

Estimation of grizzly bear population size for the Swan Hills management unit using DNA sampling and habitat-relative occupancy models.

Report prepared for Alberta Sustainable Resource Development, October 2009.

John Boulanger, Integrated Ecological Research, Nelson, B.C. boulange@ecological.bc.ca,

Jerome Cranston, Arctos Ecological Consulting, Hinton, Alberta, arctos@telus.net

Scott Nielsen, Department of Renewable Resources, University of Alberta, Edmonton, Alberta, scottn@ualberta.ca

Gordon Stenhouse, Foothills Research Institute, Hinton, Alberta, Gordon.Stenhouse@gov.ab.ca

1. Abstract

Grizzly bear population inventory work has been underway in various population units along the eastern slopes of Alberta. As of the time of the preparation of this report two population units have not been inventoried, the Swan Hills and the Alberta North units. In order to provide a science based estimate of possible grizzly bear population size in the Swan Hills unit we utilized existing data sets from the previous DNA inventory work to provide estimates for the purpose of a species status review. We used an objective, multi-scale approach to estimating occupancy-habitat associations based on DNA hair snag information and predicted (extrapolated) occupancy to similar habitats (natural sub-regions) in the Swan Hills grizzly bear management unit. Assuming similar habitat and population conditions among reference areas (the foothills adjacent to the Rocky Mountains) and the Swan Hills, we estimated population size for the Swan Hills Grizzly Bear Management Unit.

Estimates of population size ranged from 11.6 to 21.2 for the core Swan Hills area and a population size of 2.0 to 3.9 individuals for the edge area. The model-averaged estimate for the Swan Hills was 23.2 (CI=5.9-70.9) bears. We suggest that if required, the best way to test these model predictions would be to sample bear DNA in the Swan Hills using a reduced sampling effort design to create a data set to further refine relative occupancy models.

Additional data are presented from research findings of GPS collared bears illustrate the isolation of the Swan Hills grizzly bear population. Despite no recorded inter-change among populations (Swan Hills and Grande Cache), the long-term maintenance of the Swan Hills population is likely due to periodic (albeit rare) successful colonization (dispersal) from the Grande Cache unit.

We believe that data from recent field research indicate that habitat and other ecological conditions of the most northern grizzly bear population unit (Alberta North) differ significantly from all other population units. We therefore suggest that a different sample driven approach be used to provide population estimates for this unit for future management needs as habitat-occupancy methods using reference populations are unlikely to satisfy assumptions used in the model.

2. Introduction

DNA mark-recapture methods have been applied in much of the occupied grizzly bear range in Alberta to estimate population size and density (Boulanger et al. 2006, Boulanger et al. 2008, Alberta Grizzly Bear Inventory Team 2009) (Figure 1). Another less well-explored use of DNA mark-recapture data is the examination of factors influencing habitat selection and occupancy based upon detections of grizzly bears at DNA hair snag sites. Habitat-occupancy relationships estimated from these data can then be used to plan future survey efforts to increase efficiency, cross-validate other habitat models that were based on telemetry data, and estimate population sizes for areas that have not been surveyed using habitat-occupancy relationships to estimate densities of animals based on reference populations. Detailed remote sensing data is available for all grizzly bear range in Alberta (McDermid 2005, Linke and Franklin 2006), including the 2004 through 2008 DNA survey grids and surrounding areas. One application of these data is the determination of grizzly bear habitat associations across bear range and habitat-based estimations of population size for un-sampled population units, including the Swan Hills Grizzly Bear Management Unit.

