INUVIK-TUKTOYAKTUK HIGHWAY 2013

GRIZZLY BEAR DNA INVENTORY:

ESTIMATES AND DENSITY SURFACE MODELLING

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Abstract

This report summarizes field collection and analyses for a grizzly bear (*Ursus arctos*) DNA mark-recapture study conducted as part of the Wildlife Effects Monitoring Program WEMP) for the Inuvik to Tuktoyaktuk Highway development project. The main objective of the first year of study was to collect baseline population abundance and density estimates for grizzly bears in the area surrounding the proposed highway. A grid of 93 DNA collection tripods spaced in 10x10 km cells were placed from the Mackenzie Delta, west and east of the proposed highway. Tripods were sampled for 4 sessions from mid-June to mid-August 2013. Seventy five grizzly bears (46 females, 29 males) were detected during DNA sampling. Detections were highest in the northwest corner of the grid and decreased towards the southeast corner. An estimate of the superpopulation of bears in the grid and surrounding area was 122 (CI=87-263). Spatially explicit mark-recapture methods that modelled the layout of DNA collection tripods and excluded ocean areas of non-habitat were used to estimate density. Grizzly bear density was estimated to be 11.1 bears per 1,000 km^2 (CI=6.7-18.4) and the average number of bears that used the grid was 103 (CI=45-124). Spatially explicit methods estimated that bears whose home range centers were within 20-25 km of the proposed highway were most likely to be detected in the vicinity of the highway. Density of grizzly bears on the sampling grid was related to deciduous, wet herbaceous and other habitat types. The number of bears within 20 km of the proposed highway was estimated to be 36 (CI=16-82) female and 16 (CI=10-26) male bears. Future analyses will fit models to describe variation in density on the sampling grid and to determine optimal sampling designs to monitor grizzly bear populations during road construction and operation.

INTRODUCTION

Grizzly bears (*Ursus arctos*) are a high-profile species of local, national and international interest. Grizzly bears are an important furbearer species in the Inuvialuit Settlement Region (ISR) and have been managed under a quota since the late 1980s - early 90s. Inuvialuit have exclusive rights to hunt grizzly bears in the ISR and do allow the transfer of that right to guided hunters. COSEWIC has assessed the status of the grizzly bears in Canada as *Special Concern* (Committee on the Status of Endangered Wildlife in Canada(COSEWIC) 2011). In the Northwest Territories (NWT), grizzly bears are ranked as *Sensitive* by the NWT General Status Ranking Program and are slated for assessment by the NWT Species at Risk Committee in 2015. The inclusion of grizzly bears in the Wildlife Effects Monitoring Program (WEMP) for the construction of the Inuvik-Tuktoyaktuk Highway is based on this status, their low tolerance to human disturbance, and concern over how the proposed highway may result in changes in distribution and increased mortality of the species.

Industrial development presents several threats to bear populations including the potential for increased destruction of 'problem' bears, potential for collisions with vehicles, and the alteration and fragmentation of habitat. The highway may increase ease of access and possibly cause increased mortality resulting from hunting. However, hunting is managed under a quota system and all human caused mortalities are counted under the quota. Any increases in mortalities due to bear-people conflicts or collisions will cause a decrease in tags available to harvesters.

Developments within the Arctic may present a relatively high risk to grizzly bear populations due to the natural low density of bears in these areas at the northern fringe of their range, the relative scarcity of high quality habitat and corresponding large area requirements, and the increased vulnerability of bears in open tundra habitats (Ross 2002). During and after construction, grizzly bears may use areas along the highway less than expected as a result of noise from construction activity, camps, and vehicle traffic. Alternatively, grizzly bears may be attracted to camps, cabins, or construction activity if waste and odours are not properly managed; these individuals may be removed from the local population as problem wildlife. After the highway is opened, additional mortalities may occur if grizzly bears that are attracted to ungulate kill sites near roads are themselves hunted or trapped (ungulate kill sites would occur if future harvesting of caribou or other species occurs along the highway or because of animals killed by vehicles). Direct grizzly bear mortality associated with vehicle collisions is expected to be a rare event.

As part of the WEMP, grizzly bear abundance monitoring in the Inuvik-Tuktoyaktuk Highway area was initiated in 2013 during the preconstruction phase of the highway. The study design employed hair snagging for DNA analysis within the Regional Study Areas (RSA). There are many challenges to monitoring the effect of the road on grizzly bears given the large extent of their movements relative to the road area, and the likely large but unknown scale of impacts. The planned approach for monitoring grizzly bears is to estimate bear abundance prior to road construction, during road construction, and during regular use once constructed. Open mark-recapture models will be used here to analyze the bear hair snag DNA data over time. This will allow demographics estimates and will help infer mechanisms for population change in the study area. The study area will be large enough to allow a "control" area and an "impact" area. Spatially explicit mark-recapture methods will also be used to estimate changes in bear density relative to the road area over the course of monitoring.

The objectives of the 2013 grizzly bear DNA inventory were to:

- Assess whether sample sizes of bears, study area extent, and other study design features were adequate to monitor grizzly bear abundance relative to road construction;
- Estimate grizzly bear abundance and distribution during the pre-construction period within the Inuvik to Tuktoyaktuk Highway area;
- Build baseline habitat-based models of grizzly bear distribution relative to the road to be used to infer changes in bear distribution and density relative to the road once construction occurs.

Here grizzly bear population and density estimates from sampling conducted in 2013 are described with an emphasis on determining the adequacy of the sampling design. The primary focus of this analysis is estimation of grizzly bear population size, density, and modelling of variation of density on the sampling grid.

The intent is for this to be the first of a 2-year program to establish baseline distribution, abundance and density estimates for grizzly bears in the study area.

METHODS

The field design for the grizzly bear DNA inventory was based on studies conducted elsewhere in the Arctic (GN study near Kugluktuk (Dumond et al. 2014); Newmont project near Hope Bay (C. Kent, Rescan, unpubl. data); NWT diamond mines study near Lac de Gras (B. Milakovic, Rescan, unpubl. data); and Izok project (K. Poole, Aurora Wildlife Research, unpubl. data)), which were developed from research initiated in British Columbia (Woods et al. 1999, Boulanger et al. 2002, Proctor et al. 2010).

The Inuvik-Tuktoyaktuk Highway grizzly bear DNA inventory was conducted by helicopter from 17 June to 20 August 2013. The initial study area consisted of 100 grizzly bear hair-snagging tripods set out in 10 x 10 km grids within a 10,000 km^2 study area (Figure 1), which buffered the proposed highway alignment by 30-40 km, and included Richards Island and the northern portion of the Mackenzie Delta; this western area is to serve as a spatial "control" where it is assumed that bear demographics will not be affected by the road. Part of the north-western section of the study area was too wet for tripod deployment, thus 15 cells within islands were removed and another 8 cells were added to better buffer the highway and to reduce edge effect to result in 93 10 x 10 km cells within a 9,300 km^2 study area (Figure 1).

The 10 x 10 km cell size was based upon the results of previous barren-ground grizzly bears studies which achieved adequate detection rates for barren-ground grizzly bear populations (Boulanger 2013, Dumond et al. 2014). In addition, the 10 x 10 km cell size is smaller than the smallest annual home range of a female with cubs ($\overline{x}$ = 294 km^2) as determined from an earlier grizzly bear study in the project area(Edwards 2009).

Tripod design was based on recent work at Izok Lake (Aurora Wildlife Research and EDI Environmental Dynamics Inc., unpubl. data) and consisted of six 2” x 4” pieces of lumber 5’3” in length and secured at the corners with aircraft cable. Each upright 2” x 4” leg was wrapped with double-stranded 15 1/2 gauge 4-point high-tensile barbed wire to trap grizzly bear hair (Photo 1). Tripod materials were prepared prior to deployment (drilling holes, wrapping barbed wire, cutting aircraft cable, etc.) and assembled in the field by teams of two using a single A-Star B2 helicopter for transportation. Tripods were deployed near or within 1-2 km of each grid cell centre in the best apparent grizzly bear habitat available – sparsely vegetated or shrubby areas adjacent to water (Edwards 2009) – although large water bodies or avoidance of cabins occasionally resulted in placement slightly further from the cell centre. Tripod bases were not anchored because large rocks were extremely uncommon on the landscape.

Photo 1: Grizzly bear hair snagging tripod.

Lures were spread or poured atop the tripod on a piece of felt underlain by moss for absorption, and on a pile of moss and other vegetation in the centre of the tripod. Sites were revisited four times at approximately 14-day intervals to collect hair and re-bait with different combinations of blood, fish oil, and trapping lures (Table 1). At the end of each session, hair samples were removed with forceps, placed in coin envelopes, and labeled with tripod number, session number, leg number, and cluster and barb number (an alpha-numeric combination) to facilitate subsampling at the lab. A propane torch was used to remove any remaining hair. Hair samples were dried each night and stored cool and dry.

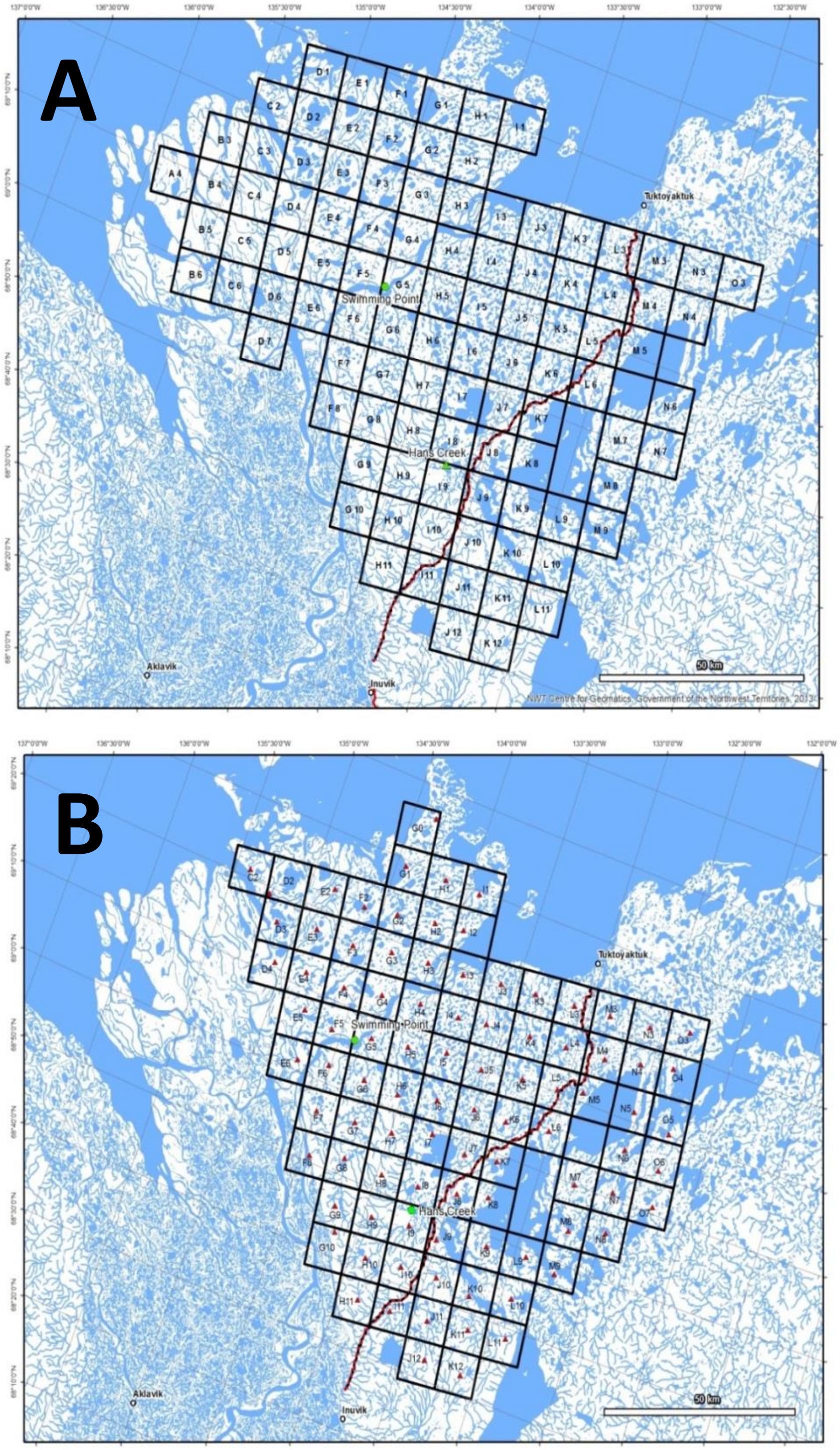

Figure 1. Inuvik-Tuktoyaktuk Highway grizzly bear DNA Sampling Grid, June to August, 2013. A. Initial design. B. Final design after modifications due to sites being too wet in June.

