grizzly bears. The results of this study suggest that estimates of black bears are possible even when the spacing of detectors is relatively large compared to a black bear's home range and movements.

## 2. Introduction

This report describes a spatially explicit mark-recapture population estimate of black bears in south Jasper National Park based on DNA sampling that occurred during the summer of 2014. Recent advances in spatially explicit mark-recapture methods (SECR) can produce more robust population estimates (Efford and Fewster 2013) by modelling the layout of detectors as well as bear movements and detection rates.

This black bear study was conducted in conjunction with a grizzly bear population estimate on the same study area (Stenhouse et al. 2015). There was no intent, initially, to conduct a black bear population estimate, however during the field work we collected a lot of black bear hair in addition to the grizzly bear hair. Also, Jasper National Park recorded an unusual number of black bear mortalities in 2014 (mostly occurring on the highway and railway, but also two management destructions). Concern over the mortalities and availability of samples convinced us to take advantage of the situation and calculate a black bear population estimate.

The Jasper and accompanying Alberta Bear Management Area 3 (BMA 03) project was designed to take advantage of spatially explicit modelling (Boulanger and Efford 2014). In particular, sampling intensity was varied by geographic area based on management objectives, habitat, and logistic challenges. In addition, areas of non-habitat were sampled with lower intensity and effort was reallocated to areas of contiguous habitat.

## 3. Methods

### 3.1. Study area

South Jasper National Park (JNP) consists of the region south of Highway 16 from the British Columbia border in the west to the JNP park boundary in the east, and south to Highway 11 at the Banff National Park boundary. Elevation ranged from 880m to 3,365m and included a diversity of habitats. Sub-alpine areas consisted primarily of Engelmann spruce (*Picea engelmannii*) and sub-alpine fir (*Abies lasiocarpa*) whereas upland forests consisted of aspen (*Populus tremuloides*), white spruce (*Picea glauca*), and open stands of lodgepole pine (*Pinus contorta*). Lowland forests were characterized by mixed forests of black spruce (*Picea mariana*), tamarack (*Larix laricina*), and lodgepole pine while wetlands and riparian areas were dominated by willow (*Salix spp.*) and shrub-graminoid communities. Important bear foods occurring in the study area include buffaloberry (*Shepherdia canadensis*), alpine sweet vetch (*Hedysarum alpinum*), cow parsnip (*Heracleum lanatum*), and various blueberry species (*Vaccinum spp.*). Other large predators include grizzly bears (*Ursus arctos*), wolf (*Canis lupus*), and cougar (*Puma concolor*). JNP hosts a number of recreational activities along the two major highway corridors (Highways 16 and 93), and the town site of Jasper occurs at the junction of the Athabasca and Miette river valleys. The majority of the park is not accessible by either road or trail (Stenhouse et al. 2015).

### 3.2. Study design

Spatially explicit mark-recapture models parameterize the movement of black bears on the sampling grid as well as the layout of sites within the sampling grid. Therefore, this approach is robust to heterogeneity of detection rates caused by trap layout relative to bear home ranges and as a result “holes” in trap coverage are allowed (Efford and Fewster 2013). In addition, edge effects and closure violation are not a biasing factor and therefore radio-collar based corrections

of estimates are not needed. However, the SECR approach relies on estimating average density across a known region of interest (South Jasper National Park). Therefore, every part of this region should have a known, non-zero chance of being sampled with a hair snare or rub tree to ensure unbiased estimates. Subsequently, a sampling design exercise was undertaken for Jasper National Park and BMA 03 to ensure a random representative sample of bear habitat Jasper National Park while optimizing sampling for areas of likely bear occurrence (Boulanger and Efford 2014). The sampling design was intended for grizzly bears, however we hoped it would prove to be adequate for black bears as well.

Jasper National Park contains substantial areas of rock and ice which were not considered suitable habitat for grizzly or black bears (Figure 1). This area, as defined by barren land cover above 2000m, was not considered for site placement in the design of the Alberta BMA 3 and Jasper National Park project (Boulanger and Efford 2014). The total area of south Jasper National Park was 7,899 km<sup>2</sup> of which 3,564 km<sup>2</sup> was barren land cover at greater than 2000 m elevation. This resulted in 4,335 km<sup>2</sup> of habitat area within the park used for SECR based sampling and analysis.

For the Jasper and BMA 03 grizzly bear study, a 7 x 7 km grid was overlaid on the Jasper Park area. Only cells in which the centroid intersected bear habitat received a single hair snag site.

This approach resulted in a random sample of sites with a probability of selection of each cell for a site weighted by proportion of habitat area in each cell (Boulanger and Efford 2014). A subset of cells also contained rub trees that were near the hair snag sites.

In some cases, cells that were chosen during the design process did not end up being sampled due to logistical constraints. Most notably, two valleys in the vicinity of the Columbia Icefields in the south and southwestern portion of Jasper Park did not receive sites (Figure 1). As discussed later, this will not necessarily bias estimates if it can be

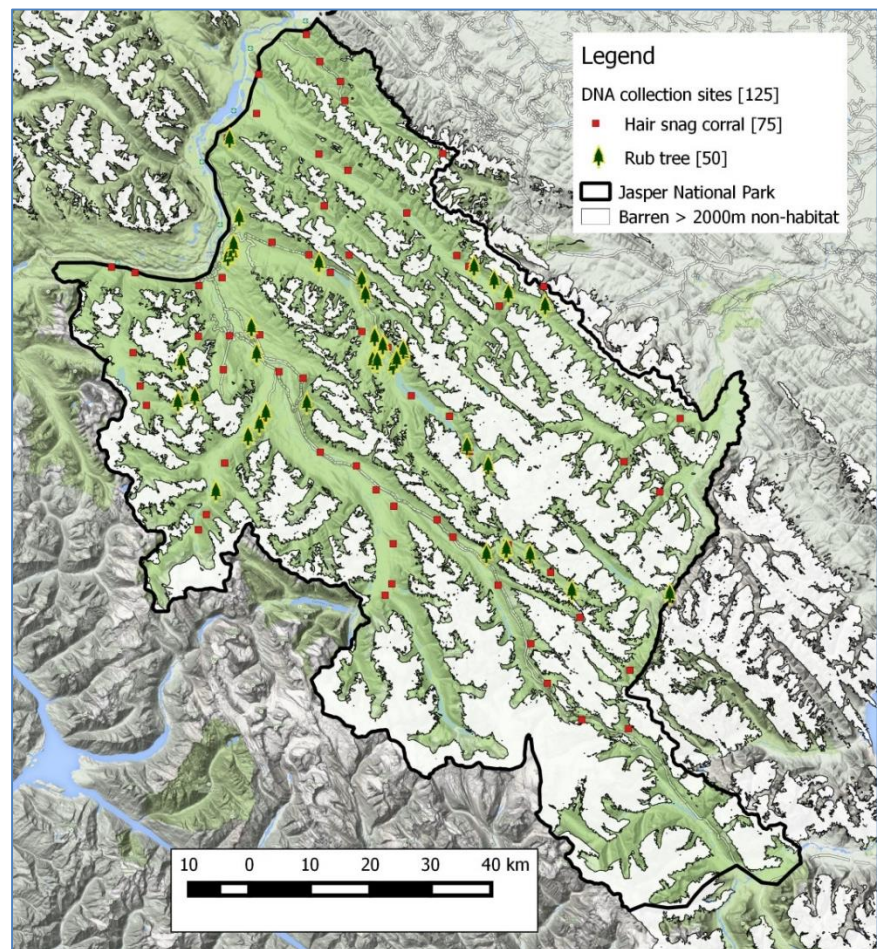


Figure 1. The south Jasper National Park study area with hair snag and rub trees detectors. The number of detectors is given in brackets.

assumed that densities of bears in the area of these sites was similar to other areas in the study area.