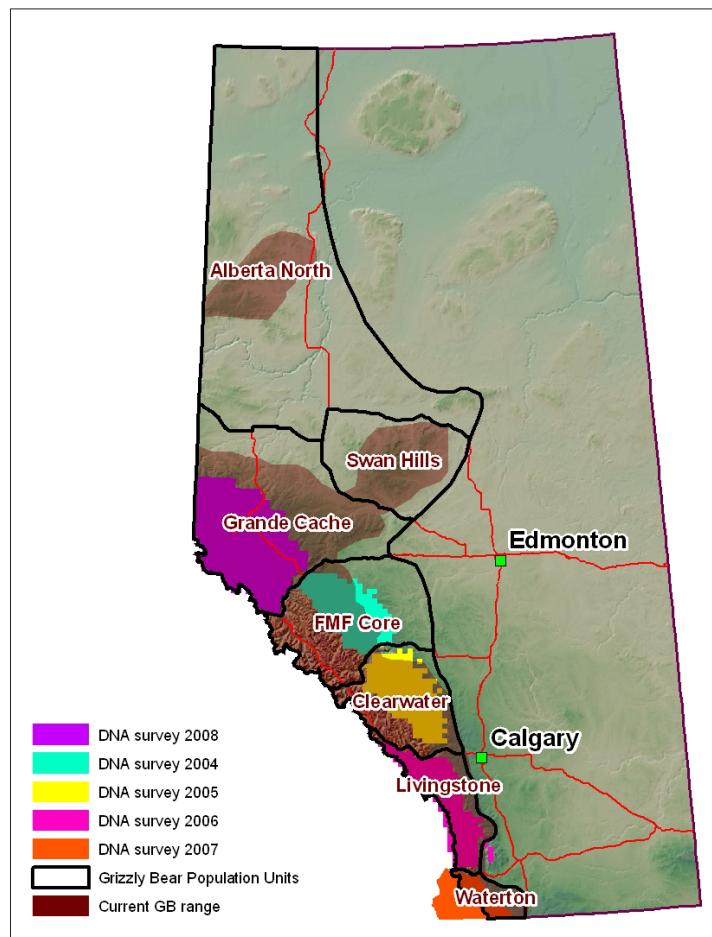


Figure 1: Swan Hills in relation to other GBU areas that have been DNA sampled in Alberta

The objective of this report is to detail relative habitat-occupancy modeling approaches used and the subsequent derivation of population estimates for the Swan Hills Grizzly Bear Management Unit based on habitat-relative occupancy relationships and a reference population density from the area east of the Swan Hills (Figure 2). This information has been requested by SRD for inclusion in the 2009 status review of grizzly bear populations in Alberta. Although the Swan Hills area harbors a population of grizzly bears, the small number of individuals that likely exists here made application of DNA mark-recapture estimates of population potentially problematic as well as being costly. As a consequence, we derive a population size estimate for SRD using models (rather than sampling) based on habitat-based density associations.

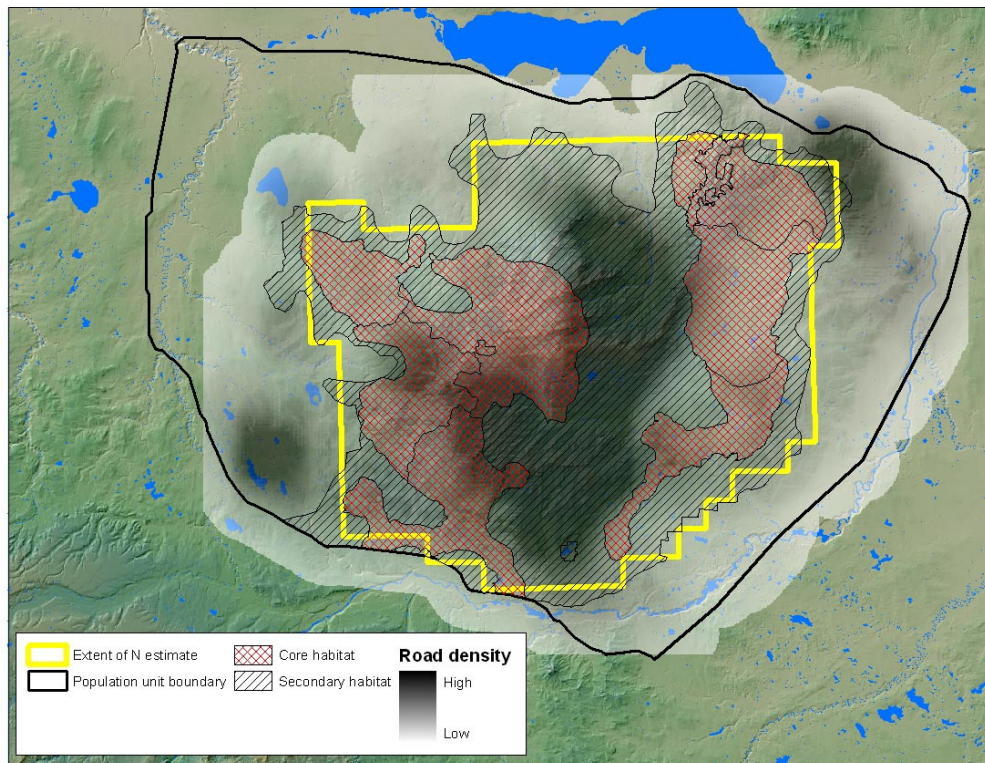


Figure 2: Swan Hills grizzly bear management unit with grizzly bear population study area, core, secondary and relative road density shown

3. Methods

3.1. Study area and habitat variables considered

Figures 1 and 2 illustrate the location of DNA grids considered for this analysis. Remote sensing-based landcover (McDermid 2005, Linke and Franklin 2006) and related GIS data were used to predict bear distribution (Table 1). As discussed later in the report, variables were summarized at various scales as part of the modeling exercise.

Table 1: Habitat variables considered in the analysis. Variables were summarized at different buffer radiuses based upon assumptions regarding the scale of association between bear occupancy and habitat attributes.