All samples were sent to Wildlife Genetics International (WGI; Nelson, BC, Canada) for microsatellite genotyping. Individuals were identified using 7 genetic markers, including 6 microsatellites and a gender marker. WGI analyzed 1 sample per leg, except when there were multiple clusters on a given leg, in which case up to 2 samples were analyzed per leg. In addition, up to 2 samples were analyzed from the ground per collection device, for a total of up to 8 analyzed samples per cell/check combination. A quality threshold of a minimum of 2 guard hair roots or 20 underfur hairs were used.

Closed population mark-recapture analysis to estimate population size

Closed model population estimates were used to obtain an estimate of the superpopulation of grizzly bears in the grid and surrounding area. The superpopulation estimate corresponds to the population of bears on the grid and surrounding area that use the grid area at least some of the time, if it can be assumed that movements to and from the grid were random and non-directional during sampling (Kendall 1999). The superpopulation estimate is most meaningful for future monitoring efforts. In addition, grizzly bear studies (Boulanger et al. 2002, Proctor et al. 2010) have primarily used closed models for estimation and therefore estimates of detection rates from these models can be compared to past studies. See Appendix 1 for background information on mark-recapture estimation.

The Huggins closed model (Huggins 1991) in program MARK (White and Burnham 1999) was used for model selection and population estimation. Sexes of grizzly bears were entered as groups in this analysis, testing whether sexes displayed differing forms of detection probability variation. Models with time, heterogeneity, and behaviour variation were considered in the analysis. In addition, detection probabilities were modelled as a function of distance from edge to determine if closure violation affected detection probabilities (Boulanger and McLellan 2001). Distances from all edges of the grid and distance from the non-ocean edge (Figure 1) were calculated since it was likely that closure violation only occurred on the non-ocean edge of the grid. Mixture model heterogeneity estimators (Pledger 2000), as incorporated in the program MARK, were used to model the heterogeneity variation of detection probabilities. Heterogeneity was modelled by letting detection probabilities come from more than one detection probability distribution. There are three parameters within the 2-detection probability distribution mixture model: 1. the probability that a given detection probability will come from the first detection probability distribution (π), 2. the mean detection probability of the first distribution (θ_1), and 3. the mean detection probability of the second distribution (θ_2). The probability that the detection probability comes from the second distribution is 1- π (Pledger 2000). Closed population models were evaluated in terms of relative support using information theoretic model selection methods (Burnham and Anderson 1998).

Spatially explicit mark recapture analysis to estimate grizzly bear density and population size

Spatially explicit capture-recapture (SECR) methods (Efford 2004, Efford et al. 2004, Efford et al. 2009, Efford 2011), also known as spatially explicit mark-recapture methods, were used to estimate grizzly bear density. Spatially explicit methods estimate the spatial scale movement for bears that are detected repeatedly to estimate the area that individual bears covered during sampling. Unlike closed models, that pooled data from multiple tripods within each session for each bear, the SECR method used multiple detections of bears at unique tripods within a session were to model bear movements and detection probabilities. Using this information, the detection probabilities of grizzly bears at their home range center (g_0), spatial scale of grizzly bear movements (σ) around the home range center, and bear density were estimated. An assumption of this method is that grizzly bear home range can be approximated by a circular symmetrical distribution of use (Efford 2004). The actual shape and configuration of the sampling grid was used in the process of estimating home range, scale of movements and density, therefore accounting for the effect of study-area size and configuration on the degree of closure violation and subsequent density estimates. For the study area a habitat mask, that accounted for areas unusable to grizzlies such as the ocean and large lakes within and in the immediate area of the sampling grid, was used to ensure the study area size included only useable habitat.

Data were initially summarized to assess the number of unique detections of bears and unique tripods visited by bears. This summary included detections of bears at unique tripods within a single session and therefore was different than closed model summaries that pooled within session data for each bear. In addition, the distance moved by bears detected multiple times was estimated to assess raw estimates of distances moved.

Analyses were conducted primarily in the R (R Development Core Team 2009) program SECR (Efford 2014b) with data screening conducted in the Windows-based program DENSITY (Efford et al. 2004). Program SECR uses a maximum likelihood approach to estimate model parameters (Borchers and Efford 2008, Efford et al. 2009). Full likelihood models were used for model fitting. Models that considered the effects of sex, temporal variation, and behavioural response on the home range center (g_0) and scale of movements (σ) were evaluated in terms of their relative support by using information theoretic model selection methods (Burnham and Anderson 1998). Estimates of parameters were model averaged based on relative support.

Spatially explicit models estimate the approximate distances moved by bears during sampling as well as the area in which they would most likely be detected using DNA sampling. This information was used to further evaluate the sampling grid and in particular the size of the grid relative to bear movements and the proposed road.

Variation in grizzly bear density

Structural relationships between habitat covariates using density surface modelling

Spatially explicit mark-recapture models were used to model variation in bear density on the study grid area and to estimate population size and density for areas that were in the proximity of the Inuvik-Tuktoyaktuk road. This approach also provided a baseline model of density in the study area, and will allow estimation of the zone of influence of the road on grizzly bear density once the road is in place.

Spatially explicit mark-recapture methods estimate density for a systematic grid of points/centroids that are overlaid on the study area (termed the habitat mask; Figure 2). For non-spatial models it is assumed that bear density is equal for each mask point. Density surface models estimated bear density at each mask centroid based upon habitat covariates summarized around the mask point. The fit of each of the density surface models was then compared to models that assumed similar density for each mask point.

This approach is similar to RSF models that are fit to detection frequencies at DNA collection sites with the strong advantage that the response surface is a systematic grid of points rather than trap locations (Efford and Dawson 2012, Efford and Fewster 2013, Royle et al. 2013, Royle et al. 2014).

Remote sensing data and previous RSF analyses based upon collared grizzly bears were used (Edwards 2009) to formulate density surface models. The covariates used for density surface modelling included RSF scores, which categorized each 28.5m^2 patch of vegetation, from Edwards (2002) as well as habitat covariates used to formulate the RSF models (Table 1). The coverage of the RSF surface included all tripod sites but excluded some of the areas in the southeast of the sampling grid (Figure 3); RSF scores for these areas were based upon scores of the closest mask centroid. Coverage of the RSF model extended to where the hair collection sites occurred and therefore the overall effect of missing RSF scores for peripheral areas probably was not substantial.

Table 1: Habitat covariates used for density surface modelling based upon Edwards (2009)

Habitat covariate	Dominant landcover features
Closed spruce	Closed mixed needleleaf
Deciduous	Closed birch
Dwarf shrub	Dwarf shrub other/Low shrub
Herbaceous	Mesic dry meadow
Low shrub lowland	Low shrub willow alder
Low shrub upland	Low shrub-tussock tundra
Non-vegetated	Non-vegetated
Open spruce	Open spruce
Sparse vegetation	Sparse
Tall shrub	Closed tall shrub
Tussock lichen	Lichen
Water	Clear water
Wet herbaceous	Aquatic

Habitat covariates were extracted within a 1 km buffer around each centroid. The proportion of area of each covariate was measured. Habitat covariates within a 500 m buffer of each tripod location were also extracted to determine if habitat also influenced detection rates at tripod sites.

It is likely that the proportion of habitat classes across centroids were structurally related given the similarity of land cover and likely associations among different vegetative types. Of most interest in modelling was determination of the most parsimonious combinations of covariates to describe grizzly bear density and therefore it was useful to assess this structure. Principal components analysis was used to discern structural relationship between habitat covariates to allow further interpretation of density surface modelling results(Tabachnick and Fidell 1996, McGarigal et al. 2000).

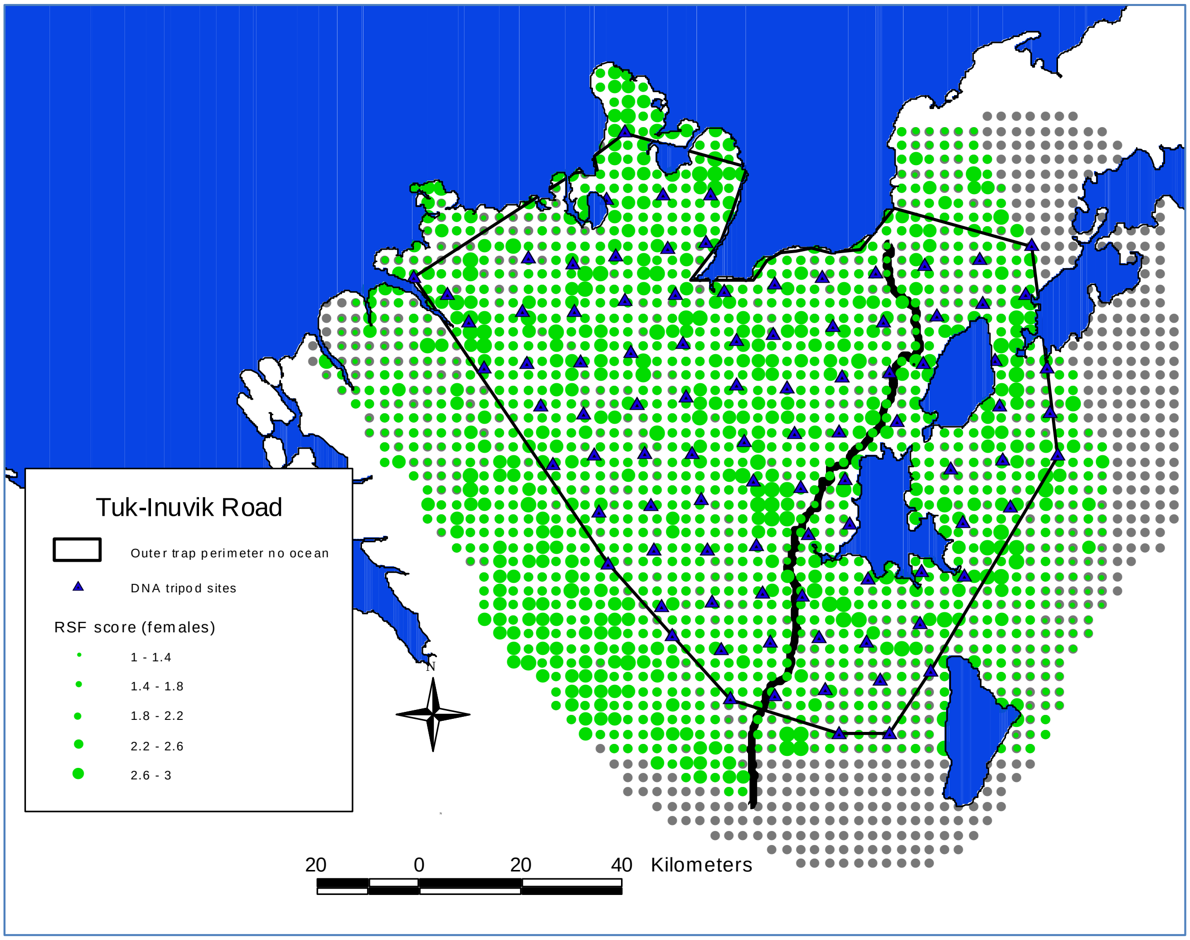

Figure 2: Habitat mask centroids, DNA tripod sites, and RSF scores for each centroid for the female season 1 habitat model (Edwards 2009).

Density surface models were built separately for male and female grizzly bears given likely differences in habitat selection and previous RSF modelling (Edwards 2009). The most supported SECR model from the initial SECR analysis was used as a base model for the density surface analysis. Habitat covariates were added individually to compare support to the base model. Models with the most supported habitat covariates were then considered. As with previous analyses, information theoretical methods were used to compare support of models.