### 3.3. Field and genetic methods

Field methods for hair snags followed the protocols outlined in previous studies (Woods et al. 1999, Proctor et al. 2010) of grizzly bears. Rub tree locations were either previously mapped by Parks Canada staff (n=25) or found during the 2014 field season by Foothills Research Institute research staff (n=25). Rub trees were set up with a zig-zag “Z” formation of barbed wire on the rubbed surface using 4 strands of barbed wire with 3 barbs each, positioning the first three wires to cover as much of the rubbing surface as possible. The fourth strand was placed below the zig-zag at a height of approximately 25cm as a “cub rub”. Rub trees were not baited with scent lure (Stenhouse et al 2015). Hair samples were sent to Wildlife Genetics International (Nelson, BC). Genetic methods followed the protocols developed for grizzly bears (Paetkau 2003) as further detailed in Stenhouse et al (2015).

### 3.4. Estimation methods

Spatially explicit capture-recapture (SECR) is a recently developed method for estimating animal density on geographically open study areas (Borchers and Efford 2008) (Efford et al. 2004, Borchers and Efford 2008, Gardner et al. 2009). Traditional capture/recapture methods are prone to bias depending on how the study area is defined, but SECR estimates density as the intensity of points that are unobserved central locations of animal home ranges. SECR does assume demographic closure. The simplest SECR model has two parameters: the detection probability at home range center, or ( $g_o$ ); and the spatial scale of animal movement around that home range center, or ( $\sigma$ ). The detection probability ( $g_o$ ) can be thought of as the probability of detection if a trap had been placed at the spatial center of the animal’s home range. Spatial scale around home range center ( $\sigma$ ) can be thought of as the distance between home range center and the sampling site. Spatial scale ( $\sigma$ ) plus the shape of the detection probability function describes how detection probability declines with distance between home range center and the trap (Efford et al. 2004, Howe et al. 2013). SECR uses ( $g_o$ ), ( $\sigma$ ), and the shape of probability function to estimate animal density.

Both ( $g_o$ ) and ( $\sigma$ ) can be described as functions of covariates. An assumption of this method is that black bear home range can be approximated by a circular symmetrical distribution of use (Efford 2004). By using the shape and configuration of the sampling grid in the process of estimating parameters, we could examine the effect of study-area size and trap configuration on closure violation and density estimates.

For our study, model selection efforts considered likely individual, temporal, and behavioural variation in both detection at home range center ( $g_o$ ) and spatial scale of black bear movements ( $\sigma$ ) around the home range center. The main types of variation modelled with associated symbols are listed in Table 1. In addition, rub tree and hair snag specific detection rates as well as scale of movement relative to detector type was considered. The support of models was evaluated using information theoretic model selection methods (Burnham and Anderson 1998).

Spatially explicit methods utilize a ‘mask’ to estimate density with the size of the mask being equal to the sampling area and the surrounding area where bears traverse over the course of sampling. An initial analysis was conducted to estimate the size of the mask (relative to study



area size) needed to minimize bias in density estimates. The `esa.plot` and `suggest.buffer` functions in program `secr` were run for male and female bear specific models. From this analysis, a buffer width of 16 km was chosen to minimize bias in density estimates. Mask centroids were spaced at 1 kilometer for all analyses. A sensitivity analysis of mask spacing suggested minimal change in estimates for mask spacings from 500 meters to 3 kilometers. The one kilometer spacing allowed reasonable computation times (less than 1 hour) for any given SECR model.

Expected population size and density estimates were estimated by all the SECR models. Expected population size is the expected number of bears that would be contained within the study area or regional area at one time (Efford and Fewster 2013). Density is then estimated as the expected number of black bears divided by the entire area of the grid, or the habitat area within the grid. Log based confidence intervals of expected population size and density were generated using formulas from Efford and Fewster (2013). All spatially explicit analyses were done in program `secr` (Efford 2014b) in the R statistical package (R\_Development\_Core\_Team 2009). In addition, data was screened using program DENSITY (Efford et al. 2004). The main screening procedure involved checking distances between repeated detections of individual bears to double check that any longer distance movements of individuals were not due to data entry or genotyping errors. Map figures were produced using program QGIS (QGIS\_Foundation 2015).

Table 1: Summary of spatially explicit model types and parameter symbols used for the black bear analysis.

Symbol	Definition
t	Temporal variation
T	Linear trend in parameters
h <sub>2</sub>	Undefined heterogeneity
b	Change in parameter after initial detection
B	Change in parameter based on detection in the previous session
HS	Hair Snag
RT	Rub Tree
(.)	Denotes parameter that was held constant
b <sub>HS</sub>	Denotes a behavioural response for hair snags with change in parameter after initial detection
B <sub>HS</sub>	Denotes a behavioural response for hair snags with change in parameter based on previous session

### 3.5. Adjustment of sessions

The original study design called for four consistent sampling sessions. We discovered however, that the start dates for sampling had to be changed in conjunction with elevation because of differences in snowmelt. Snowmelt at some sites was so late that we could not complete four sessions for all sites (Figure 2).

In the original data the sessions for each site were numbered sequentially (Figure 3). This created a potential issue for modelling temporal change in detection probabilities and behavioural responses based on seasonality. We therefore recoded the session numbers to reflect discrete sampling periods, which resulted in five synchronized sessions (Figure 4 and Table 2), however no one site was visited more than four times. X-matrices were formulated for each site to inform the SECR model as to when sites were operational.

Sampling in August (berry season) is not desirable – visits to lure sites can decrease because of the abundance of berries. In our case, however, the later sites were high in elevation where berry ripening is also late.

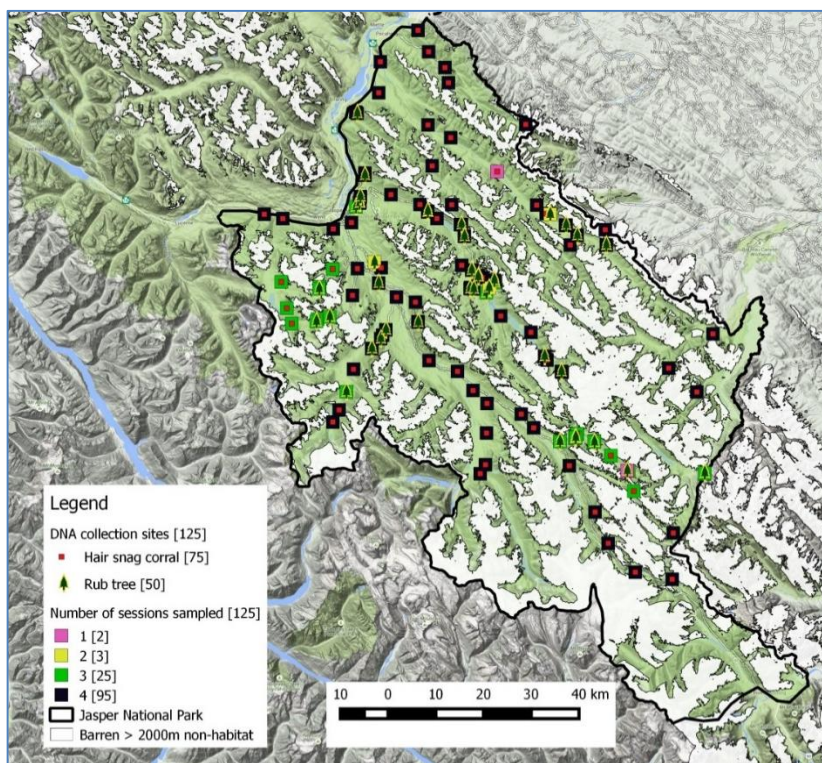


Figure 2. Study area sample sites, including number of sampling sessions for each site. Barren areas above 2000m are highlighted..