Habitat variable	Description
Natural sub-region	Five natural sub regions considered: lower & upper foothills, montane, subalpine, alpine
Crown closure	Crown closure (McDermid 2005)
Grizzly mortality risk	Risk of mortality (Nielsen et al. 2004)
Grizzly habitat (RSF)	RSF score from radio-collared bear analysis (Nielsen et al. 2006).
Elevation	Elevation (metres) from a DEM
CTI	Compound topographic index (a soil moisture index; Gessler et al. 1995)
TRI	Terrain ruggedness index (Riley et al. 1999)
Regeneration age	Regeneration age (yrs)
Regeneration habitat	Proportion regeneration habitat (what scale)
Forest age	Forest age
Percent conifer	Percent conifer
Distance to stream 100	Negative exponential decay (100m parameter) distance to stream
Distance to stream 500	Negative exponential decay (500m parameter) distance to stream
<u>Landcover variables</u>	
Upland tree	Proportion upland tree
Upland herb	Proportion upland herb
Wetland herb	Proportion wet herbaceous
Wetland treed	Proportion wetland tree
Shrub	Proportion shrub
Water	Proportion water
Forest	Proportion forest
Wetland	Proportion wet herbaceous and wetland tree pooled into a single wetland category
<u>Anthropogenic covariates</u>	
Past mortalities	Known mortalities that occurred within 1km of site
Percent protected	Percent area protected (parks, reserves etc) in a 10-km radius
Distance to protected	Km from protected areas
Distance to whitezone road density	Km distance from Alberta's white zone (private lands)
Human pressure index-1	Human pressure index based on diffusion from human population sources (scalar 1); (Nielsen unpublished)
Human pressure index-2	Human pressure index based on diffusion from human population sources (scalar 2); (Nielsen unpublished)
Distance to cities	Km distance from cities
Distance to smrvlg	Km distance from small rural villages
Distance to twnmv	Km distance from towns, villages, and municipalities
Cost distance to roads	Cost (TRI) weighted distance to roads
Distance to road	Distance from roads (km)

3.2. Statistical methods to estimate and model bear occupancy and distribution.

We used logistic regression to contrast presence/not detected of grizzly bears at a DNA hair snag site to predict the probability of relative occupancy in the habitat areas surrounding the DNA site (p_{LR}) based on environmental GIS predictor variables (Table 1). We assumed that the probability of detection (i.e. hair snag) for a bear that encountered a DNA hair snag site was constant across all sites sampled but was not necessarily 1 (as discussed later). This assumption allowed us to estimate relative occupancy using the DNA hair snag data even though detection probabilities at sites are most certainly less than 1 (Boulanger et al. 2004). It was also assumed that relative occupancy would in turn influence the distribution and densities of bears in the sampling grid with areas of higher relative occupancy would also have higher densities of bears (see however, Nielsen et al. 2005; Johnson et al. 2008).

We used a multi-scale regression approach to fit models to data from the DNA survey grids. The primary emphasis of our approach was to fit an overall (global) habitat-density model to all the grids surveyed between 2004-2008 in the Clearwater (2005), Yellowhead (2004), and Grande Cache (2008) population units rather than selecting a single reference area (population) for extrapolation to the Swan Hills. Although these surveys were conducted during different years, we do not expect occurrence of bears or factors affecting occurrence of bears to change substantially over a just a few years time. All DNA sampling occurred during an eight week period in the late spring to early summer season (end of May-end of July).

3.3. Determination of reference area for extrapolation

In order to estimate a habitat-based population size for the Swan Hills, a reference population density (area with a known population size and of similar habitat) is needed. However, the Swan Hills population unit does not have the same habitat conditions represented in the other three DNA grids. In particular, the Rocky Mountain natural region (Montane, Sub-alpine, and Alpine ecosystems) is common to the other three grids, while it is lacking in the Swan Hills population (Figure 3). We therefore excluded, for the reference population, all Rocky Mountain environments in the 2004, 2005 and 2008 DNA grids leaving the Lower and Upper Foothills natural sub-regions as our reference area (population).