Regional estimates of population size relative to the proposed road

The realized or average number of grizzly bears that could potentially encounter the road at any one time was estimated (by spatially explicit mark-recapture models) (Efford and Fewster 2012). Estimates from models that assumed constant density throughout the study area were compared to density surface models that accounted for habitat specific variation in density.

Results

A total of 1,262 hair samples were collected for DNA analysis to determine identification of individuals (Table 2). Successful hair captures at tripods averaged 29% across all sessions. The number of tripods where hair was collected and the number of individual hair samples collected per session increased as the study progressed (Table 1). Average session length approximated 14 days for the first 3 sessions, but increased to over 18 days for session 4 (Table 1) because of poor weather preventing helicopter flights.

Table 2. Schedule of lures used throughout the Inuvik-Tuktoyaktuk Highway grizzly bear DNA study sessions, June to August, 2013, along with mean session interval, total number of hair samples collected and the percent of tripods with successful hair captures.

Session	Lures used[1]	$\bar{x}$ interval (days)	Total samples	Tripods with hair samples
1	Rancid hogs blood, rancid fish oil[2], Predator Long-distance Call lure	14.4	231	18 (19%)
2	Rancid hogs blood, rancid fish oil, K9 Triple Take lure	13.6	271	26 (28%)
3	Rancid hogs blood, rancid fish oil, aged beluga oil	14.1	282	29 (31%)
4	Rancid hogs blood, rancid fish oil, beaver castor lure	18.4	478	35 (33%)

[1]Lures supplies by Forsyth Animal Lures, Alix, Alberta, except for aged beluga oil (supplied locally). All tripods received ~700 ml blood and ~300 ml fish oil. Lures were applied at ~15 ml/site.

[2]Rancid fish oil was mixed with rancid shellfish oil and oil of anise.

Summary of DNA data

Overall, 75 grizzly bears (46 females, 29 males) were detected over the 4 sampling sessions (Table 3). Detections per sampling period were relatively similar except with reduced female detections in session 1. The number of unmarked (bears not previously detected and genotyped) bears in each session decreased moderately for females and markedly for males suggesting sampling for males was efficient but it was likely there were unmarked bears on the grid at the end of sampling. Detection frequency, which is the number of sessions that each bear was detected, demonstrated that sampling was efficient with 41 bears detected once and 34 bears detected more than once.

Table 3: Summary statistics of the number of grizzly bears detected during the Inuvik-Tuktoyaktuk Highway grizzly bear project in 2013. All samples from an individual bear were pooled within each session for this summary for 'Bears detected,' 'Unmarked bears,' and 'Cumulative bears.' Detection frequencies refers to number of individual bears captured during 1 to 4 sessions during the study.

	Session			
Statistic	**1**	**2**	**3**	**4**
Females				
Bears detected	11	20	22	21
Unmarked bears	11	15	12	8
Cumulative bears	11	26	38	46
Detection frequencies	25	15	5	1
Males				
Bears detected	12	13	13	11
Unmarked bears	12	8	7	2
Cumulative bears	12	20	27	29
Detection frequencies	16	7	5	1
Males + Females				
Bears detected	23	33	35	32
Unmarked bears	23	23	19	10
Cumulative bears	23	46	65	75
Detection frequencies	41	22	10	2

The summaries in Table 3 pooled within-session detections of bears. For example, it was possible that a bear might be sampled at two tripods within the same session. Summaries of bear detections including within-session detections revealed that some bears were detected at up to 7 unique tripod-session combinations but the majority of bears were only detected at a single tripod (Figure 3).

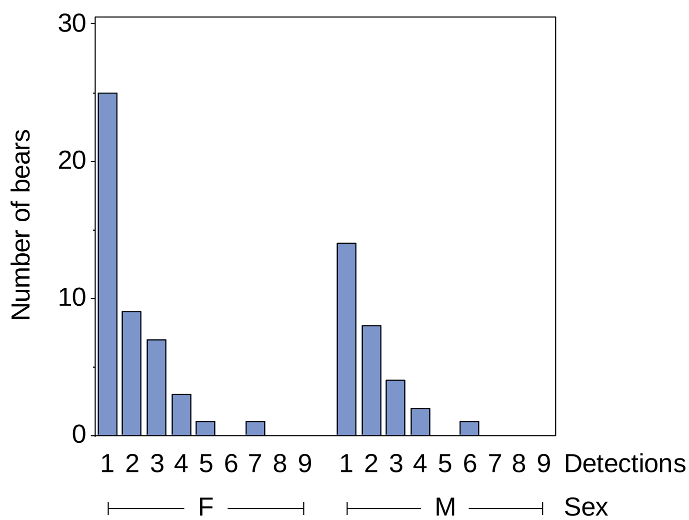

Figure 3: Frequencies of detections for bears including within-session redetections during the 2013 Inuvik-Tuktoyaktuk Highway grizzly bear DNA project.

When the distribution of bears as categorized by the number of unique tripods was examined, where a bear was detected during the entire study, it was found that both males and females bears were detected at up to 5 unique tripods (Figure 4). Spatially explicit mark-recapture uses information from Figures 2 and 3 to model movements and estimate the distances that bears traversed during sampling as related to detection rates.

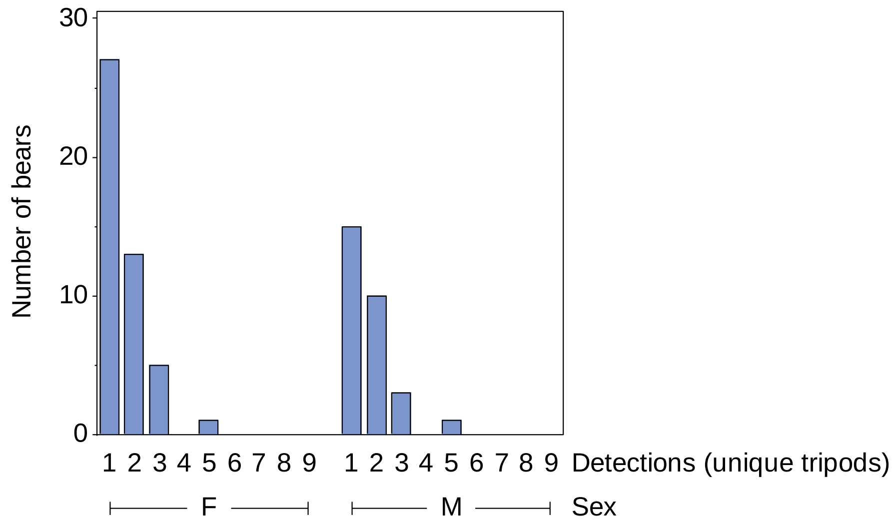

Figure 4: Detections of grizzly bears at unique tripods within the study area for all sessions during the 2013 Inuvik-Tuktoyaktuk Highway grizzly bear DNA project.

Summary of distribution of bears on the sampling grid

A plot of detections by tripod illustrates that the northern part of the grid had the most detection with fewer detections in the southeast portion of the grid (Figure 5).

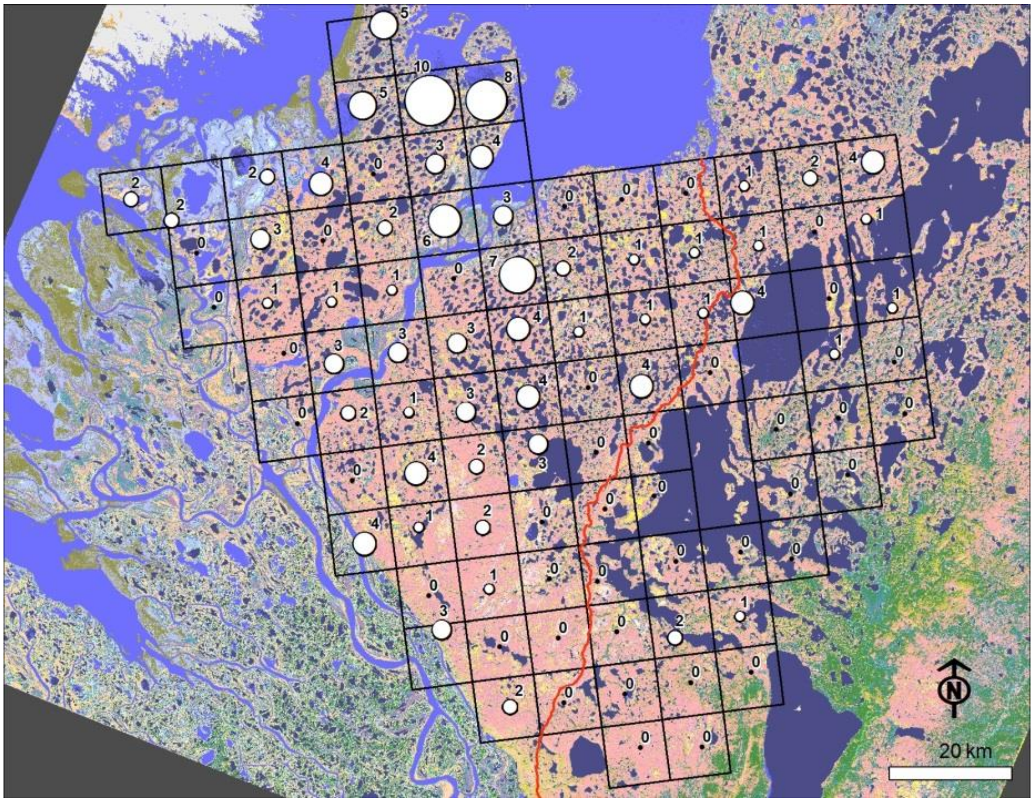

Figure 5: Frequencies of detection of bears pooled across sessions at each tripod. Circles are scaled to the number of detections.

A plot of individual grizzly bear mean detection locations (home range center) also illustrates the density gradient with a majority of grizzly bear mean detection locations to the west of the proposed Inuvik-Tuktoyaktuk Highway (Figure 6). Only 11 (7 females, 4 males) out of 75 bears had home range centres to the east of the proposed road alignment.