Table 2: Dates of sessions and the number of active sites per session

Session	Dates		Number of sites active		
	Start	End	Hair snag	Rub tree	Total
1	May 26, 2014	June 19, 2014	32	21	53
2	June 20, 2014	July 5, 2014	63	39	102
3	July 6, 2014	July 18, 2014	74	48	122
4	July 19, 2014	August 1, 2014	74	48	122
5	August 2, 2014	August 15, 2014	42	23	65

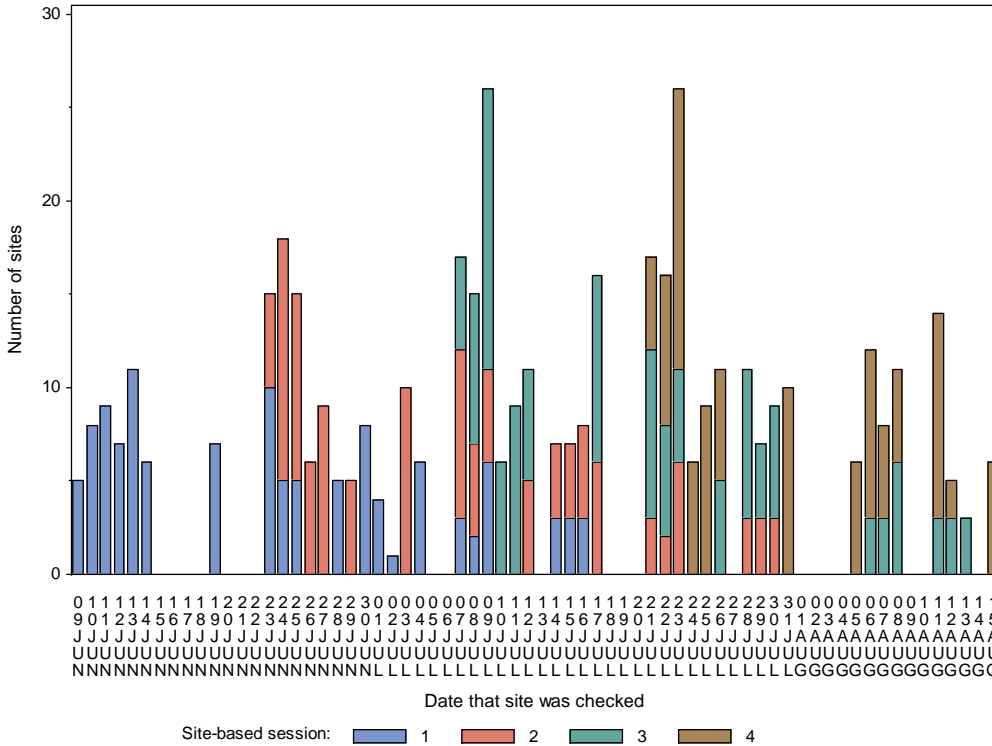


Figure 3. Original session numbers. Sessions were defined by the initial sampling date for each site.

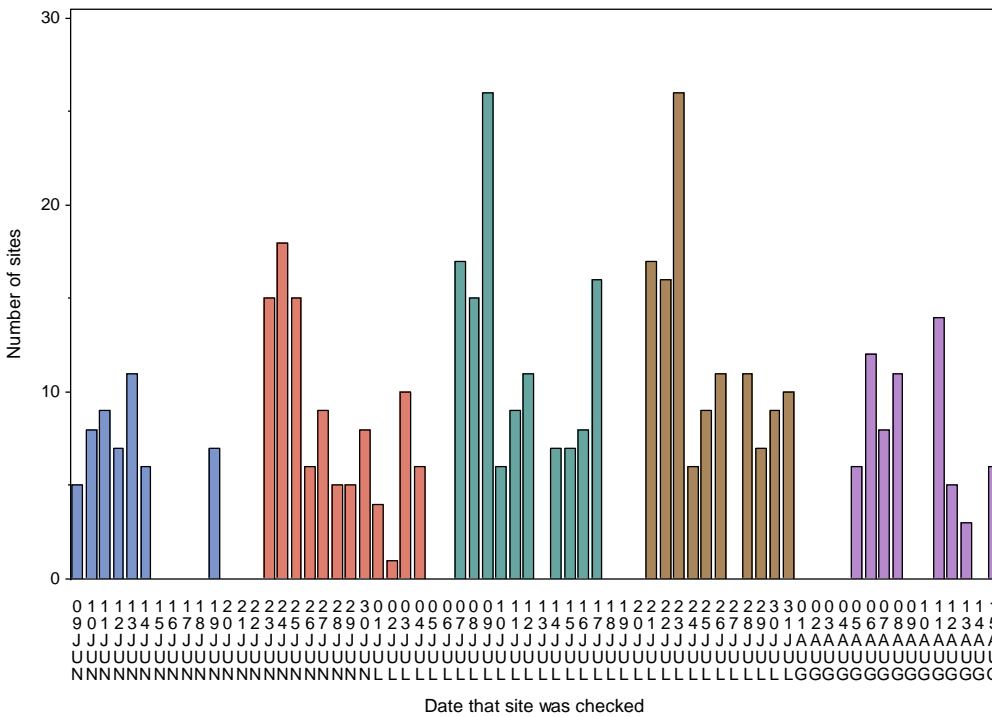


Figure 4. Recoded session numbers to reflect temporal clustering of site checks. Sessions are defined by the temporal cluster of site checks. The recoding resulted in the creation of a 5<sup>th</sup> session.

## 4. Results

### 4.1. Summary

Overall, 93 bears (45 females, 48 males) were detected during the study (Figure 5). Mean detection locations revealed a large number of detections in sites near the Jasper town site, Maligne Lake Road, Miette Hotspings Road and Athabasca Valley highway corridor with lesser frequencies in the more remote sites. This contrasts with grizzly bear detections that mainly occurred in the more remote sites (Stenhouse et al. 2015).

The majority of detections occurred at hair snag sites with the most detections occurring in sessions 2 and 3 (Figure 6). The number of active sites was reduced in sessions 1 and 5 (Table 2) which may have affected the number of bears detected. Our spatially explicit models can estimate temporal trends in detection while accounting for the number of active sites.

A relevant issue is the number of detections, including visits to multiple sites within a single session. For spatially explicit modelling, bears need to visit more than one site over the duration of sampling to facilitate estimation of movements. The distribution of unique detections including visits to the same site across multiple sessions suggested that female bears were detected up to 3 times whereas males were detected up to 5 times with 26 females and 17 males being detected more than once (Figure 7, left). This resulted in 62 redetections for males and 53 redetections for females. If only visits to unique sites are considered (sessions pooled) then it can be seen that the majority of bears visited a single site with 13 females and 14 males visiting more than a single site (Figure 7; right) resulting in 26 redetections for males and 32 redetections for females. The majority of rub tree visits were to a single rather than multiple sites.