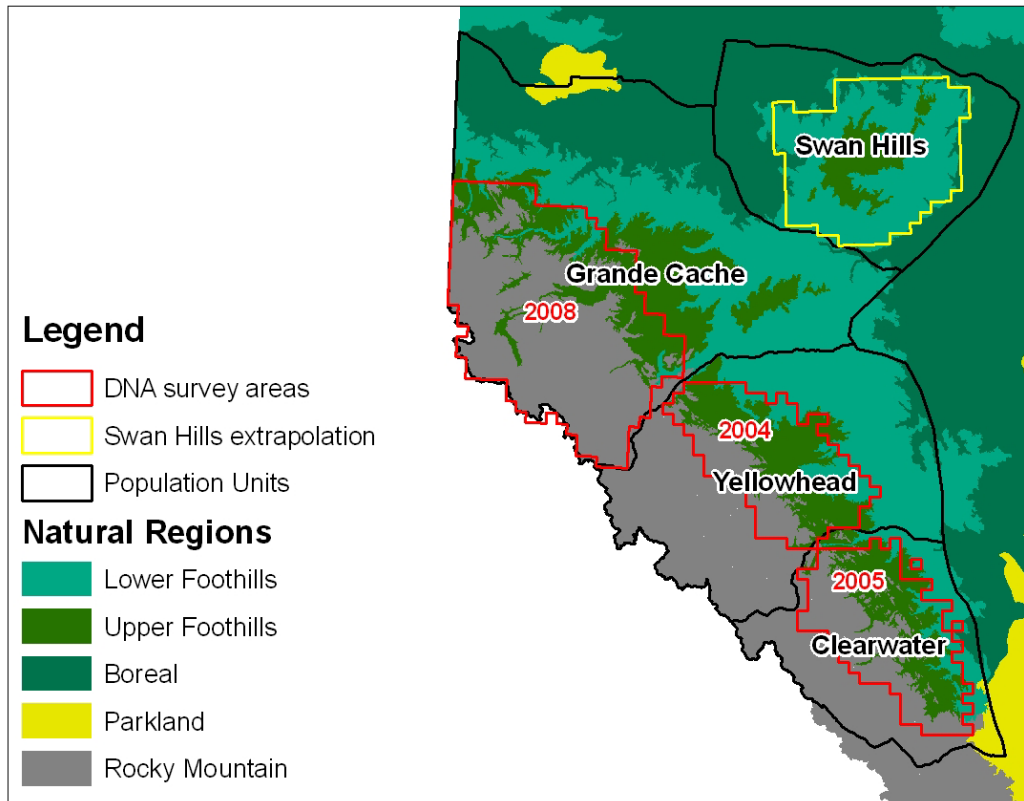


Figure 3: Natural sub-regions (NSR) relative to the 2004, 2005, 2008 DNA grids and the Swan Hills area.

3.4. Biologically-based candidate models.

Hierarchical models of bear (relative) occupancy were developed at the landscape scale, DNA grid-scale, and habitat-patch scale. Scale in this case was based upon the extent in which habitat variables were summarized in a GIS relative to hair snag sites with the landscape scale based upon an extent of 10 kilometers surrounding hair snag sites corresponding to bear home range areas (Nielsen et al. 2004) and the scale at which humans often plan and influence land use activities (i.e., the township). DNA grid-scales were based upon an intermediate distance of a 3.95 kilometer radius from hair snag sites (the approximate distance between adjacent hair snag sites when sampled at 1 site per 49 km² cell), while the habitat patch scale was based on a 300 meter radius representing the habitat conditions immediately surrounding a hair snag site.

Models were evaluated using the sample-size-corrected Akaike Information Criterion (AICc) index of model fit (Burnham and Anderson 1998). The model with the lowest AICc score was considered the most parsimonious, thus optimizing the tradeoff between bias and precision (Burnham and Anderson 1998). The difference between any given model and the most supported ($\Delta AICc$) was used to evaluate the relative fit of models when their AICc scores were similar. In general, any model with a $\Delta AICc$ score of ≤ 2 is considered to be supported by the data. Models were also evaluated using ROC scores (a measure of model predictive accuracy) to assess overall fit to the reference data (Fielding and Bell 1997).

3.5. Habitat-based estimation of population size

The logistic regression model estimated probability of a grizzly bear detections at a hair snag sites, which we use as an index of relative occupancy since we do not know detectability (i.e., detectability of <1, but not necessarily varying among sites). These probabilities were then applied to each pixel (100m X 100m=1 ha.) in a GIS to create a surface of predicted probabilities of occurrence (p_i). The mean of p_i for all of the pixels was then estimated (\bar{p}_{SA}). The ratio of each probability of occurrence to the mean predicted probability of occurrence could then be used to index the relative density for each pixel compared to other pixels in the study area. For example, a ratio of 1 would suggest the pixel had the same density as the reference density whereas a value that is greater than 1 would suggest a higher density, and a value below 1 would suggest a lower density.

Using this ratio and an estimate of reference density per pixel for the entire study area (D_{SA}), relative densities per pixel could be estimated across the study area using the product of the ratio and reference density per pixel as described in Eq. 1 below.

$$D_i = D_{SA} \left(\frac{p_i}{\bar{p}_{SA}} \right) \quad (1)$$

The population size was then estimated for each pixel and summed to obtain an estimate of population size (\hat{N}_{SA}) for the entire grid (Boyce and McDonald 1999). More formally, the population size estimated for the new area (Swan Hills) is estimated as,

$$\hat{N}_{SA} = \sum_{i=1}^n D_i * Area \quad (2).$$

Upper and lower confidence intervals on p_i (probabilities of occurrence) and reference density D_{SA} were substituted for p_i to obtain confidence intervals on D_i (density) and \hat{N}_{SA} (estimated population size).

3.6. Reference densities for the Swan Hills

As discussed in Section 2.3, we only used for habitat-occupancy modeling data from DNA hair snag sites that occurred in the Upper and Lower Foothills in the 2004 (Yellowhead), 2005 (Clearwater), and 2008 (Grande Cache) grids. To estimate population size for the Swan Hills, we therefore needed the corresponding reference density for these two natural sub-regions. We therefore first estimated densities by NSR to obtain an applicable reference density. We did this using a logistic regression model with NSR as a categorical predictor of relative probability of occurrence as applied across the full set of DNA data sets. For the 2008 Grande Cache DNA grid, the non-protected population size and density estimates were used since these best applied to the Lower and Upper Foothills sub-region (Alberta Grizzly Bear Inventory Team 2009) (Table 2). Probabilities of occurrence for each site were then used in the equations (1) and (2) to estimate densities by sub-region using a mean reference density (combined grids in Table 2) of 8.99 (CI=7.99-11.01) bears per 1000-km².