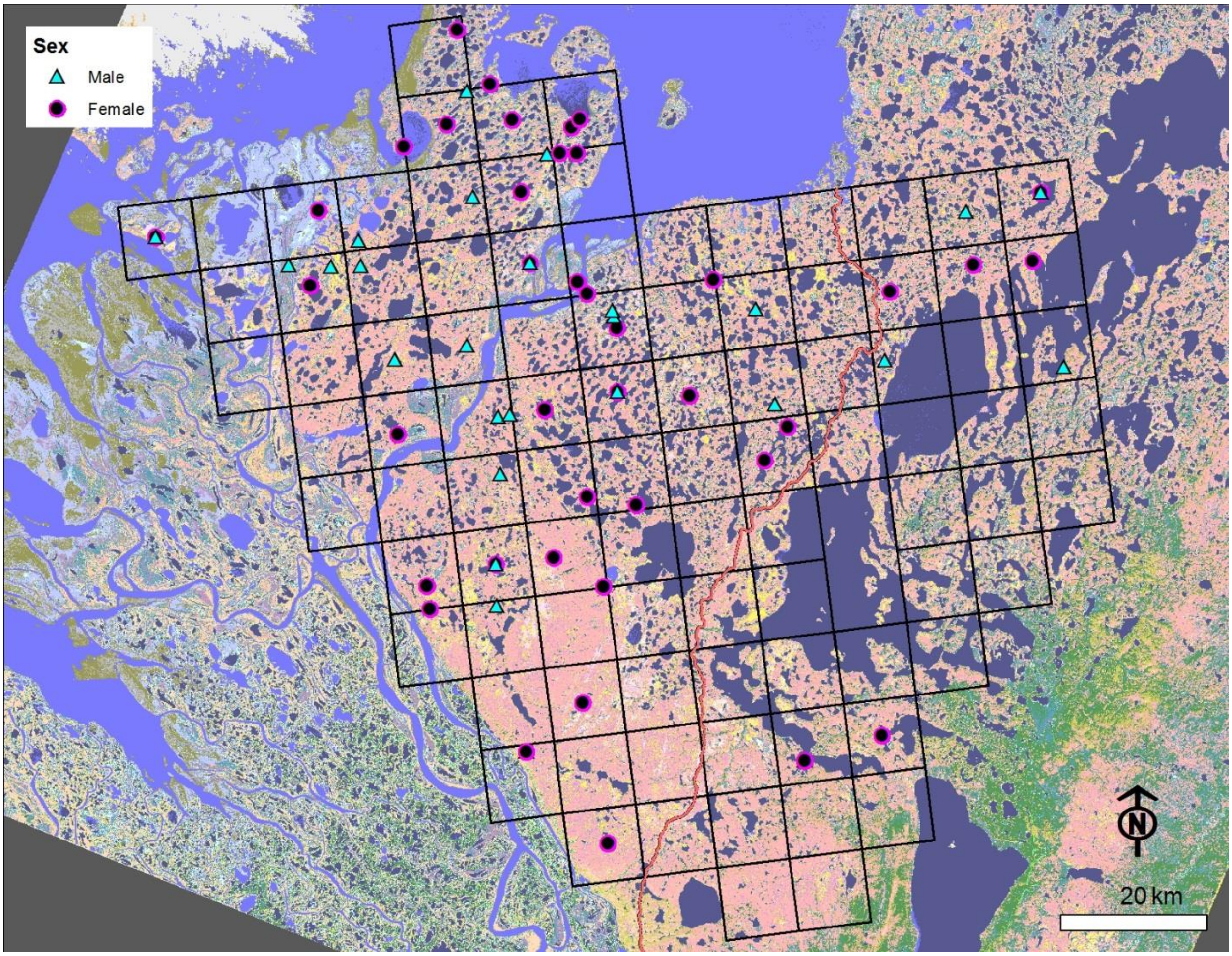

Figure 6: Mean detection of male and female bears during the 2013 Inuvik-Tuktoyaktuk Highway grizzly bear DNA project. In some cases more than one bear had the same home range center and therefore not all bears detected are displayed.

Closed population mark-recapture analysis to estimate population size

Closed model selection suggested that detection rates varied as a function of distance from the non-ocean edge of the grid (Table 4, Models 1-4). Sex-specific differences in detection were not supported; however, a model (Model 1, Table 4) with different initial detection and redetection rates was supported suggesting a behavioural response to DNA sampling. Interestingly, a model with equal detection and redetection rates (Model 2) was also marginally supported. This suggests the overall difference in rates of grizzly bear initial detection and subsequent redetection was not a strong effect.

Table 4: Huggins closed model selection. Models are denoted by the assumption made about initial detection probabilities, redetection probabilities (after initial detection), and the influence of distance from all borders or distance from the non-ocean edge of detection and redetection rates. Constant = the detection rate parameter was similar for all sessions and for male and female bears. t_1 = detection rates were unique for the first sampling session. Heterogeneity mixture models are denoted by π and ϴ. AIC_c = sample size adjusted Akaike Information Criterion , ΔAIC_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 deviance are given.

No	Detection (p)	Redetection	Grid edge	AIC_c	ΔAIC_c	w_i	K	Deviance
1	constant	constant	log(ocean)	369.9	0.00	0.52	4	361.8
2	constant		log(ocean)	371.8	1.83	0.21	2	367.7
3	sex		log(ocean)	373.2	3.24	0.10	3	367.1
4	t_1		log(ocean)	373.8	3.87	0.08	3	367.7
5	t_1		ocean	374.8	4.83	0.05	2	370.7
6			ocean	376.0	6.05	0.03	3	369.9
7	t_1			378.3	8.34	0.01	2	374.2
8	t_1	constant		380.2	10.26	0.00	3	374.1
9	sex+t_1			380.3	10.34	0.00	3	374.2
10	constant			382.7	12.80	0.00	1	380.7
11	t_1		all borders	383.2	13.29	0.00	2	379.2
12	sex	sex		383.3	13.38	0.00	4	375.2
13	sex+Ft_1	sex		383.3	13.38	0.00	4	375.2
14	sex			383.9	13.93	0.00	5	373.7
15	π(sex) $\Theta_{1\&2}$(sex)			384.6	14.62	0.00	2	380.5
16	sex*t	Sex *t		389.8	19.84	0.00	6	377.5

Model averaged estimates of detection and redetection for males were 0.32 (SE=0.08, CI=0.19-0.48) and 0.35 (SE=0.05, CI=0.27-0.45), respectively, whereas estimates of detection and redetection for females were 0.30 (SE=0.07, CI=0.18-0.46) and 0.34 (SE=0.05, CI=0.26-0.44), respectively. These estimates suggested a moderate “trap-happy” response where detection increased after initial encounter with the site. In plain terms, bears that had visited a tripod and left a hair sample were more likely to be redetected when compared to bears that had not yet been detected. This could result in an overestimate of detection probability of unmarked bears and a resulting negative bias in superpopulation estimates. Model averaged estimates that included a behavioural response of to multiple hair snag sessions (Model 1) and with no behavioural response (Model 1 removed) were 122 and 111, respectively, suggesting that the level of bias was not large (Table 5). Estimators for behavioural response models are less precise and therefore precision was low (CV>30%) with behavioural responses included (Model 1), and slightly better (CV>20%) when behavioural responses were not considered.

Table 5: Model averaged superpopulation estimates ($\widehat{N}$)from the Closed Huggins model analysis Coefficient of variation (CV) is given as an indicator of precision.

Parameter	Individuals detected	$\widehat{N}$	SE($\widehat{N}$)	Confidence limit	CV
Behavioural response					
Females	46	75	22.63	53-158	30.3%
Males	29	47	14.97	33-104	31.9%
Pooled	75	122	37.85	87-263	31.1%
No behavioural response					
Females	46	68	14.38	53-117	21.0%
Males	29	42	7.90	34-68	18.7%
Pooled	75	111	24.89	85-198	22.5%

Spatially explicit mark-recapture analysis to estimate grizzly bear density, home range, and scale of movement

Assessment of movement of grizzly bears between sites throughout the study period estimated that grizzly bears moved an average of 10.6 ± 1.3 km(SD)(females)) and 12.9 ±2.2 km (SD)(males) between detections. A spatial representation of movements (using repeat detections of individual bears within and across sessions) showed large-scale (>50 km) movements for both males and females (Figure 7). Movements and densities of males were greater in the northwest half of the sampling grid with females showing more movement and higher densities in the mid-part of the grid closer to where the highway will occur.

As an initial step in the modelling process the effective sampling area (termed the habitat mask) of the grid was estimated. The effective sampling area in the context of spatially explicit modelling is the grid and surrounding area where a bear could be detected. Using an iterative process this was estimated to be the grid and a buffer area of 27 km surrounding the grid. Significant water bodies such as the ocean and large lakes were also modelled as non-habitat and density was set to 0 in these areas (Figure 7).

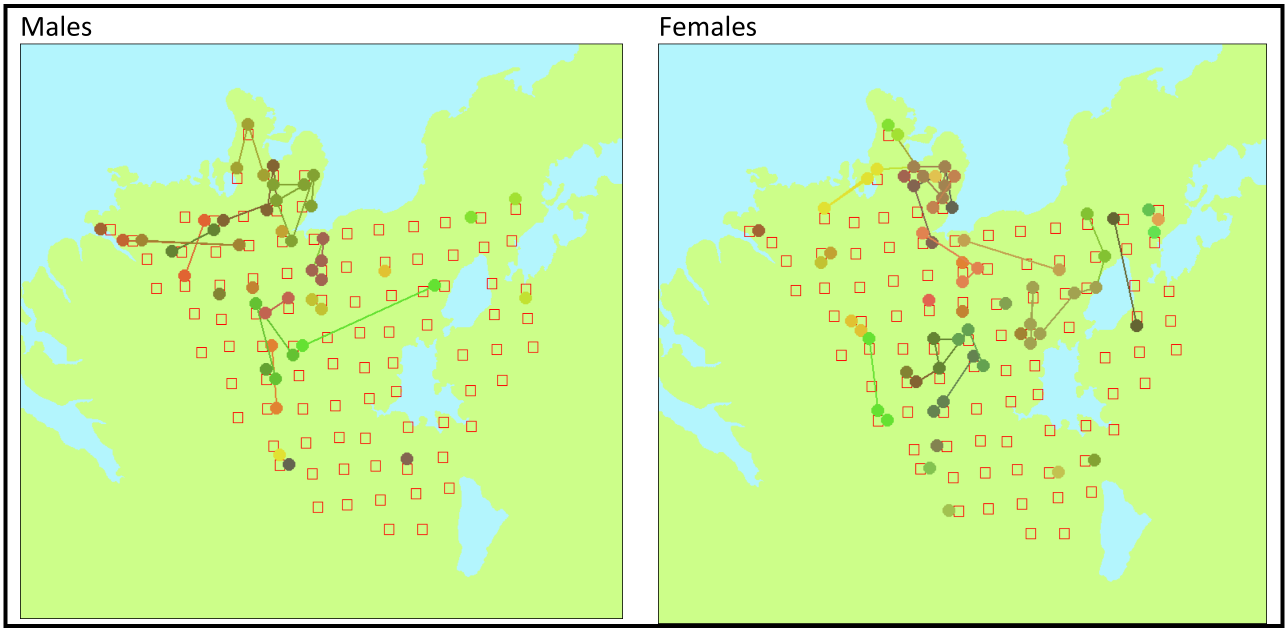

Figure 7: Movements of grizzly bears on the sampling grid for all sessions as indexed by detections at different tripods. Individual bears are indicated by unique colors. The green area was considered habitat whereas blue areas (ocean and lakes) were denoted as non-habitat for the spatially explicit analysis.

Spatially explicit model selection focused on variation in detection probability at home range center (g_0) and movement (sigma, σ). Models that considered behavioural change in g_0 were most supported (Table 6, Models 1-4). Models that considered change in detection probability of individual bears based on detection in the previous occasion (Models 1 and 2: denoted by 'B') were more supported than models that assumed change in detection probabilities after initial detection across all sessions (denoted by 'b'; Models 3 and 4). The most supported model suggested this change was similar for males and females (Models 1) in contrast to a model that considered unique change for males and females (Model 2)

Table 6: Spatially explicit model selection with models indicated by assumptions made about detection at home range center g_0 and scale of movement (σ). Sex =sex-specific estimates, B =the change in detection rate if the bear was detected in previous occasion, b = change in detection if the bear was detected previously (in any session), T =linear trend, t =session-specific parameters, constant =single value for parameter, t_1 =specific estimate for session 1, and h_2 =2-mixture model for heterogeneity of detection rates. Sample size adjusted Akaike Information Criterion (AIC_c), the difference in AIC_c from the most supported model (ΔAIC_c), AIC_c weight (w_i), number of model parameters (K) and log-likelihood are given.

No	Detection (g_0)	Scale (σ)	AIC_c	ΔAIC_c	w_i	K	Log-Likelihood
1	sex+B	sex	1108.8	0.00	0.543	7	-546.6
2	sex*B	sex	1110.8	1.98	0.201	8	-546.3
3	sex+b	sex	1112.1	3.25	0.107	7	-548.2
4	sex*b	sex	1112.1	3.31	0.104	8	-547.0
5	sex*T	sex	1116.6	7.82	0.011	8	-549.2
6	sex	sex*T	1117.2	8.35	0.008	8	-549.5
7	sex+t	sex	1117.7	8.90	0.006	9	-548.5
8	sex	sex+b	1117.7	8.93	0.006	7	-551.0
9	constant	constant	1118.1	9.31	0.005	4	-554.8
10	sex	sex	1118.3	9.51	0.005	6	-552.5
11	sex	sex+B	1118.7	9.87	0.004	7	-551.5
12	constant	sex	1119.4	10.55	0.000	5	-554.2
13	sex*h_2	sex	1119.9	11.08	0.000	9	-549.6
14	sex	constant	1120.1	11.24	0.000	5	-554.6
15	sex+t_1	sex	1120.7	11.94	0.000	7	-552.5
16	sex	sex+t_1	1120.7	11.94	0.000	7	-552.5
17	sex	sex*h_2	1120.8	11.98	0.000	9	-550.0
18	sex*t	sex	1122.0	13.17	0.000	12	-546.5
19	sex*t_1	sex	1123.3	14.45	0.000	8	-552.5

Plots of the detection function from Model 1 revealed that males displayed lower detection at home range center but had larger scale movements compared to females that had a higher detection probability at the home range center but lesser movements (Figure 8). In both cases detection probabilities were above 0 at distances greater than 10 km suggesting that the 10 km tripod cell size was adequate. Redetection rates at home range center (after initial detection) increased to 0.11 (males) and 0.20 (females) ,.