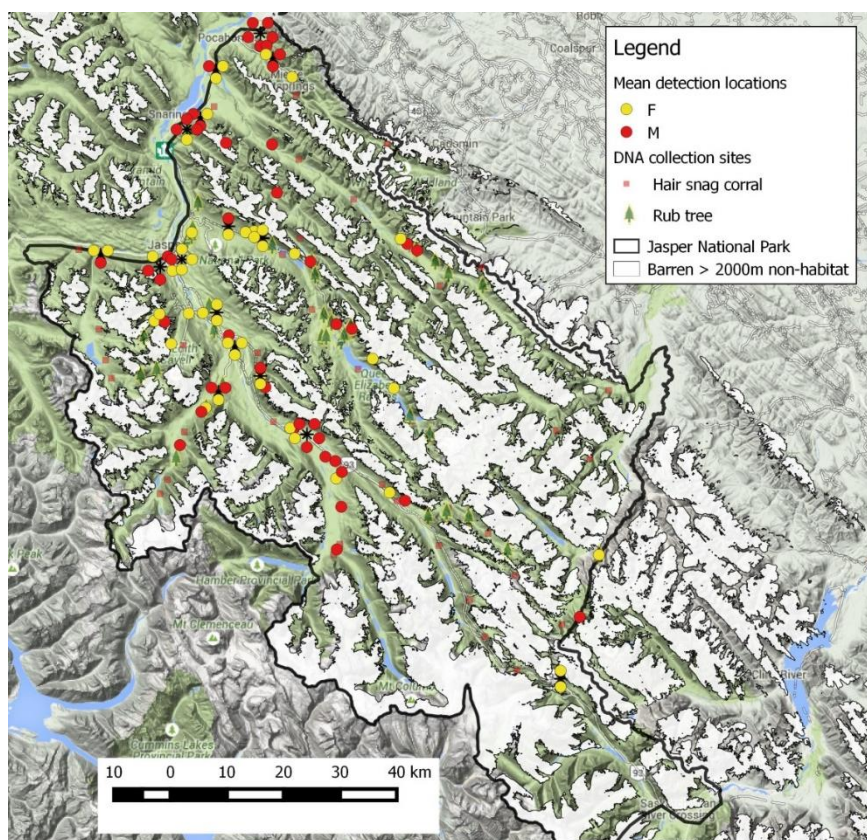


Figure 5. Mean detection locations of male (M) and female (F) bears on the sampling grid based on cumulative detections at hair snags and rub trees. Multiple mean detection locations are presented in a concentric ring with the central point denoted as a \*.

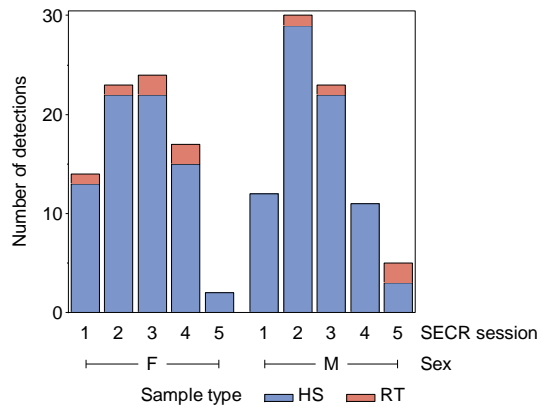
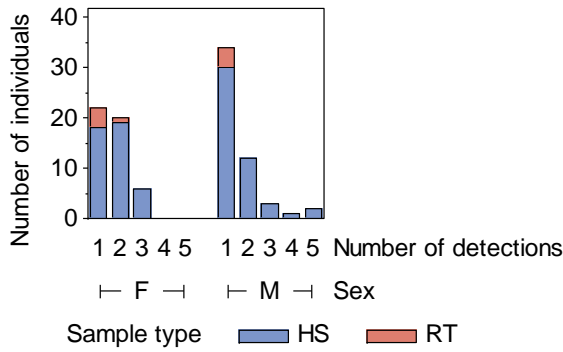


Figure 6. Number of detections as a function of hair snag (HS), and rub tree (RT) detectors.

All detections including repeat visits



Detections at unique sites

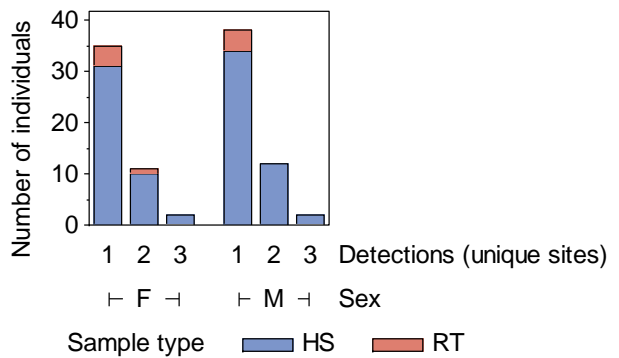


Figure 7: The number of detections including within session detections for bears. The left graph includes multiple detections at the same site (different sessions) whereas the right graph only includes unique sites.

## 4.2. Mortalities or translocations during sampling

Over the course of the spring and summer of 2014, there were 15 (7 females, 8 males) mortalities and 2 live capture/translocations (2 females) near the DNA sampling grid (Figure 8). Both of the live captures were released with no subsequent known mortality. One mortality occurred before DNA sampling, 10 (5 females, 5 males) occurred during DNA sampling, and 4 occurred after DNA sampling (Figure 8). Of most interest are the 10 bears that were removed during DNA sampling. Of these, 7 occurred within the DNA sampling area (5 in the core area) with the rest occurring just to the northeast of the DNA grid along the Trans Canada (Highway 16) corridor (Figure 8). Two of the 10 bears of interest were detected in DNA sampling. In terms of timing of mortalities, 3, 1, 2, 3, and 1 mortalities occurred in sessions 1,2,3,4, and 5

respectively. Of the two detected bears that were mortalities, one mortality occurred in session 1, and one in session 4. Of the 2 live captures, one was captured during DNA sampling on the grid and one was captured after DNA sampling just off the grid. Both live captured bears were detected in DNA sampling. As discussed later, the low number of detected bears that were also mortalities made it difficult to incorporate the effects of mortality into the analysis.

## 4.3. Spatially Explicit Analyses

Spatially explicit analyses were conducted separately for each sex of bear given the likelihood of sex-specific parameters as well as sex-specific distributions of bears on the sampling grid. This approach was simpler than attempting pooled sex analysis with sex-specific terms for each parameter.

### 4.3.1. Females

Females were detected in lower numbers during sessions 1 and 5, however this could have been due to the lower number of active detectors in these sessions (Table 3). The number of unmarked bears decreased to 0 in the 5<sup>th</sup> session suggesting that sampling efforts were relatively effective in detecting the majority of bears within the vicinity of detectors. Detection frequencies also suggested effective sampling with more bears detected more than once (24) than bears detected only once (23).

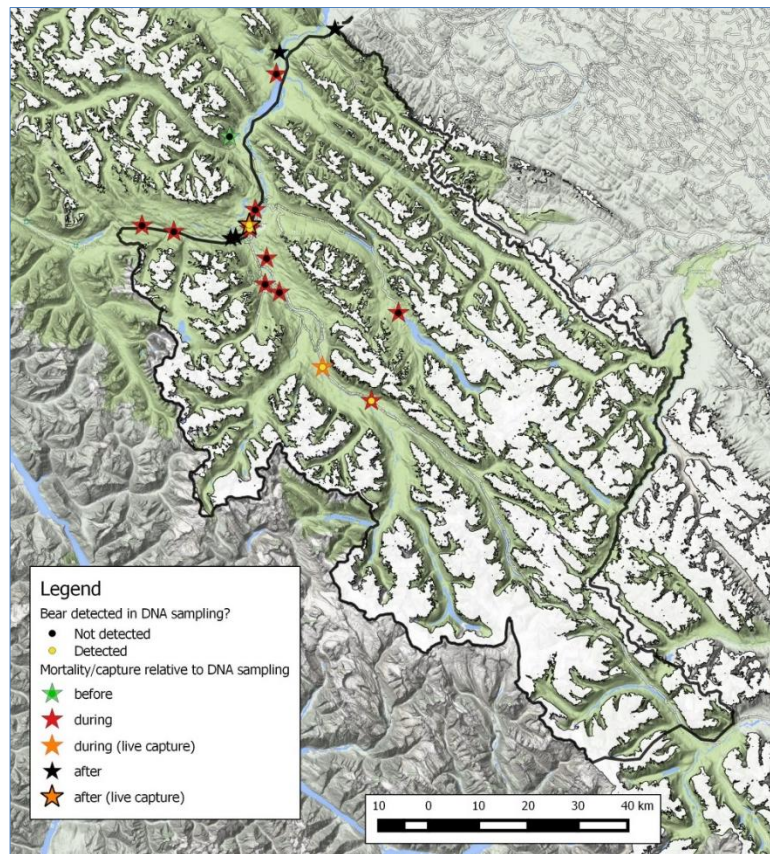


Figure 8. Locations of known mortalities and live captures of black bears in 2014.