Table 2: Summary of DNA grids, average population size estimates, and associated density estimates for entire grid areas. Density expressed in bears per 1000 km².

Unit-DNA grid	Year DNA	Area (km ²)	\hat{N}	CI(\hat{N})	\hat{D}	CI(\hat{D})
Yellowhead	2004	8,820	42	36.0-55.0	4.76	4.08-6.24
Clearwater	2005	8,477	45.4	41.0-52.0	5.36	4.84-6.13
Grande Cache ¹	2008	9,464	153.1	135.3-187.5	16.18	14.29-19.82
Totals		26,761	240.5	212.3-294.5	8.99	7.933-11.005

¹Estimate based upon non-protected areas on the 2008 grid (Alberta Grizzly Bear Inventory Team 2009).

4. Results

4.1. Habitat-occupancy models

Initially, landscape-scale models (where predictor variables were evaluated at 10 kilometer extents around hair snag sites) were considered (Table 3). Of these models, a model with road density, upland tree landcover, wetland landcover, and terrain ruggedness was most supported (Model L-9 in Table 3).

DNA grid-sampling scale models, which assumed associations between predictors and relative occupancy at moderate (3.95 kilometer) spatial scales, were also considered (Table 3). Of these models, bear habitat based on an RSF using collared bears, moose abundance index, terrain ruggedness, and wetland landcover type was most supported (Model Grid-6 in Table 3). However, the overall support of this model compared to models at landscape scales was low.

At local scales (habitat patch scales), we considered factors that were most likely relevant at the site/stand-level, such as ungulate densities, local topography (valleys as indicated by distances to stream), canopy closure, terrain ruggedness and distance to roads. Of these, a model (model Hab-3) with RSF score, moose abundance, distance to stream, and terrain ruggedness was most supported. However, support for all habitat patch models, including the most supported model, was even lower than DNA grid-sampling and landscape-scale models.

Multi-scale models combined the most dominant predictors from each of the landscape, DNA grid-sampling, and habitat patch scales. A number of models were supported as indicated by the grey shading in Table 4 and AICc weights that were greater than 0.01. The highest supported model (Model MS-1) considered road density (10-km radius), wetland landcover type (3.95 km radius), upland forest landcover type (10-km radius), regenerating forest landcover type (10-km radius), and terrain ruggedness (10 km radius) at DNA grid-sampling and landscape scales, while compound topographic index was the only local scale (300 m) predictor. Population estimates from any model that had an AICc weight of greater than 0.01 were model averaged to estimate population size in the Swan Hills. Coefficients for the most supported models are given in Appendix 1.

Table 3: Models considered in the analysis. Models that are shaded grey were supported ($w_i > 0$). Akaike Information Criteria (AIC_c), the difference in AIC_c values between the i th and most supported model (ΔAIC_c), Akaike weights (w_i), and number of parameters (K) are presented.

Model	AIC_c	ΔAIC_c	w_i	K	Variables
<i>Landscape scale (variables summarized at 10km extent)</i>					
Landscape-1	847.4	81.16	<0.01	2	roads
Landscape-2	821.9	55.65	<0.01	4	roads, km_whtzone, km_smrvg
Landscape-3	814.5	48.25	<0.01	5	roads, km_whtzone, km_smrvg, NSR (foothills)
Landscape-4	786.1	19.84	<0.01	6	roads, km_whtzone, km_smrvg, NSR (foothills), TRI
Landscape-5	780.1	13.81	<0.01	7	roads, km_whtzone, km_smrvg, NSR (foothills), TRI, RSF
Landscape-6	774.8	8.50	<0.01	7	roads, km_whtzone, km_smrvg, NSR (foothills), RSF, wet
Landscape-7	773.2	6.92	<0.01	6	roads, km_whtzone, km_smrvg, RSF, wet
Landscape-8	781.3	15.07	<0.01	5	km_whtzone, km_smrvg, RSF, wet
Landscape-9	768.3	2.06	0.06	6	roads_10km, uptree, wet, TRI, TRI ²
<i>DNA Grid sampling scale (variables summarized at 3.95 km extent)</i>					
DNA grid-1 (Canopy & roads)	877.2	111.00	<0.01	4	CC, drd_km, CC X_drdkm
DNA grid -2 (Forestry habitat model)	831.5	65.24	<0.01	6	regen, regen ² , rgnage, rgnage2, shrub
DNA grid -3 (RSF/moose habitat model)	822.1	55.83	<0.01	3	RSF, moose
DNA grid -4 (RSF/moose & terrain model)	788.6	22.33	<0.01	5	RSF, moose, TRI, TRI ²
DNA grid -5 (Forestry + TRI)	802.5	36.16	<0.01	8	regen, regen ² , rgnage, rgnage ² , shrub, TRI, TRI ²
DNA grid -6 (RSF/terrain + wetlands)	783.1	16.83	<0.01	5	RSF, moose, TRI, wet
<i>Habitat-patch scale (variables summarized at 300 m. extent)</i>					
Hab-1 (RSF/moose)	846.3	80.10	<0.01	3	RSF, moose
Hab-2 (general edge/canopy/streamsidings)	874.0	109.68	<0.01	4	CC, CC ² , dedge, stream100
Hab-3 (RSF + selective environments)	817.6	51.32	<0.01	7	RSF, moose, dstream100, drd, TRI, TRI ²
Hab-4	830.8	61.94	<0.01	7	moose, CTI, CTI ² , TRI, TRI ² , drd
<i>Multi-scale (extents denoted with variables)</i>					
MS-1	766.4	0.00	0.50	10	roads(10k), wet (10k), regen (10k), regen ² (10k), uptree (10k) TRI(10k), TRI ² (10k), CTI(300m), CTI ² (300m)
MS-2	777.0	10.72	<0.01	6	km_smrvg, km_whtzone, wet(10k), TRI(10k), TRI(300m)
MS-3	768.4	2.12	0.06	9	Roads (10k), wet(10k), uptree(10k), TRI(10k), TRI ² (10k), moose(300m) CTI (300m), CTI ² (300m)
MS-4	766.8	0.50	0.31	8	roads(10k), wet (3.95k), uptree(10k), TRI(10k), TRI ² (10k), CTI (300m), CTI ² (300m)
MS-5	767.9	2.06	0.06	6	roads(10k), wet(10k), uptree (10k), TRI(10k), TRI ² (10k)