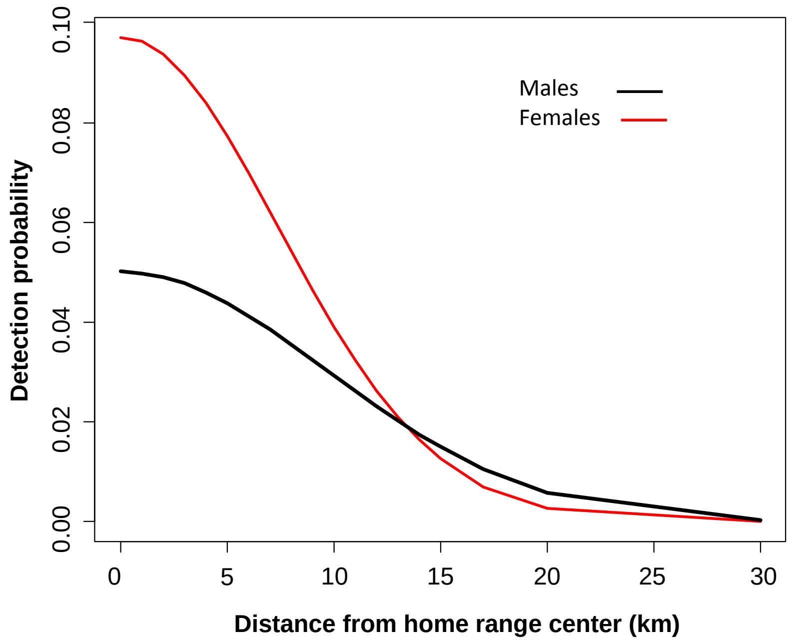

Figure 8: Spatially explicit detection function from Model 1 (bears with different initial detection and redetection rates) (Table 4) for males and females. The plot shows estimates of initial detection probability. Redetection probability (if detected in previous occasion) at home range center increased to 0.11 and 0.20 for males and females, respectively.2013 Inuvik-Tuktoyaktuk Highway grizzly bear DNA project.

Model averaged estimates of density were run with and without the behavioural response models (Table 6; Models 1-4) to assess the sensitivity of estimates to behavioural response. Estimates of density and average population size were higher and less precise with the behavioural response models (Table 7). For both cases of the non-behavioural response models both pooled sex estimates and sex-specific estimates had acceptable precision (CV<20%).

Table 7: Model averaged estimates of density (bears per 1,000 km^2) and average number of bears (Ave N) on the sampling grid for all models in the analysis and with the behavioral response models excluded. Confidence limits (95%) are also given.

Sex	Density bears/1,000km	SE	Conf. Limit	CV	Ave # of bears	SE	Conf.Limit
All models							
Females	6.84	1.79	4.13-11.32	26.1%	63.6	16.6	38.4-105.3
Males	4.24	1.14	2.53-7.11	26.9%	39.4	10.6	23.5-66.2
Males + Females	11.08	2.12	6.66-18.43	19.1%	103.0	19.7	45.0-124.3
No behavioural models							
Females	5.49	1.10	3.72-8.10	20.0%	51.1	10.2	34.6-75.3
Males	3.44	0.67	2.35-5.01	19.5%	32.0	6.2	21.9-46.6
Males + Females	8.93	1.29	6.08-13.11	14.4%	83.0	12.0	41.0-88.6

The spatially explicit estimates were also used to assess the area of detectable influence of the road based upon detection function estimates for male and female bears. The detectability of bears becomes negligible at distances greater than 20km for females and 25 km for males (<0.005)(Figure 8). This can be conceptualized to mean that if a bear had its home range center on the road, that bear could be detected up to 20-25 km from the road. Conversely, a bear whose home range center was 20-25 km from the road might be just be detectable by a DNA tripod placed near the road (Figure 8). Therefore, these estimates help define the sample size of bears that were within detectable range of the road based upon their mean detection locations. Using the 20 km (female) and 25 km (male) km distances, 9 males and 11 females were in detectable range of the road. Of the bears not in detectable range, 3 females and 2 males were to the east of the road and 23 females and 11 males were in the northwestern section of the grid.

The grid of dots in Figure 9 illustrates the habitat mask used in the program SECR as the mask centroids overlaying the trapping area. In the program SECR, bear density is estimated for each centroid. For analyses in this document grizzly bear density was assumed to be equal for each centroid. The extent of the mask is based upon a liberal estimate of a maximum bear detection distance of 27 km (as formulated in an initial step of the analysis). Comparison of the extent of the mask and the buffer distance from the road provides an estimate of the total area of inference for the DNA sampling grid. From this comparison, it can be seen that additional areas to the north and south of the road could be sampled to further increase the sample size of bears that are within detectable range of the road (Figure 9). This would also extend the mask surface further to the north and south.

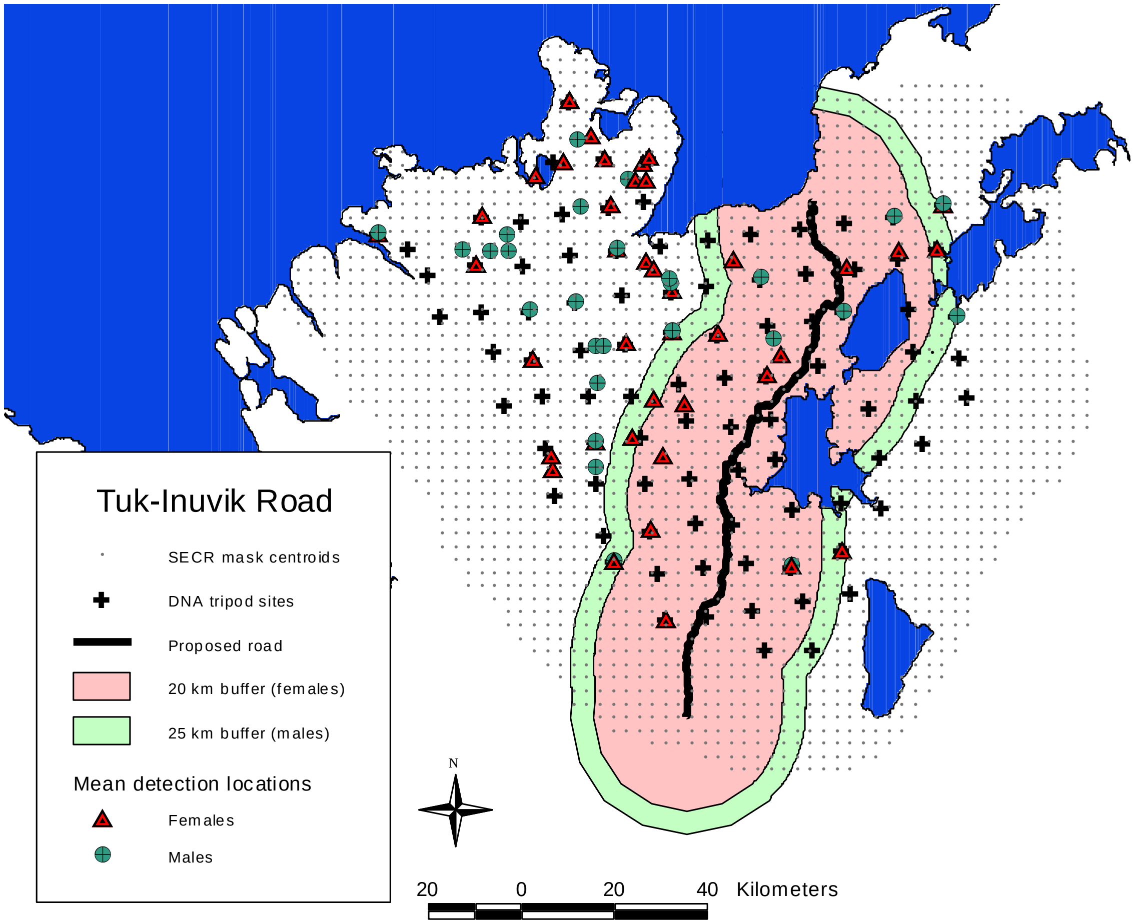

Figure 9: Proposed Inuvik-Tuktoyaktuk Highway with SECR based buffers of 20 km (females) and 25 km (males) which define the potential area of greatest influence of the road on grizzly bears during sampling. Also shown are mean detection locations for male and female bears, DNA tripod sites and dominant water bodies that were modelled as non-habitat in the SECR analysis. In addition, centroids of the habitat mask used by the SECR model are shown.

Variation in grizzly bear density

Structural relationships between habitat covariates using density surface modelling

Principal components analysis was used to assess structural relationships among the primary habitat covariates. The principal components model explained 57% of the variation in the covariate data with the three principal components. Principal component scores suggested the higher association of shrub and lichen for the first component, closed spruce and deciduous (positive) and non-vegetated/sparse vegetated (negative) for the second loading and low shrub lowland and wet herbaceous for the third component (as determined by loads of greater than 0.5) (Table 8).

Table 8: Standardized component scores for principal components analysis of SECR habitat mask remote sensing data. Significant factors are in bold.

Variable	Factor1	Factor2	Factor3
Closed spruce	0.17	**0.61**	-0.33
Deciduous	0.07	**0.59**	-0.48
Dwarf shrub	**-0.84**	0.14	-0.02
Low shrub lowland	0.47	-0.09	**0.67**
Low shrub upland	**-0.83**	-0.13	0.20
Open spruce	0.32	0.35	-0.06
Tall shrub	0.48	0.38	0.18
Tussock lichen	**-0.71**	-0.18	0.31
Water	0.24	-0.27	-0.18
Wet herbaceous	0.47	0.35	**0.56**
Herbaceous	0.40	-0.45	0.23
Non-vegetated	0.41	**-0.65**	-0.30
Sparse vegetation	0.27	**-0.62**	-0.39

Inspection of principal component plots suggested positive associations of higher elevation communities (dwarf shrub, low shrub upland, tussock lichen) for the first component (Figure 10). The second component was positively associated by closed canopy vegetation (closed spruce/deciduous/closed birch) but negatively associated with sparse/non-vegetation areas. The third component was less associated with any particular class. These results suggest that the dominant gradients are towards association of higher elevation communities (first component) and closed cover in opposition to sparse/non vegetated classes in the second component. The main interpretation of this result is that association of any particular habitat class may indicate a general gradient in the data set as opposed to a single association (as discussed later).

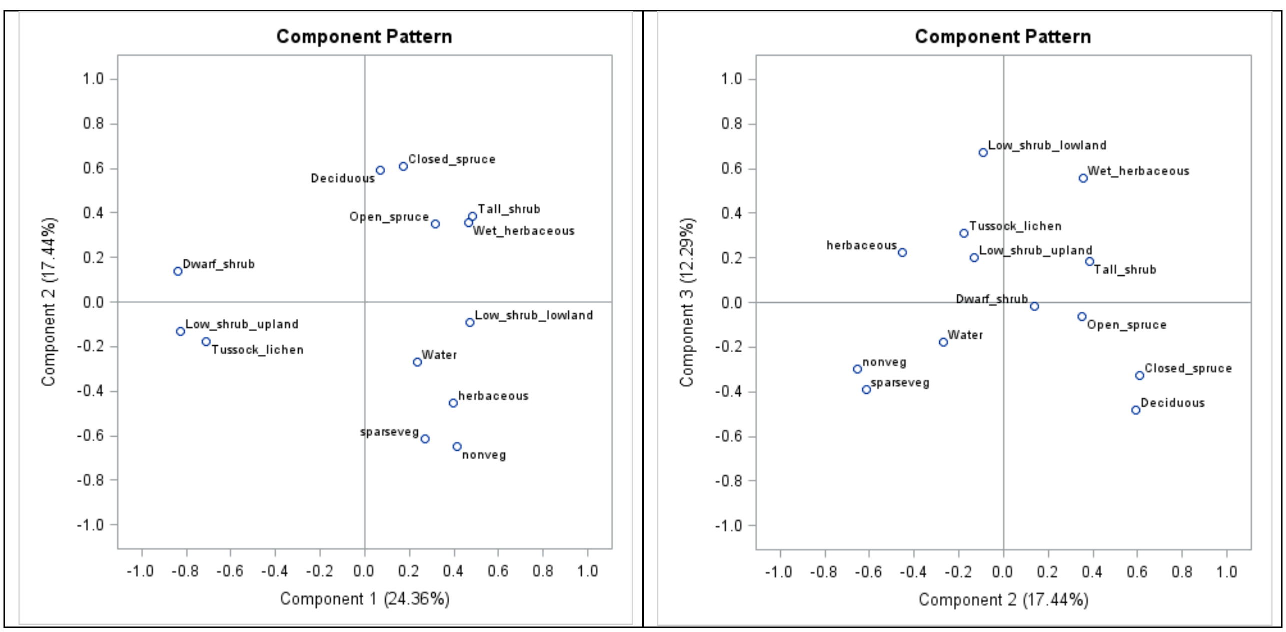

Figure 10: Plots of principal component scores (Table 8) for mask centroid covariates.