The majority of detections occurred in the main Athabasca Valley corridor as well as the road to Maligne Lake (Figure 9). The largest cluster of detections occurred with the vicinity of the Jasper townsite. Movements between detections occurred along the Maligne Lake Road corridor as well as in valleys along the Athabasca Valley corridor (the actual paths are approximate because the sequence of detections is not known). Few detections or movements occurred in the southern or eastern portion of the park. The mean distance moved between detections was 3.5 kilometers, however, this statistic is sensitive to trap layout. The best method to assess movements is through spatially explicit detection functions which are presented later.

Model selection efforts initially focused on identifying base variation in detection probability at home range center ( $g_0$ ) and spatial scale of movements ( $\sigma$ ). Models considered included temporal variation

(symbolized by  $t$ ), linear trends in parameters (symbolized by  $T$ ), undefined heterogeneity (symbolized by  $h_2$ ), and behavioural response (a change in a parameter after initial detection, symbolized by  $b$ ), or a change in detection based on detection in the previous session (symbolized by  $B$ ). Parameter symbols are described in Table 1. It was most likely that hair snags could create a behavioural response given that a lure was used to attract bears and therefore many of the behavioural response models were specific to hair snags (terms  $B_{HS}$  or  $b_{HS}$ ).

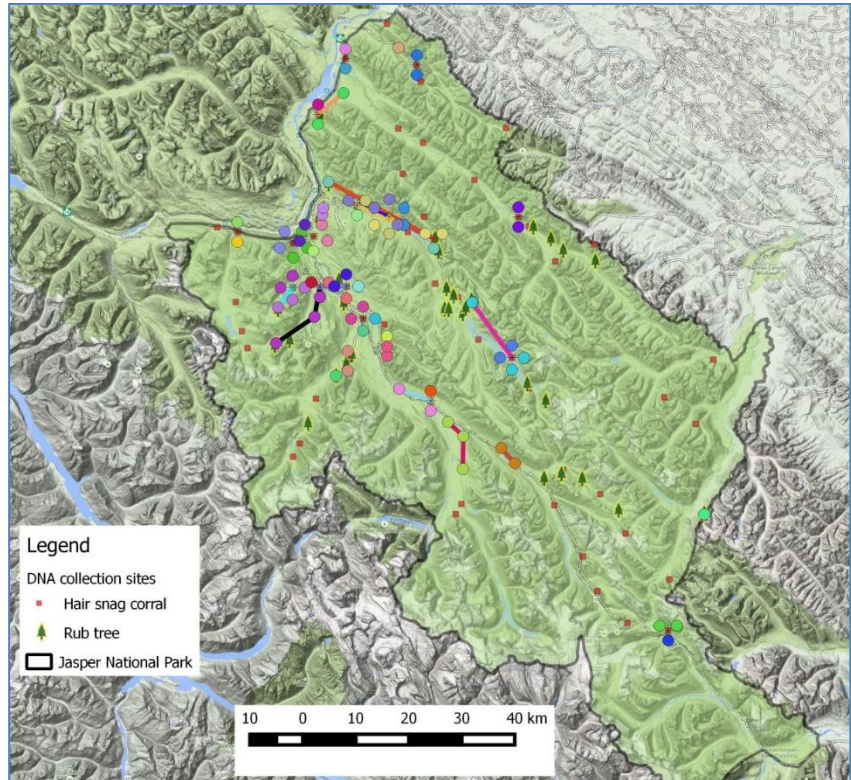


Figure 9. Detection locations and approximate movement paths of female black bears (one colour per bear). Multiple detections at a site are denoted by a \* with offset symbols.

Table 3: Summary statistics for detections of females in the Jasper 2014 sampling grid.

Statistic	Session(j)					Total
	1	2	3	4	5	
Detections (nj)	11	20	24	15	2	72
Unmarked (uj)	11	16	13	5	0	45
Cumulative marked (Mt+1)	11	27	40	45	45	45
Frequencies (fsessions)	23	18	3	1	0	45
Total site visits <sup>A</sup>	14	23	24	17	2	80
Detectors visited	12	21	19	15	2	69
Detectors available	53	102	122	122	65	464

<sup>A</sup>Includes multiple visits to different sites within single sessions.

Of the models considered, a model with rub tree (RT) and hair snag (HS)-specific detection probabilities at the home range center ( $g_0$ ) with constant scale of movement (Table 4, Model 1) was the most supported. Models that assumed behavioural response specific to hair snags (parameter  $B_{HS}$ , Models 3-4, 6-9) were not supported nor were models that assumed similar detection rates for hair snags and rub trees. Estimates from the models varied, with rub-tree specific formulations displaying slightly lower estimates than models that assumed similar detection rates between rub trees and hair snags. All estimates showed reasonable precision with coefficients of variation less than 20%.

Table 4: Female SECR model selection results and expected population size estimates. AICc = sample size adjusted Akaike Information Criterion,  $\Delta AICc$  = the difference in AICc between the model and the most supported model, AICc weight =  $w_i$ , K = the number of model parameters, and LL = the log-likelihood. Baseline constant models are shaded for reference with covariate models. Parameter symbols are described in Table 1.

No	Model	AICc	$\Delta AICc$	$w_i$	K	LL	$\hat{N}$	SE	CV	Conf. Limit
1	$g_0(RT) \sigma (.)$	549.6	0	0.54	4	-270.3	77.7	12.1	15.6%	57.4 105.2
2	$g_0(RT) \sigma (RT)$	552.1	2.5	0.15	5	-270.3	77.7	12.1	15.6%	57.4 105.2
3	$g_0(RT+B_{HS}) \sigma (.)$	552.2	2.6	0.15	6	-269.0	89.1	18.5	20.7%	59.6 133.1
4	$g_0(RT+b_{HS}) \sigma (.)$	553.2	3.6	0.09	6	-269.5	75.2	14.7	19.6%	51.4 109.9
5	$g_0(.) \sigma (RT)$	555.4	5.8	0.03	4	-273.2	78.6	12.4	15.8%	57.8 107.0
6	$g_0(.) \sigma (RT+ B_{HS})$	556.6	6.9	0.02	6	-271.2	88.0	16.8	19.1%	60.7 127.6
7	$g_0(RT+B_{HS}) \sigma (RT+ B_{HS})$	558.3	8.6	0.01	9	-267.6	88.5	18.6	21.1%	58.8 133.1
8	$g_0(.) \sigma (RT+ b_{HS})$	558.4	8.8	0.01	6	-272.1	84.3	17.7	21.0%	56.1 126.7
9	$g_0(RT+ b_{HS}) \sigma (RT+ b_{HS})$	560.9	11.3	0.00	9	-268.9	74.6	14.7	19.7%	50.9 109.3
10	$g_0(.) \sigma (h_2)$	580.9	31.3	0.00	5	-284.7	111.0	26.1	23.5%	70.5 174.8
11	$g_0(T) \sigma (.)$	582.9	33.3	0.00	4	-286.9	81.2	13.3	16.4%	59.0 111.7
12	$g_0(.) \sigma (T)$	583.4	33.8	0.00	4	-287.2	87.8	14.3	16.3%	63.9 120.6
13	$g_0(.) \sigma (.)$	584.6	35.0	0.00	3	-289.0	84.2	13.0	15.5%	62.3 113.9
14	$g_0(T) \sigma (T)$	585.4	35.8	0.00	5	-286.9	77.7	12.1	15.6%	57.4 105.2
15	$g_0(t) \sigma (.)$	586.8	37.2	0.00	7	-284.9	84.2	13.0	15.5%	62.3 113.9
16	$g_0(.) \sigma (B)$	586.8	37.2	0.00	4	-288.9	86.5	14.8	17.1%	62.1 120.7
17	$g_0(.) \sigma (t)$	587.1	37.5	0.00	7	-285.0	86.5	14.8	17.1%	62.1 120.7
18	$g_0(h_2) \sigma (.)$	589.6	39.9	0.00	5	-289.0	111.0	26.1	23.5%	70.5 174.8

Estimates of detection probability at home range center ( $g_0$ ) from model 1 ( $g_0(RT) \sigma (.)$ ) were 0.23 for hair snags (SE=0.046, CI=0.15-0.33) and 0.028 for rub trees (SE=0.013, CI=0.01-0.069). The common estimate of scale of movement ( $\sigma$ ) was 3,639.3 m (SE=309.7, CI=3081.1-4298.5). A plot of the detection function from model 1 estimates illustrates the higher detection probabilities for hair snags with non-zero detection probabilities occurring within 10 kilometers of the home range center of female bears (Figure 10).