Maps of estimated relative occupancy based on habitat conditions suggest areas of higher relative occupancy in the Swan Hills area. These areas had lower road densities (Figure 4), lower upland tree habitat types, and higher proportion regenerating habitat (in this case from the Virginia Hills, Agnes and Chisholm fires that occurred from 1990-2001).

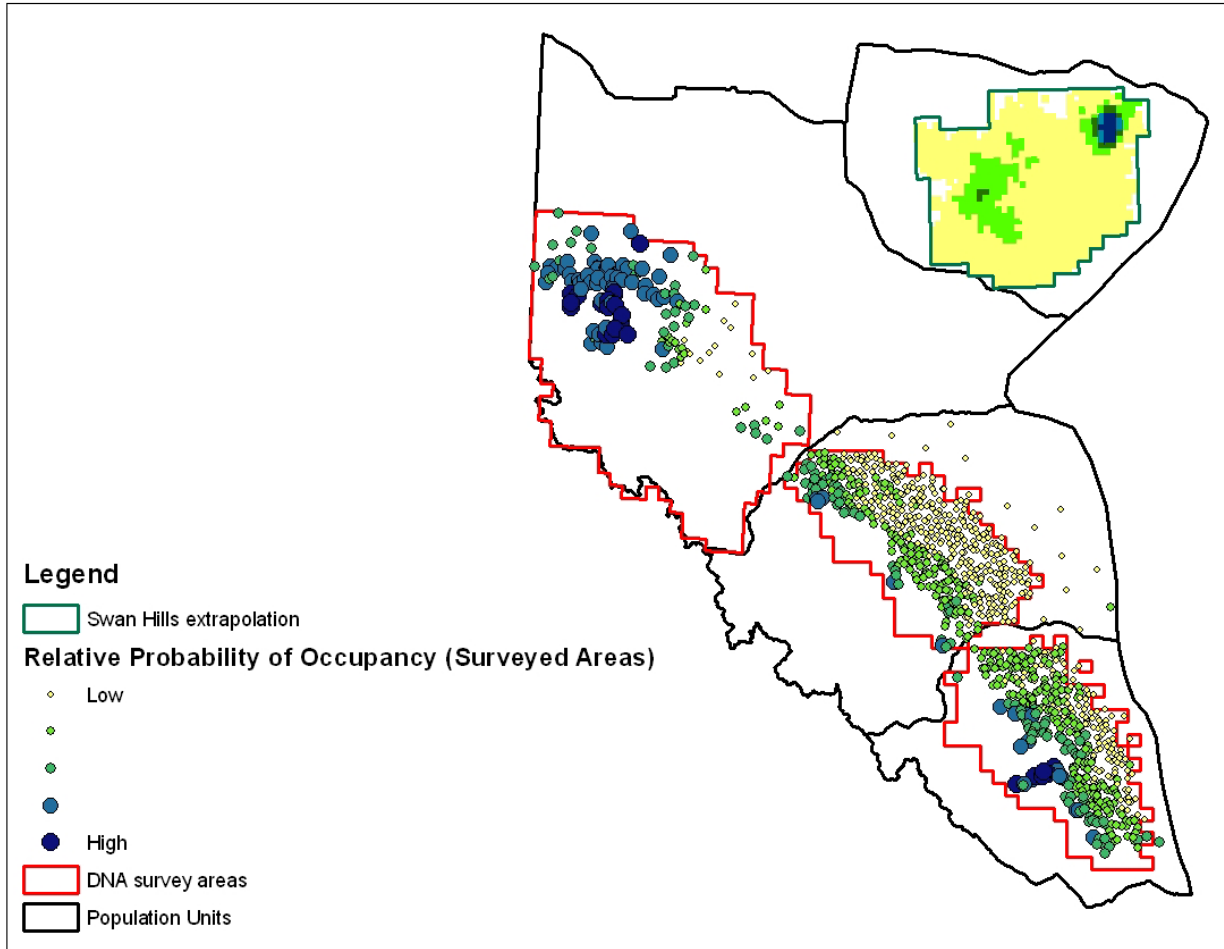


Figure 4: Estimated relative occupancy for the reference DNA grids and Swan Hills area using the most supported relative occupancy model (Model MS-1 in Table 4)

4.2. Estimates of reference density

Reference density was determined by first stratifying the combined densities of the 2004, 2005, and 2008 sampling grids by natural sub-region (NSR) and modeling relative occupancy for each NSR. NSR was a significant predictor of relative occupancy ($\chi^2=137.03$, $df=4$, $p<0.0001$). Population size estimates from the NSR model suggested that the highest density occurred in the subalpine, alpine, and montane-transition (montane areas adjacent to the sub-alpine) zones compared to the upper and lower foothills zones (Table 4). The combined density of the lower and upper foothills zone was 5.38 (CI=3.89-8.27) bears per 1000 km² which we used as the base reference density for extrapolation to the Swan Hills area.

Table 4: Population size estimates and partitioned densities by natural subregion from the 2004, 2005, and 2008 DNA grids. Density is expressed in bears per 1000 km².

Natural Sub-region (NSR)	Area (km ²)	\hat{N}	CI (\hat{N})	\hat{D}	CI (\hat{D})		
Montane transition zone	1,323	13.92	8.60	25.21	10.52	6.50	19.05
Lower foothills	4,851	16.65	9.88	29.27	3.43	2.04	6.03
Upper foothills	12,446	76.33	57.41	113.82	6.13	4.61	9.15
Subalpine	7,644	109.89	85.59	159.00	14.38	11.20	20.80
Alpine	833	15.85	10.86	25.42	19.03	13.04	30.52

4.3. Population estimates for the Swan Hills

Population estimates were derived from the most supported models as indicated by AICc weights that were greater than 0.01. ROC scores suggested that the fit of these models was adequate as indicated by ROC scores that were greater than 0.7 (Table 5). When estimating population size based upon the most supported model (MS-1), it was apparent that recent fires (i.e., regenerating forests) were more dominant in the Swan Hills than the reference DNA grids. This habitat difference, along with a