Variation in female grizzly bear density – analysis with surface modelling

Initial analyses of a female grizzly bear density surface model considered the best baseline model for detection probabilities and it was sigma based on the most supported models from the combined sex analyses in Table 6. A model that included a change in the probability in grizzly bear detection after the initial detection at the home range center (g_0(b)) and a constant scale of movement (σ) was most supported (Table 9, model 16). Models that constrained site detection probabilities to be a function of covariates were not supported (Models 25-27). Models that assumed a linear rather than exponential relationship between habitat covariates and density were also not well supported (Models 28-29).

Table 9 : Female spatially explicit density surface modelling model selection results. A base model (g_0 (b), sigma (.) was used for all analyses except when noted. An exponential relationship between covariates and density was assumed except where noted. The base model (with no density covariates) is shaded in grey. Sample size adjusted Akaike Information Criterion (AIC_c), the difference in AIC_c between the most supported model for each model (ΔAIC_c), AIC_c weight (w_i), number of model parameters (K) and deviance are given.

No	Density surface model	AIC_c	ΔAIC_c	w_i	K	LL
1	Deciduous	624.83	0.00	0.35	5	-306.66
2	Decidous+Wet herbaceous	625.91	1.08	0.20	6	-305.88
3	Deciduous+Closed spruce	626.99	2.16	0.12	6	-306.42
4	Deciduous+Dwarf shrub	627.14	2.31	0.11	6	-306.49
5	Deciduous+ Non-vegetated	627.45	2.62	0.09	6	-306.65
6	Deciduous+Non-vegetated+Wet herbaceous	628.78	3.95	0.05	7	-305.92
7	Closed spruce	629.29	4.47	0.04	5	-308.90
8	Closed spruce+Deciduous+Dwarf Shrub	630.22	5.39	0.02	7	-306.63
9	RSF mean	633.42	8.60	0.00	5	-310.96
10	Dwarf shrub	634.13	9.31	0.00	5	-311.32
11	Low shrub upland	635.46	10.63	0.00	5	-311.98
12	Wet herbaceous	635.65	10.82	0.00	5	-312.07
13	Non-vegetated	636.17	11.34	0.00	5	-312.33
14	Elevation	636.21	11.38	0.00	5	-312.36
15	Sparse/non-vegetated	636.91	12.08	0.00	5	-312.70
16	Constant density	636.93	12.10	0.00	4	-313.98
17	Herbaceous	637.72	12.89	0.00	5	-313.11
18	constant (g_0(B model)	637.94	13.11	0.00	4	-314.48
19	Water	637.98	13.16	0.00	5	-313.24
20	Sparse vegetation	638.05	13.23	0.00	5	-313.28
21	Low shrub lowland	638.55	13.72	0.00	5	-313.52
22	Open spruce	639.14	14.32	0.00	5	-313.82
23	Tussock Lichen	639.34	14.51	0.00	5	-313.92
24	Tall shrub	639.43	14.61	0.00	5	-313.97
25	constant (g_0 elevation)	639.44	14.62	0.00	5	-313.97
26	constant (g_0 constant)	645.08	20.25	0.00	3	-319.25
27	constant (g_0 RSF mean)	651.04	26.21	0.00	5	-319.77
28	Linear (RSF)	651.56	26.74	0.00	5	-320.03
29	Linear(Deciduous)	651.65	26.82	0.00	5	-320.08

Female grizzly bear density surface models revealed a large number of associations between density and habitat covariates as indicated by support of individual models (Table 9, Models 1-15) compared to models assuming constant density across the study area (Model 16). Of these models, the most parsimonious has deciduous (primarily closed birch) as a single predictor variable. Models with wet herbaceous and closed spruce also had some support from the data as indicated by ΔAIC_c values of less than 2. Plots of predicted densities for mask centroids and covariates revealed a negative relationship between deciduous (closed birch) cover where bear density was above 0 only when the proportion of deciduous cover was less than 0.1 (Figure 11). Wet herbaceous vegetation defined areas of higher density when modelled with deciduous cover (Model 2). Closed spruce cover was similar to deciduous with larger confidence limits on predictions. RSF score was positively associated with density, however, confidence limits were wide as also indicated by lower support of the RSF habitat predictor model.

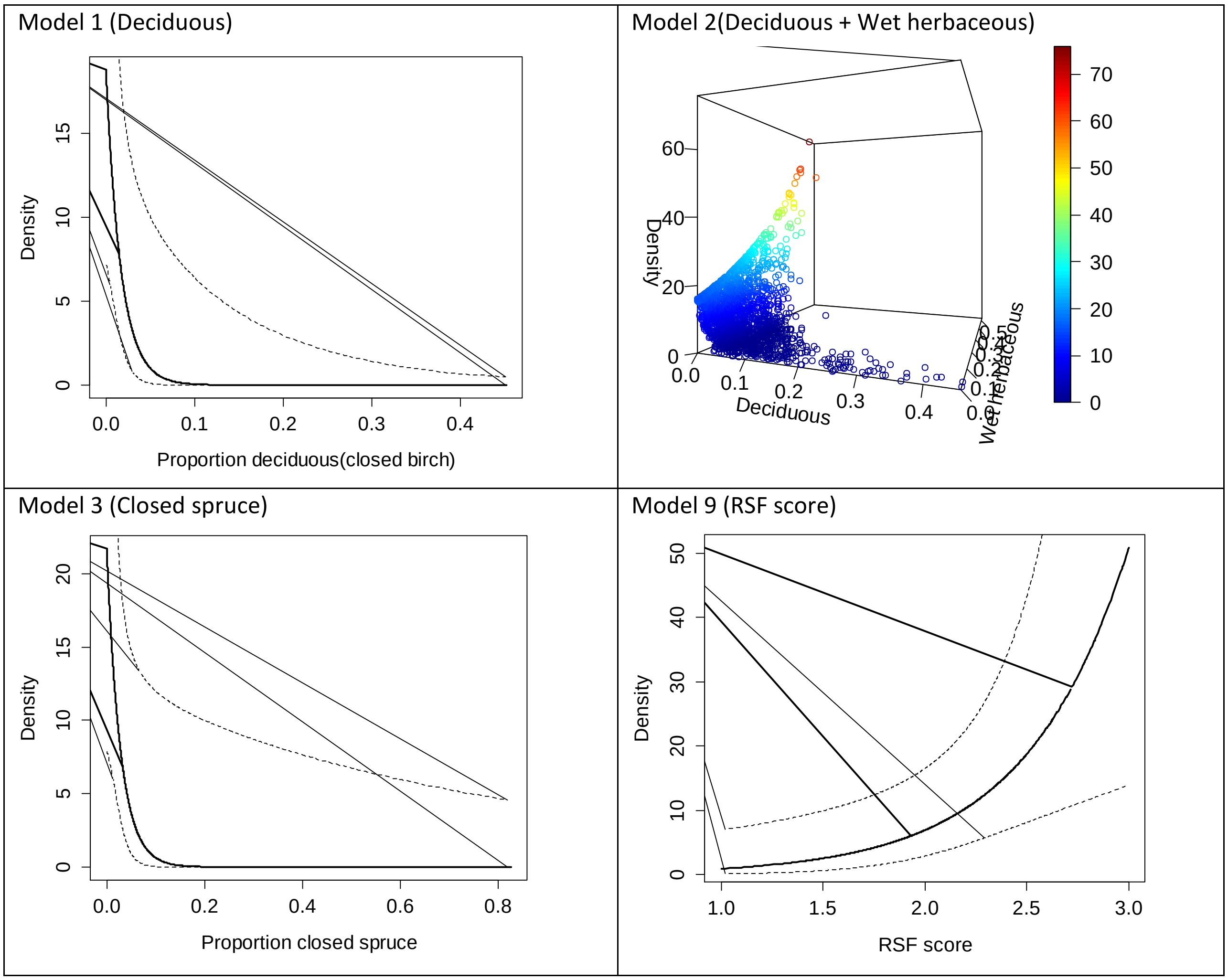

Figure 11: Plots of predicted female densities for mask centroids as a function of deciduous cover (upper left), deciduous + wet herbaceous cover (upper right), closed spruce (lower left) and RSF score (lower right). The color bar in the upper right plot corresponds to levels of density (the z-axis). Density is expressed in bears per 1000 km^2.

Spatial plots of Models 1 and 2 revealed that both models predicted lower densities in the southern part of the sampling grid with Model 2 predicting the highest densities in the northern corner (in association with higher wet herbaceous habitat type). Mean detection locations of females also followed this general pattern with the most detections in the northern part of the study area and the least detections in the south.

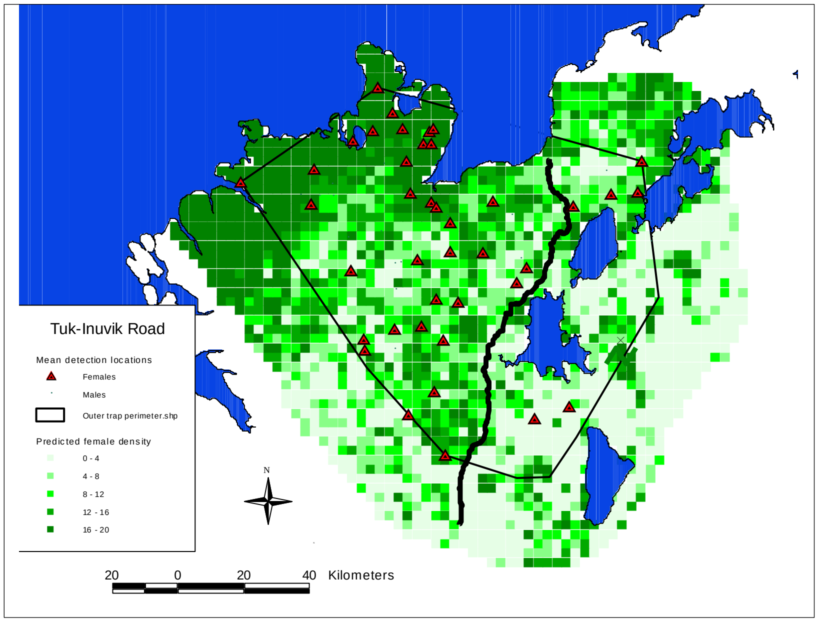

Figure 12: Predicted female grizzly bear density of mask centroids based upon deciduous (closed birch) habitat Model 1 (Table 9)

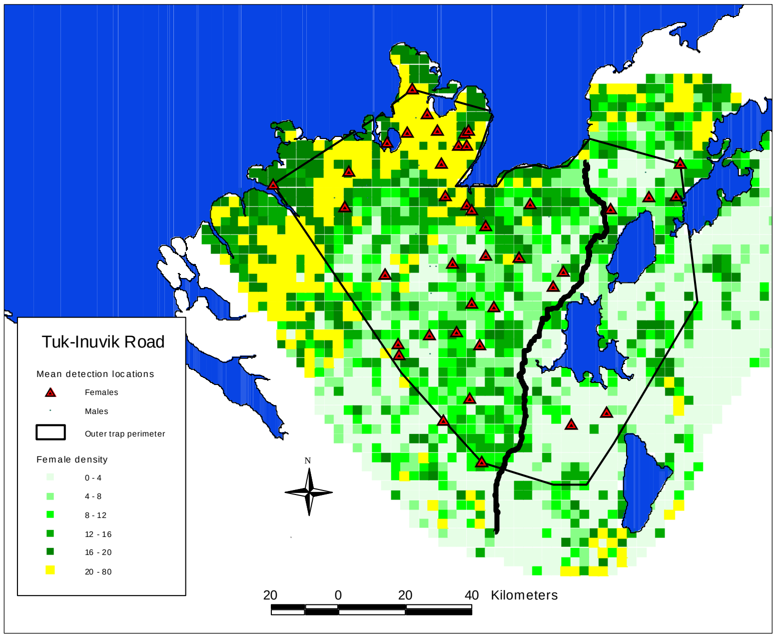

Figure 13: Predicted female grizzly bear density of mask centroids based upon deciduous (closed birch) and wet herbaceous (aquatic) habitat Model 2 (Table 9)

Male density surface modelling

Initial analyses considered the best baseline model for detection probabilities and sigma based on the most supported models from the combined sex analyses (Table 6). A model with change in detection probabilities based upon detection in the previous session (g_0(B)) with constant sigma was most supported (Table 10, Model 5). A single model with deciduous (closed spruce) was supported by the data with few covariate models showing greater support than the constant density model (Model 5).