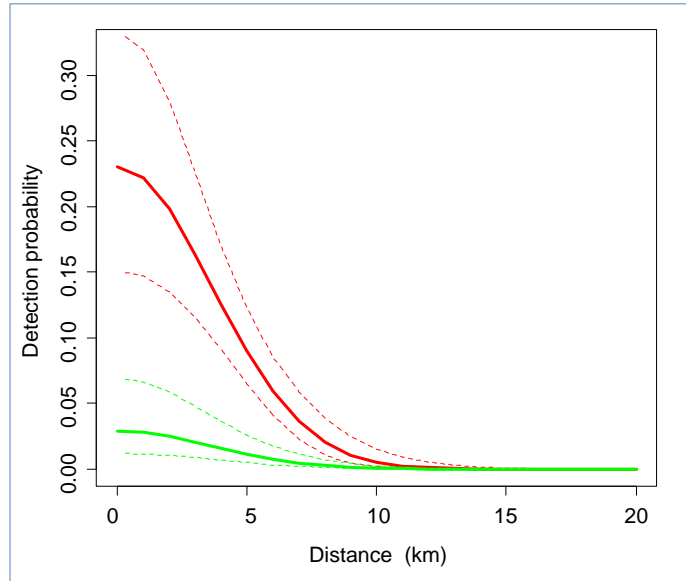


Figure 10. Detection probability plots for model  $g_0(RT) \sigma(\cdot)$  for female bears. The red and green lines are the detection functions for hair snags and rub trees respectively. Confidence limits are

### 4.3.2. Males

Males were detected in lower numbers during sessions 1 and 5, however this could have been due to the lower number of available detectors in those sessions (Table 5). The number of unmarked bears decreased to 1 in the 5th session suggesting that sampling efforts were relatively effective in detecting the majority of bears within the vicinity of detectors.

Detection frequencies suggested moderate sampling effectiveness with 14 males being detected more than once and 34 males being detected once. The number of site visits was reasonably higher (30) in session 2 than unique detectors visited (17). This indicates that there were a reasonable number of inter-session movements of bears. The mean distance moved for males was 5.4 kilometers as estimated by detections across different sites. As with females, the best interpretation of male movements is through SECR detection functions.

Table 5: Summary statistics for detections of males in the Jasper 2014 sampling grid. Detections were pooled across detector types.

Statistic	Session(j)					Total
	1	2	3	4	5	
Detections ( $n_j$ )	11	22	19	9	4	65
Unmarked ( $u_j$ )	11	20	10	6	1	48
Cumulative marked ( $M_{t+1}$ )	11	31	41	47	48	48
Frequencies ( $f_{sessions}$ )	34	11	3	0	0	48
Total site visits <sup>A</sup>	12	30	23	11	5	81
Detectors visited	10	17	18	11	5	61
Detectors available	53	102	122	122	65	464

<sup>A</sup>Includes multiple visits to different sites within single sessions.

The distribution and movements of males revealed a large number of detections along the Athabasca Valley corridor with less detections than females near the Jasper townsite and Maligne Lake corridor. Males displayed longer distance movements with some detections occurring up to 25 kilometers apart (Figure 11). Many of the detection locations were on the border of the Park area making it likely that the home ranges of some of the bears occurred outside of the focal study area.

Model selection for males revealed various

forms of variation in both detection at home range center and scale of movement. Most notably, a behavioral response in scale of movement for hair snag sampling as well as rub-tree and hair snag specific scale of movement was detected (Table 6, Model 1). Support for this model suggests that males display different movement patterns for hair snags, potentially based on the attractant, compared to rub trees. Furthermore, movements of male bears change after initial detection at the hair snag site. Models with behavioural response (Models 1-5) had greater support than models without behavioural response (Models 6, 8, and 9) but still with rub-tree specific detection and movements. Estimates for the behavioural response models were lower than non-behavioural response models by about 10 bears. All estimates showed reasonable precision with coefficients of variation less than 20%.

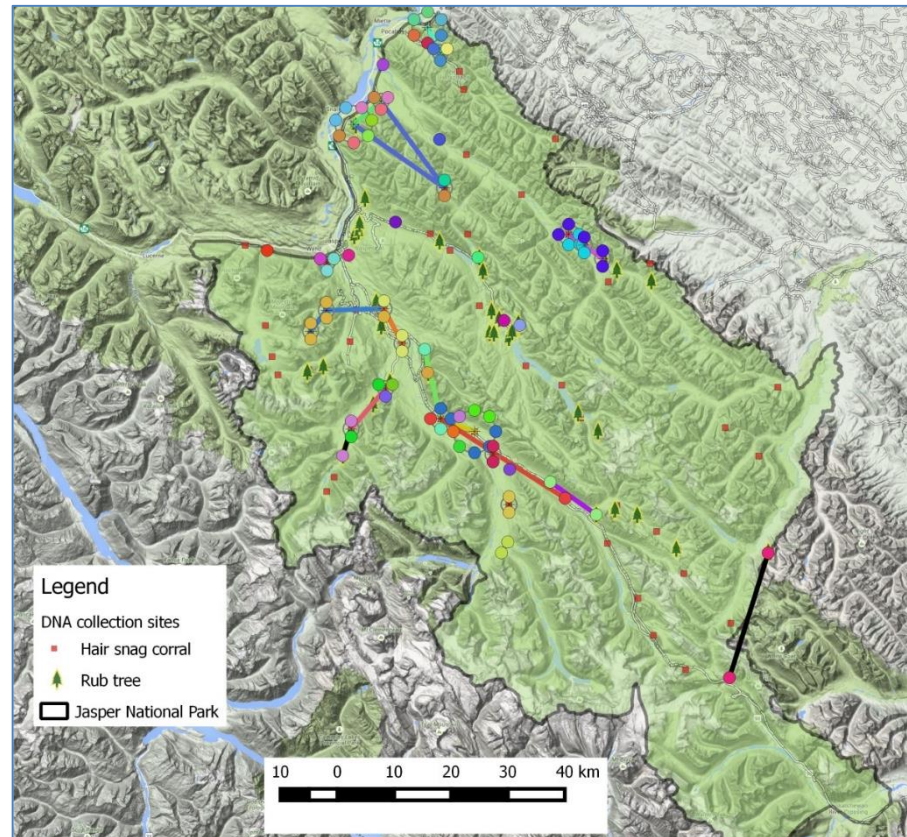


Figure 11. Detection locations and approximate movement paths of male black bears (one colour per bear). Multiple detections at a site are denoted by a \* with offset symbols.

Table 6: Male SECR model selection results and expected population size estimates.  $AIC_c$  = sample size adjusted Akaike Information Criterion,  $\Delta AIC_c$  = the difference in  $AIC_c$  between the model and the most supported model,  $AIC_c$  weight =  $w_i$ ,  $K$ , the number of model parameters and log-likelihood ( $LL$ ) are given. Baseline constant models are shaded for reference with covariate models. Symbols used in models are summarized in Table 1.