non-linear (quadratic) term (coefficient) for regeneration in the MS1 model resulted in over-estimates of occupancy in the northeastern part of the Swan Hills (the area of the recent burn). These increases in occupancy inflated population estimates for the Swan Hills. To address this issue, we estimated population size using model MS-1 for individual “cells” at a scale (49 km²) matching the original DNA-based sampling methods. Since the other candidate models were less sensitive to the regeneration extrapolation, population size was estimated using a pixel-sized (1 ha.) unit.

Estimates of population size ranged from 11.6 to 21.2 for the core Swan Hills area and a population size of 2.0 to 3.9 individuals for the outer area. The model-averaged estimate for the Swan Hills was 23.2 bears (CI=5.9-70.9) (Table 5). Confidence interval widths encompassed both variance introduced by uncertainty in original DNA mark-recapture density estimates (Table 2), foothills reference densities (Table 4), and uncertainty based upon estimation of relative occupancy probabilities. On average, 58.3% of the variance introduced into estimates were due to uncertainty in relative occupancies, with the remaining variance due to uncertainty in reference density estimates.

Table 5: Model fit statistics and population estimates from the most supported models in Table 4 (as indicated by AICc $w_i > 0$). Coefficients for models are given in Appendix 1.

Model	Model fit			Population estimates				
	AICc	Δ AICc	w_i	ROC	Core \hat{N}	Edge \hat{N}	Total unit \hat{N}	CI (\hat{N})
MS-1	766.4	0	0.47	0.794	21.2	3.9	25.1	4.6-80.3
MS-4	766.8	0.45	0.30	0.790	14.7	2.5	21.9	6.7-69.9
MS-5	767.9	1.51	0.10	0.784	16.5	2.8	20.1	8.0-73.0
L-9	768.3	1.98	0.07	0.783	13.8	2.5	24.3	6.1-68.0
MS-3	768.4	2.09	0.06	0.789	11.6	2.0	17.9	4.2-63.6
Naïve avg \hat{N}					15.6	2.7	21.9	5.6-74.6
AIC wt. \hat{N}					17.7	3.2	23.2	5.9-70.9

5. Discussion

We used an objective, multi-scale approach to estimating occupancy-habitat associations based on DNA hair snag information and predicted (extrapolated) occupancy to similar habitats (natural sub-regions) in the Swan Hills grizzly bear management unit. Assuming similar habitat and population conditions among reference areas (the foothills adjacent to the Rocky Mountains) and the Swan Hills, we estimated population size for the Swan Hills Bear Management Unit of Alberta.