Table 10 : Male spatially explicit density surface modelling model selection results. A base model (g_0 (B), sigma (.) was used for all analyses except when noted. An exponential relationship between covariates and density was assumed except where noted. The base model (with no density covariates) is shaded in grey. Sample size adjusted Akaike Information Criterion (AIC_c), the difference in AIC_c between the most supported model for each model (ΔAIC_c), AIC_c weight (w_i), number of model parameters (K) and deviance are given.

No	Covariates	AIC_c	ΔAIC_c	w_i	K	LL
1	Deciduous	469.6	0.00	0.36	5	-228.5
2	Deciduous+Wet herbaceous	472.2	2.60	0.08	6	-228.2
3	Closed spruce	472.6	2.98	0.08	5	-230.0
4	Deciduous+herbaceous	472.8	3.14	0.06	6	-228.5
5	constant g_0(B)	472.9	3.33	0.07	4	-231.6
6	constant (g_0 constant)	473.0	3.37	0.07	3	-233.0
7	elevation	473.0	3.42	0.07	5	-230.2
8	herbaceous	473.5	3.93	0.05	5	-230.5
9	wet herbaceous	474.1	4.50	0.04	5	-230.7
10	minimal vegetation	474.1	4.52	0.04	5	-230.8
11	tall shrub	474.7	5.06	0.03	5	-231.0
12	low shrub lowland	475.3	5.65	0.02	5	-231.3
13	constant (g_0 b)	475.3	5.71	0.02	4	-232.8
14	non-vegetated	475.6	5.95	0.02	5	-231.5
15	sparse/non veg	475.6	6.03	0.02	5	-231.5
16	tussock lichen	475.6	6.04	0.02	5	-231.5
17	dwarf shrub	475.7	6.08	0.02	5	-231.5
18	low shrub upland	475.7	6.08	0.02	5	-231.5
19	sparseveg	475.8	6.17	0.02	5	-231.6
20	water	475.8	6.18	0.02	5	-231.6
21	RSF	475.9	6.27	0.02	5	-231.6
22	open spruce	475.9	6.27	0.02	5	-231.6
23	g_0(rsf)	480.4	10.76	0.00	5	-233.9
24	g_0(elevation)	1011.7	542.11	0.00	5	-500.4

Plots of male density versus deciduous habitat revealed a similar relationship with females but the precision of predictions was poor as evidence by large confidence limits on predictions (Figure 14).

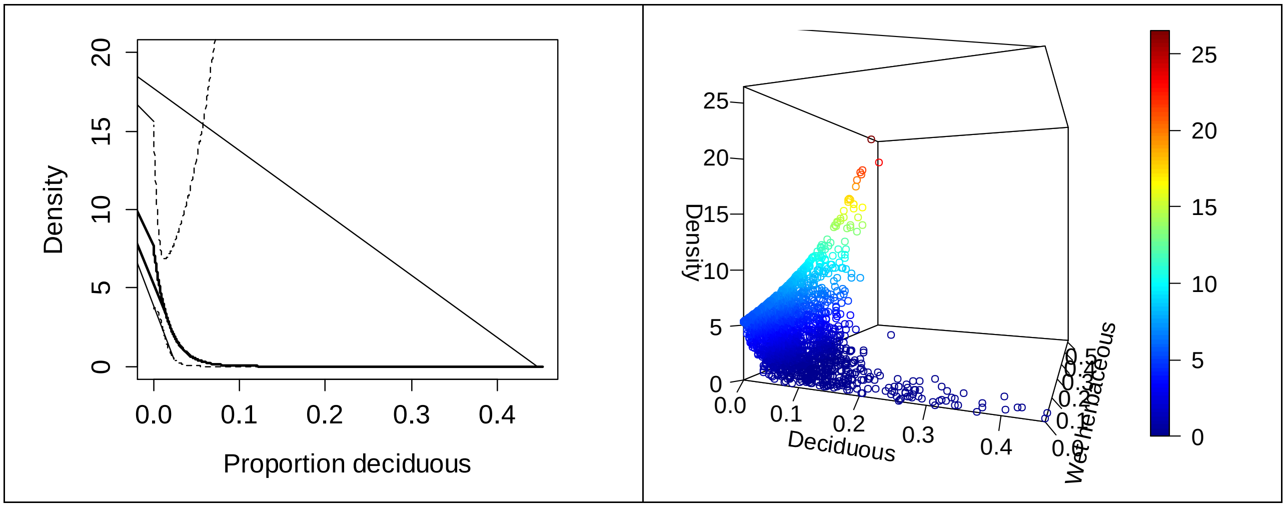

Figure 14: Predicted density of male grizzly bears as a function of deciduous habitat from Model 1 and deciduous and wet herbaceous habitat (Model 2, Table 9). Density is expressed in bears per 1000 km^2.

Predictions from the deciduous habitat model (Model 1) were plotted and compared with detection locations. The distribution of males based upon mean detection locations coincided with density predictions especially for the southern part of the sample area where few males were detected with corresponding low predicted density (Figure 15).

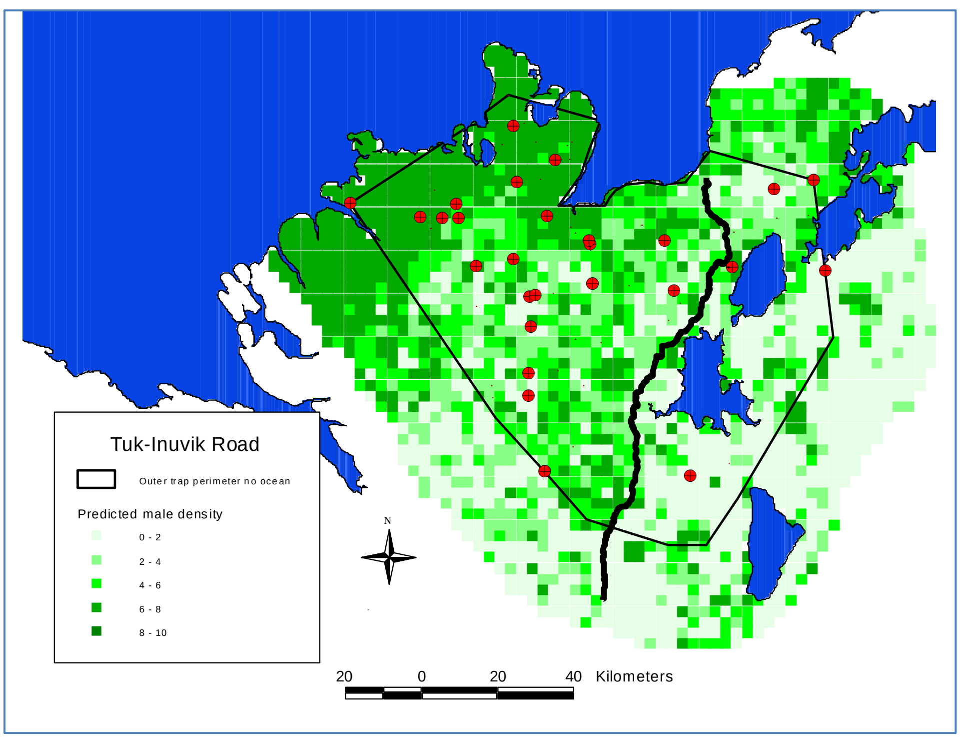

Figure 15: Predicted density at mask centroids for male grizzly bears based on deciduous (closed birch) habitat (Model 1, Table 10). Mean detection locations for males are given as red circles.

Regional estimates of population size relative to the proposed road

Regional population size estimates were generated for areas within 20 and 25 km of the proposed road which was the buffer distance estimated for females and males respectively. These estimates correspond to realized population size of bears or the average number of bears that would be within 20-25 km of the road at any one time. The 20-25 km buffer would ensure that the bears included in the estimate would have home ranges that would encompass the road, based on female and male grizzly bear scales of movement. Estimates from the density surface models were less than the constant density models which was presumably due to lower habitat specific densities near the road compared to areas further from the road such as the northern Richardson Island area (Figures 12-15). Precision of estimates was reduced compared to the pooled sex estimates. Future analyses will combine sexes which should enhance precision.

Table 11: Estimates of average numbers of bears within 20 km of the Inuvik-Tuktoyaktuk road from sex-specific SECR density surface models (Tables 9 and 10)

Density model	Estimate	SE	Confidence limit		CV
Females (20 km buffer)					
Constant	48	20.2	22	106	0.42
Deciduous	38	16.5	17	86	0.43
Deciduous+Wet herbaceous	36	16.0	16	82	0.44
Males (25 km buffer)					
Constant	26	6.02	16	40	0.23
Deciduous	20	5.09	13	33	0.25

Discussion

The main objectives of this study were to estimate baseline population size and density of grizzly bears in the Inuvik-Tuktoyaktuk Highway and surrounding area, and assess whether sample sizes of bears, study area extent, and other study design features were adequate to monitor grizzly bear populations relative to road construction and operation. This analysis identified a reasonably large population of bears with results suggesting that sampling was adequate to provide an estimate of baseline population size and distribution.

The presence of a behavioural response with detection rates increasing after subsequent capture was somewhat unique to this study. The usual mechanism for a trap happy response is that the animal gets a nutritional award from the site and is then more likely to revisit it. However, a habituation response to sites that were not moved between sessions was detected in a study in Alberta (Boulanger et al. 2006). The lure types used in this survey are identical to those in studies of both southern and barren-ground grizzly bears which have not shown a large degree of behavioural response. This type of response to DNA sampling was less supported in the Izok barren ground grizzly bear DNA study (Boulanger 2013), however, this may have been due to lower sample sizes and subsequent lower power to detect detection probability variation. Two types of behavioural response were suggested. For the combined sex analysis and the male-only density surface analysis, a model with detection probability changed based upon detection in the previous session was supported (denoted by a B). For the female only density surface analysis, a model with detection probability change after initial capture, independent of whether it was the previous session was most supported (denoted by b). Other studies, such as the Kitikmeot study, only used 2 sessions which precluded testing for behavioural response (Dumond et al. 2014). The main effect of behavioural response is negative bias in estimates which can be offset by use of behavioural response models which are less precise but presumably more accurate. It is likely that the lower precision of these models will be offset by the increased sample sizes from an additional year of data from sampling to be conducted in 2014. We suggest that four sampling sessions are conducted again in 2014 to allow adequate testing and modelling of behavioural response of detection probabilities.