No	Model	$AIC_c$	$\Delta AIC_c$	$w_i$	$K$	$LL$	$\bar{N}$	SE	CV	Conf. Limit	
1	$g0(.) \sigma(RT+bHS)$	544.1	0.00	0.56	6	-265.0	51.5	6.8	13.2%	39.8	66.6
2	$g0(T) \sigma(RT+bHS)$	546.0	1.93	0.21	7	-264.6	54.4	8.3	15.3%	40.42	73.24
3	$g0(RT) \sigma(RT+ bHS)$	546.7	2.59	0.15	7	-264.9	51.4	6.8	13.2%	39.8	66.4
4	$g0(RT+bHS) \sigma(RT+ bHS)$	549.4	5.33	0.04	9	-263.3	52.5	7.5	14.2%	39.8	69.3
5	$g0(RT+b) \sigma(RT+b)$	550.6	6.51	0.02	7	-266.9	52.8	7.5	14.2%	40.1	69.6
6	$g0(T) \sigma(RT+THS)$	556.3	10.29	0.00	7	-269.8	72.1	11.0	15.3%	53.5	97.1
7	$g0(.) \sigma(RT+BHS)$	557.8	13.73	0.00	6	-271.9	61.4	9.1	14.8%	46.0	82.0
8	$g0(.) \sigma(RT)$	559.5	15.45	0.00	4	-275.3	69.6	10.5	15.0%	51.9	93.3
9	$g0(RT+bHS) \sigma(.)$	559.8	15.77	0.00	6	-272.9	56.8	8.0	14.1%	43.2	74.9
10	$g0(RT) \sigma(RT+BHS)$	560.5	16.46	0.00	7	-271.9	61.4	9.1	14.8%	46.0	82.0
11	$g0(RT) \sigma(RT)$	562.0	17.95	0.00	5	-275.3	69.6	10.5	15.0%	51.9	93.3
12	$g0(RT+bHS) \sigma(RT+bHS)$	563.0	18.96	0.00	9	-270.1	63.0	10.0	15.8%	46.3	85.7
13	$g0(RT) \sigma(.)$	564.0	19.97	0.00	4	-277.6	69.8	10.4	15.0%	52.1	93.4
14	$g0(RT+bHS) \sigma(.)$	566.6	22.53	0.00	6	-276.3	66.1	10.4	15.7%	48.6	89.7
15	$g0(T) \sigma(.)$	594.1	49.99	0.00	4	-292.6	71.9	10.4	14.5%	54.2	95.3
16	$g0(.) \sigma(t)$	595.0	50.93	0.00	7	-289.1	72.1	10.4	14.5%	54.4	95.6
17	$g0(t) \sigma(t)$	595.9	51.81	0.00	11	-283.3	76.0	11.4	15.0%	56.8	101.8
18	$g0(t) \sigma(.)$	595.9	51.83	0.00	7	-289.6	71.2	10.3	14.4%	53.7	94.3
19	$g0(T) \sigma(T)$	596.4	52.36	0.00	5	-292.5	72.0	10.4	14.5%	54.3	95.5
20	$g0(h2) \sigma(.)$	598.0	53.98	0.00	5	-293.3					
21	$g0(.) \sigma(h2)$	598.2	54.11	0.00	5	-293.4	82.2	13.9	17.0%	59.1	114.3
22	$g0(.) \sigma(.)$	600.2	56.1	0.00	3	-296.8	70.1	10.0	14.3%	53.0	92.7

Estimates of detection at the home range center ( $g_0$ ) for model 1 for rub trees and hair snags were the same at 0.15 (SE=0.14, CI=0.02-0.62). Estimates of  $\sigma$  were 3,068 meters (SE=449.9, CI=2305-4083) for rub trees and 5,716 meters (SE=558.8, CI=4722-6921) for initial detection at hair snags. Spatial scale ( $\sigma$ ) was reduced to 3,068 meters (SE=449.9, CI=2305.2-4083.4) meters after initial detection for hair snags. These results are best viewed as a detection function (Figure 12) which illustrates the similar detection probabilities for rub trees and hair snags but at different spatial scales. This result indicates that rub trees have a smaller effective sampling area compared to hair snags. These results also

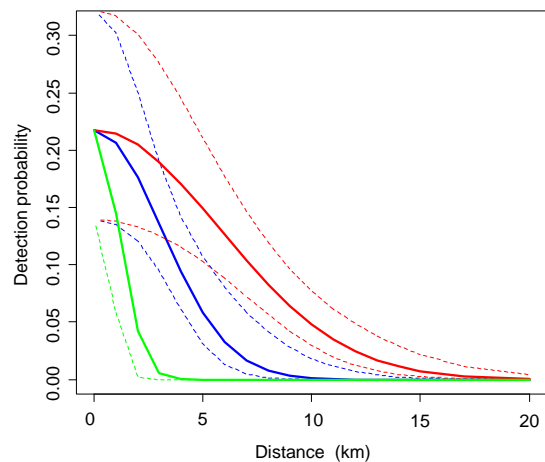


Figure 12. Detection functions for male bears. Red line is initial detection function for hair snags, blue line is the detection function after initial detection at hair snags, and green line is the detection function for rub trees.

suggest that male bear movement decreases after initial detection at hair snags due to a behavioral response.

4.3.3. Estimates of density and total population size.

Table 7 provides combined estimates for male and female bears as well as densities based on habitat area from the most supported sex-specific models in Tables 4 and 6. Population estimates were adjusted slightly to account for difference in how program SECR estimates habitat area compared to a GIS based estimate of area. Namely, SECR estimates habitat area as the number of mask centroids that fall on habitat (as opposed to non-habitat: barren > 2,000m). In this case, 434,500 centroids of the (1 x 1km spacing) mask fell on habitat which amount to an estimate habitat area of 4,345 km<sup>2</sup>. The GIS based estimate of area was 4,355 km<sup>2</sup> (less than 1% difference). To adjust estimates, density was first estimated based on secr habitat area and this density was then multiplied by the GIS area to obtain a GIS-based estimate. The difference in estimates based on this adjustment was trivial.

Table 7: Combined estimates of male and female bears for South Jasper National Park unit based on estimates in Tables 4 and 6. Estimates of density and expected population size are based on GIS estimated habitat area (4,355 km<sup>2</sup>).

Sex	Individuals Detected	Population estimates					Density (bears per 1000 km <sup>2</sup> )			
		Estimate	SE	Conf. Interval		CV	Estimate	SE	Conf. Interval	
Females	45	78.1	12.2	57.7	105.7	15.6%	17.88	2.78	13.21	24.21
Males	48	51.7	6.8	40.2	67.3	13.2%	11.85	1.56	9.21	15.42
Total	93	129.7	14.0	105.2	160.0	10.7%	29.73	3.19	24.09	36.66

Estimates of density based on habitat area are the most biologically meaningful since densities in non-habitat barren areas are likely to be 0 and therefore inclusion of these areas will not be meaningful. If needed, an estimate of density based on the entire park area can be derived by dividing the expected population size by the total park area. This amounts to an estimate of 16.38 bears per 1000 km<sup>2</sup> (SE=1.76, CI=13.29-20.21) for the combined sex estimate.

**5. Discussion**

Our results suggest that precise estimates of black bears are possible even when the spacing of detectors is relatively large compared to the home range and movements of the bears. There are a few potential reasons for this. First, the precision of spatially explicit methods is partially determined by the number of redetections of bears at different sites. While the number of redetections was relatively low, this was offset by the relatively large number of individual bears detected (Figure 7) which therefore resulted in a reasonable number of redetections at unique sites (27 individuals detections at more than one site for 58 redetections total at unique sites). One rule of thumb is that there needs to be at least 20 recaptures to ensure precise estimates with SECR (Efford et al. 2004). Our study achieved this goal with 58 recaptures at unique sites, and 115 recaptures if revisits to the same site across multiple sessions are allowed. If the number of individual bears were lower it would be expected that the precision of estimates would decrease due to lower overall detections.