The density surface modelling in this report represents the first attempt at describing the association of remote sensing-based habitat variables with grizzly bear density. The resulting models are reasonably simplistic in that only one or two habitat features are associated with density. This is presumably due to sample size limitations as well as the relatively large scale of habitat selection of grizzly bears detected by DNA sampling. One important point to note is that associations with habitat variables such as deciduous (closed birch) habitat most likely represent gradients of habitat selection rather than selection for the single factor. For example, principal component analysis results suggests that deciduous (closed birch) habitat is negatively related with sparse vegetation and non-vegetated site, so negative association with this habitat type also could infer positive selection for the sparse/non-vegetated habitat types. It is likely that more complex density surface models will become more supported as more years of data are collected.

For the current density surface analysis, scores for each mask centroid were based upon a 1 km buffer around each centroid. This distance represented a compromise between the relatively large scale of grizzly bear selection, the dimensions of the mask (mask centroids were spaced 2.7 km apart), and the need to ensure an adequate number of pixel sampling to derive a robust rating for each centroid. It is possible that this scale may not adequately represent finer scale RSF habitat values, and may not adequately account for the effect of water bodies and other landscape features. Future analyses will test different buffer distances to allow a sensitivity analysis of buffer distance on SECR density surface model selection and density predictions.

Further refinement of the monitoring design

The spatial information from the SECR analysis could be used for a variety of purposes. First, it could be used to define “impact” and “control” areas based upon the buffer widths. In this context, it becomes clear that the northwest portion of the grid could be considered a control area, while the road and surrounding 20 km buffer zone would serve as the impact area. These two areas could be compared in terms of demography and population size using open population models to determine apparent survival, rates of addition, and trend once a time series of data are collected. The regional population size estimates (Table 11) present a baseline estimate of bears that can be used for future estimates of trend and population size of bears relative to the road.

It was noted that estimates of the average number of bears relative to the road may not correspond to the actual cumulative number of bears that will traverse the area over an entire season. Estimates of average numbers of bears or “expected” population size are useful in that they correspond to a “snapshot” of abundance that can be easily related back to density. These estimates are useful for comparison with other studies or with average numbers of bears in other parts of a study area. For monitoring, the “superpopulation” or “realized” population size of bears, which is the cumulative number of bears that traverse through a study area over time, may be more relevant. Spatially explicit mark-recapture methods will estimate both quantities whereas closed population models estimate a quantity that is closer to a “realized” population size, but is less defined than SECR estimates given that closed models do not use spatial information when estimating population size (Efford and Fewster 2011).Realized estimates are derived under the assumption that usage in the periphery of the sampling grid, as estimated by the entire mask area (Figure 9) will decrease as described by the half-normal detection function (Figure 8). This assumption is reasonable if habitat is similar on the periphery of the grid compared to the main grid area, or the density surface model describes density well in the non-sampled area. These assumptions may be questionable for the Inuvik-Tuktoyaktuk grid given the abrupt change in habitat types on the western edge of the grid due to the Mackenzie Delta (Figure 5). Other peripheral areas of the sampling grid are delineated by ocean and are less relevant given that these areas are not modelled as habitat. The RSF density model for females rates the Mackenzie Delta habitat as higher quality (Figure 2) and the density surface models estimate reasonable densities (Figures 12, 13, and 15). Future analyses will consider radio-collared data and further consideration of the RSF predictions for this area.

The use of mark-recapture methods to monitor demography of bears has been used to assess the effect of varying levels of salmon escapement on grizzly bear populations in coastal British Columbia (Boulanger et al. 2004). Power analyses can be used to further refine sampling interval and sampling intensity to assess trend (Boulanger 2005). Often sampling can be reduced to bi-annual or tri-annual intervals with minimal loss of power once an initial set of bears is genotyped within the study area in the first few years of sampling.

It is possible that the spatial scale of movements of bears might change in response to the road, or that the road may not actually influence densities of bears in the entire 20-25 km buffer zone (Table 11). For example, more immediate areas might be influenced by traffic volume. Alternatively, mortality of bears could actually increase beyond the 20-25 km zone if the road provides enhanced access for hunters to travel beyond the immediate area of the road. In this case, the “zone of influence” of the road may not simply be defined as the 20-25 km zone of detection. The density surface analyses conducted provide baseline habitat models to estimate density variation throughout the study area. When the road is completed an additional zone of influence term can be added to assess if density changes relative to distance from the road. The main advantage to this approach is that the scale of movement of bears is taken into account in the SECR modelling process. In addition, the response variable is density rather than habitat selection. Therefore, the zone of influence in essence becomes a zone of “density change” which will allow an actual estimate of change in population size due to the road. Many potential zone of influence type shapes including piecewise curves (Boulanger et al. 2012) can be used to assess the effect of the road on grizzly bear density. By using multiple years of data it should also be possible to assess temporal change in the influence of the road by modelling the interaction of distance from road with year of survey.

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Appendices

Appendix 1 Background information on mark-recapture issues

Several fundamental mark-recapture concepts must be defined to ensure adequate understanding of the concepts discussed in this report.

Definition of a model and estimator

Mark-recapture estimation represents an improvement from traditional count-based census methods. With traditional methods bears would be counted or trapped and the number trapped would be the estimate of population size. Inherent in this is the assumption that all animals have been trapped or counted, otherwise the estimate of population size would be lower than the actual population size. In mark-recapture estimation the percentage of animals captured is estimated. This percentage is called a capture probability. This concept can be expressed by the following formula:

$$\widehat{N} = \frac{\widehat{M}}{\hat{p}}$$

In the above formula, *M* is the count of animals, $\hat{p}$ is the estimate of capture probability, and $\widehat{N}$ is the estimate of population size. With traditional census methods $\hat{p}$ is assumed to equal one. An important term can be introduced here. A *model* is a set of assumptions that correspond to an estimation method. In the case of a census, our model is based on the assumption that all animals are caught. Capture probability $\hat{p}$ is rarely equal to one, and, as a result, many models have been formulated that make differing assumptions on how $\hat{p}$ varies. For any model there is a corresponding estimator. An *estimator* is a set of mathematical formulae that allow an estimate using the assumptions of the model. In the case of a count model, the estimate is simply the count of animals caught. The subject of estimation using mark-recapture methods has seen much theoretical attention, and, therefore, many estimators exist which are much more complex than simple counts.

Bias, precision and robustness

Estimates of density and population size are evaluated using two principle measures: precision and bias. The best way to conceptualize precision and bias is to consider what a range of estimates might look like if a project was repeated many times (Figure 12).

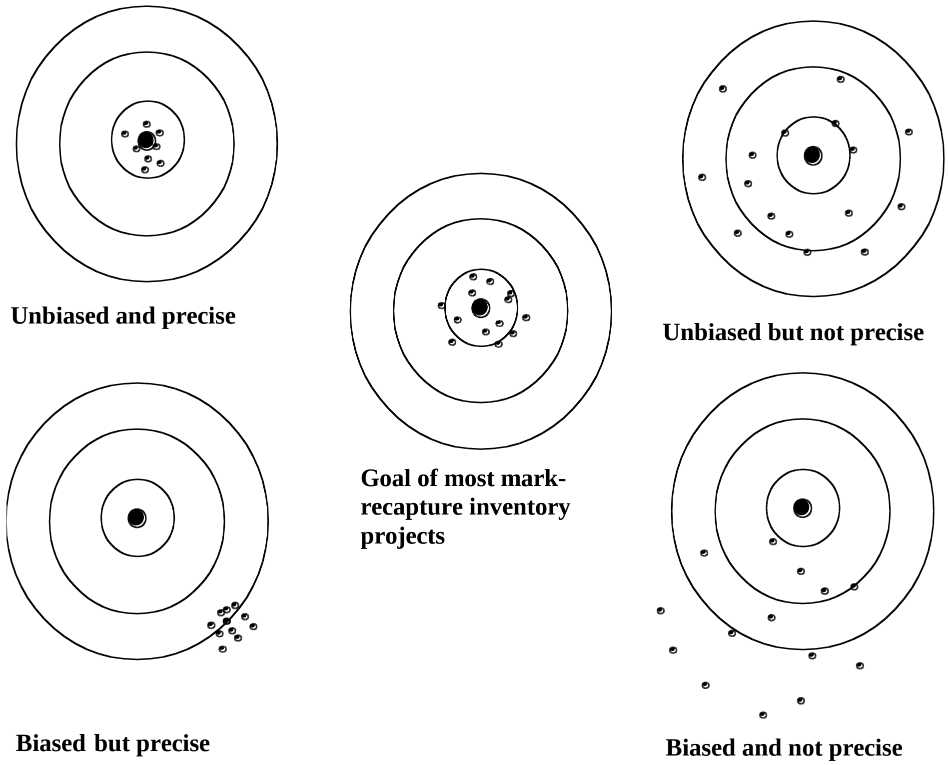

Figure 16: A conceptual diagram of bias and precision. Each target represents a possible set of estimates ("shots") from the mark-recapture experiment, if the study were repeated many times. Lack of precision is mainly caused by low sample sizes, and bias is caused by improper model selection. Unlike this target analogy, most mark-recapture experiments are only conducted once (i.e. one "shot") and the true bulls eye (true population size) is not known. Therefore, mark-recapture data should be interpreted cautiously and statistically to avoid erroneous conclusions (target figure from White et al. 1982).

Precision is the repeatability of estimates and is usually estimated by the coefficient of variation and the width of confidence intervals. *Bias* is the deviation of estimates from the true population value and is determined by how well the statistical model and estimator fit the mark-recapture data. The goal of most mark-recapture experiments is to minimize bias and maximize precision therefore minimizing potential error in estimates.

An ideal estimator of population size or density should be unbiased, precise, and robust. *Robustness* is a measure of how well an estimator will perform even when its associated assumptions about capture probability are violated. An example of a robust estimator would be one that assumes equal capture probabilities but still gives unbiased estimates when moderate capture probability variation exists in the data.

Key issues in optimal inventory design

Proper sampling design is critical to obtaining reliable population estimates. The following is a list of the three main issues in the design of projects to estimate population size (White et al. 1982).

1. *Meeting the assumption of geographic and demographic closure*: If closed population estimation models are used, then it is assumed that the population is closed or "no animals leave, enter, die

or are born during the sampling process." Violation of closure can cause substantial biases in estimates from most mark-recapture models. If closure violation is occurring, mark-recapture population estimates will pertain to the "superpopulation" of bears in the *sampling grid and surrounding area during the time that sampling was conducted*. (White 1996, Kendall 1999, Boulanger and McLellan 2001). For estimation of density and comparison of different areas the average number of bears on the sampling grid is most applicable. Recently spatially explicit methods have been developed that use the locations in which bears were captured to estimate movement of bears during sampling, detection rates at the center of home range, and density. This approach uses the same underlying models as closed models, but also allows covariates that describe trap locations and variation of density on the trapping grid (Efford 2004, Efford et al. 2009, Efford and Fewster 2013, Efford 2014a).

2. *Sample size*: Sample size is determined by the number of animals in the trapping area, the capture probability of the population, and the number of times the population is sampled. In general, higher population capture probabilities are needed for smaller population sizes to obtain adequate estimates. The primary effect of low sample size is reduced estimate precision. In addition, if sample size is low, then not enough data will be available to determine dominant capture probability variation in the data set leading to erroneous model selection.

3. *Capture probability variation*: Bears probably show unequal probabilities of capture which can lead to biased population estimates. It is possible to test data to determine the dominant type of capture probability variation, if the above issues are met. Capture probability variation can be divided into three categories.

   a) *Heterogeneity*: Each animal has a unique probability of capture that is constant throughout the study.

   b) *Behaviour*: All animals have an equal initial capture probability but this changes after initial capture.

   c) *Time*: The capture probability of bears changes evenly each time sampling occurs.

   Program CAPTURE, MARK, and SECR have estimation models that are formulated to accommodate each form of capture probability variation. The models (and corresponding capture probability assumptions) are M_o (null or equal capture probabilities), M_h (heterogeneity), M_t(time), M_b(behaviour), M_{th} (time/heterogeneity), M_{bh}(behaviour/heterogeneity), M_{tb}(time/behaviour) and M_{tbh}(time/behaviour/heterogeneity).

If the goals of study design are met, the most appropriate estimation model can be used for population estimates, which should yield the most precise and unbiased results. Conversely, if an inventory is designed poorly, a complex, imprecise model may have to be used (to minimize bias), or, if assumption violations are severe*, no estimator* will give a reliable estimate (Otis et al. 1978).