A related question would be if the spacing of detectors (7 x 7 km grid cell size) was adequate for general use in black bear sampling. A rule of thumb is that detector spacing should be between 1.5 and 2.5 times the estimated scale of movement  $\sigma$  (M. Efford, pers. comm). In our situation, spacing should be between 4 km (rub trees for males) and 8.5 km (initial detection at hair snags

for males), so 7 km is approximately correct. The geography of Jasper National Park most likely confines movement by funelling bears along valleys, and probably enhances trap encounter rates. Therefore our findings may not be transferable to other study areas. Simulations using program *secrdesign* (Efford 2015) could be used with the estimates of  $g_0$  and  $\sigma$  from this study to further refine sampling design for future studies.

Site selection for the study was primarily based upon areas closest to the centroid of each 7 x 7 km cell that contained likely grizzly bear habitat. Grizzly bear habitat may differ from black bear habitat with black bears selecting areas closer to human habitation as well as other factors. The amount that smaller-scale site selection influences estimates may not be significant as long as black bears were not excluded from areas by grizzly bears (resulting in a larger proportion of black bears with zero detection probabilities). Given that sites were available for 2 weeks and no reward was available at the site it is unlikely that this effect would have been very strong. To examine this question more closely, we could use site covariates to assess variation in detection rates and movement scale due to habitat in the proximity to sites as was done for grizzly bears (Stenhouse et al. 2015). In addition, it is possible to use density surface modelling to assess larger-scale variation in density on the sampling grid (Royle et al. 2013, Efford 2014a, Boulanger 2015). Both of these analyses, which would require further GIS analysis to define black bear site covariates and SECR centroid covariates, were beyond the scope of the current analysis.

Rub trees showed relatively low efficiency for sampling black bears with lower effective sampling areas as determined by scale of movement and detection probabilities. A similar study in Banff National Park (Sawaya et al. 2012) used a 7 x 7 km grid cell size with rub tree and hair snag sampling. This study, which used closed models for estimates, also found low detection probabilities for rub trees with black bears. A study in Glacier National Park (Stetz et al. 2014) that used rub trees found that rub trees had similar if not higher detection probabilities. However, this study utilized a very high density of rub trees which probably created higher detection rates for rub trees given that closed model detection rate will be sensitive to trap density. In comparison, the results of this study suggested that rub trees either had lower detection rates at home range center ( $g_0$ ) (Figure 10: females) or lower effective sampling area as dictated by lower scale of movement ( $\sigma$ ) values (Figure 12: Males). In each case, increasing the number of rub trees or using an attractant might offset the lower efficiency of individual rub trees. However, even higher densities of rub trees may not sample the entire bear population if an age or sex cohort does not exhibit rubbing behavior during the time that DNA sampling occurs as suggested in grizzly bear studies (Boulanger et al. 2008). A simulation study, as well as comparison of estimates with and without rub trees would help determine the viability of rub tree sampling strategies.

Behavioural response to hair snag sampling has been detected in previous DNA mark-recapture studies using closed models for grizzly bears (Boulanger 2003) as well as spatially explicit models for black bears (Drewry et al. 2013). The change in spatial scale after initial detection suggests that male bears may have reduced movements relative to hair snag sites once they were initially detected (Figure 12). This could be due to increased interest in hair snag sites, interactions with other bears, or other factors. Black bears did not get a reward from visitation to hair snag sites, however it is possible that the fresh scent lure still attracted them to sites each session.

An inherent assumption of the SECR analysis is that all areas on the grid have an initial opportunity to be sampled, however, not all bears need to have a non-zero probability of capture. The initial design of the Jasper sampling project was that the probability of a 7 x 7 cell receiving a site depended on whether the centroid of the cell was bear habitat (defined as non-barren areas below 2000m in elevation). It is hard to determine how well the 2000m cutoff applies to black bears without analysis of telemetry data to determine habitat selection. However, we don't believe that black bears utilize higher elevation barren habitats to any degree – Jasper National Park remote camera data revealed only one detection above 2,000m in 42,351 camera days. With habitat excluded, SECR will still provide an unbiased estimate in density even if there is variation in density on the grid, as long as sampling follows a stratified random sampling design (Boulanger and Efford 2014, Efford 2014a). This assumption was partially met with some areas not being sampled due to logistic considerations (Stenhouse et al. 2015). One such area was the far southern end of the Park. In this case it must be assumed that densities in these areas are similar to the sampled areas. As with other parts of the park, barren areas above 2000m were excluded from population estimates. Therefore the main assumption is that habitat areas in these areas are similar to other park areas.

There were a reasonable number of known mortalities that occurred mainly along the Trans-Canada highway during the survey (Figure 8). Spatially explicit models assume that populations are demographically closed during sampling. The low sample size of marked bears that were mortalities made it problematic to model the effect of mortalities on estimates. The main challenge for modelling mortalities is that it cannot be assumed that all are known and therefore an additional parameter, the probability that a mortality is detected (usually called reporting rate) should be estimated as well as apparent survival rate. The effect of mortalities on actual estimates was minimal given that only 2 of the detected bears were mortalities. The general effect of mortality or emigration on closed model estimates is to create a negative bias in estimates (Kendall 1999). If it is assumed that most of the mortalities are known then 8% of the male and female population (10 bears) was removed during sampling with an additional 4% (5 bears) removed after sampling. However, the main mortalities occurred along the Trans-Canada highway and therefore the overall impact on estimates (i.e. bias in detection rates) was probably not large especially given that many of these bears would not have had home ranges that were completely on the DNA sampling grid. To include these mortalities in the spatially explicit analysis would require adding an additional detector type (i.e. highway collisions on the Trans-Canada highway as a removal collector). While possible, this type of analysis was beyond the scope of this exercise.

The Alberta Black Bear Management Plan reports a black bear harvest rate of approximately 6% (although both population sizes and harvest numbers were based only on expert opinion). The stated management goal was to not exceed 20% human caused mortality. Reports of harvest rates considered to be appropriate in other jurisdictions were as high as 25%. (Czetwertynski and Schmeigelow 2012) report harvest rates of between 8% and 21% in northern Alberta. To be completely certain of the sustainability of a particular harvest rate, we would have to know both survival rates and recruitment rates, neither of which are known for JNP black bears. Adding 12% human caused mortality is probably unsustainable. Over the last 10 years, the human-caused mortality rate has been about 7 bears (though it has been highly variable), which would

represent about a 5% human caused mortality rate if the population was constant at 129. The cause(s) of the sudden increase in mortality rate for 2014 are unclear.

Our main estimate of black bear density was 30 bears/1,000 km<sup>2</sup>, however to compare with other study areas, we must incorporate the non-habitat areas, which lowers the estimate to 16.38 bears/1,000 km<sup>2</sup>. A study using similar methods in Banff National Park reported a very similar density of (28 bears/1,000 km<sup>2</sup>, (Sawaya et al. 2012). Black bear densities in other jurisdictions however are considerably higher than in the Canadian mountain national parks: 114 bears/1,000 km<sup>2</sup> in Glacier National Park (Stetz et al. 2015), 200 bears/1,000 km<sup>2</sup> in New York (Gardner et al. 2010), 257 bears/1,000 km<sup>2</sup> in the Parsnip Plateau, and 100 bears/1,000 km<sup>2</sup> in the Parsnip Mountains of British Columbia (Mowat et al. 2001) . Estimates of density from older reports tend to be a lot higher (in the multiple 100s), but these estimates may be confounded by not accounting for study area closure. Our black bear density could be low relative to other jurisdictions for several reasons, including lower primary productivity due to low precipitation and high elevation, sympatry with grizzly bears (Millar 1997, Mowat et al. 2001), and competition for the elk calves from other predators (cougars, wolves, grizzly bears).

In terms of longer-term monitoring it should be possible to use reduced effort designs and even occupancy-type data to supplement more extensive DNA surveys. A recent study (Chandler and Clark 2014) used data from DNA surveys with intermediate years of occupancy data to refine population trends for black bears. In the case of Jasper National Park, scat and remote camera data collected on the trail system could be used for this type of analysis. The main requirement is that the search area and effort is documented for samples to allow incorporation into a spatially explicit model.

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