We found most habitat-occupancy associations occurred at larger (landscape) scales suggesting that occupancy is controlled by regional patterns in habitat and human activity. Since the DNA hair snagging at a site occurred over a two week period, our estimates of occurrence reflect the probability that a bear was in the area at least once during a 2 week time period and was snagged at the DNA site. Given this, it would be expected that the scale in which DNA sampling occurs would be inherently larger scale than similar GPS-collar-based sampling regimes. Despite the large scale of DNA sampling, we were able to detect strong significant relationships between bear detections and terrain ruggedness, road density, habitat (upland trees, wet ecotypes), and forestry activities. This suggests that the scale of DNA sampling is still fine scale enough to detect heterogeneity in occupancy across grid areas. In general, we found that simpler models that assumed homogeneity in occupancy of habitat values estimated larger population sizes than more complex models that modeled heterogeneity in occupancy. This highlights the utility of a multi-scale approach to habitat relative occupancy and estimation of population size and cautions against the use of simpler models (that assume homogeneity of density) across grid areas used to extrapolate densities between sampled and un-sampled bear habitats.

In our analysis we assumed that the probability of detection of bears that encounter sites was constant so that detection at a site implies relative occupancy for the habitat surrounding the site at the various scales considered in the analysis. However, the detection probability of sites was not 100% and it has been estimated that only 60% of bears that encounter DNA hair snag sites are detected (Boulanger et al. 2004). This issue is accounted for when DNA mark-recapture methods, that estimate detection probabilities of grizzly bears, are used to estimation of population size and density (Boulanger et al 2004). This assumption does not have a large influence on the analysis unless detection rates differ substantially among sites. On-going research is testing (using occupancy models; MacKenzie et al.

2006) whether DNA sites show large variability in detection of bears based on micro-site placement of hair snags (Boulanger, in prep).

An inherent assumption of the analysis is that the same general habitat associations and relationships between bear mortality pressure and anthropogenic features (i.e. roads) that occur on the DNA grids also occur in the Swan Hill grizzly bear unit. By reducing the reference data set to only include the Upper and Lower Foothills sub-regions we ensured that the same general ecosystem was considered in the analyses for the core population of the Swan Hills. The confidence intervals on population estimates consider the degree of statistical uncertainty in logistic regression probabilities as well as reference density estimates and subsequent population estimates so these provide an indication of statistical certainty in extrapolated estimates due to all habitat-modeling components. Final confidence intervals were large due to the propagation of errors across each step of the extrapolation procedure. Future research will focus on more efficient estimation of error rates which may reduce the width of confidence intervals.

The best way to test model predictions would be to sample bear DNA in the Swan Hills using a reduced sampling effort design to control costs. For example, the occupancy design employed in the 2008 DNA grid could be applied (larger grid cell size with sites not moved between sessions) to provide a data set to test model predictions. This model would then be used to estimate more accurately the relative occupancy of the Swan Hills areas which would in turn refine population estimates and lower confidence intervals.

5.1. Connectivity of Swan Hills Population Unit

The FRI Grizzly Bear Research Program captured and GPS radio collared 8 adult bears from 2005 – 2007, with a goal of collecting habitat use and movement data for the preparation of RSF models for this population unit. Although limited in both time span and sample size, data from these bears illustrate the isolation of the Swan Hills population. No collared grizzly bears moved outside this population unit over this period. Home ranges and den site locations for all research animals were also all found to occur within the currently defined grizzly bear conservation (core) areas of the Swan Hills.

This same research team also captured and GPS radio collared 37 bears (~100,000 GPS locations) in the population unit (Grand Cache) to the west of the Swan Hills for the period 2005 – 2009. During this time period none of the study animals moved east into the Swan Hills, although three bears did move to within 40 kilometers of the western edge of the Swan Hills. However, two of these bears were killed by poachers illustrating the human-induced fragmentation of these two population units. Despite no recorded inter-change among populations, the long-term maintenance of the Swan Hills population is likely due to periodic (albeit rare) successful colonization (dispersal) from the Grande Cache unit.

5.2. Estimation of population size for Alberta North grizzly bears

The FRI Grizzly Bear Research team conducted capture and collaring operations in the Alberta North population unit from 2006 – 2008. During this time period this team captured 5 grizzly bears and 25 black bears despite extensive trapping efforts. To put this in context, over the past 10 years of intense capture efforts across all grizzly bear population units, capture success for all bear species was highest (bears captured/trapping day) in the Alberta North unit, but also the lowest capture rate of grizzly bears for any of the population units. Researchers also camera “traps” using baited sites to further

detect grizzly bears in the area. This effort identified at least 3 additional grizzly bears after 600 camera/trap nights. Although these results are inadequate to determine population size in this unit, the researchers (Stenhouse, pers. comm) believe that this unit is dominated by lower quality grizzly bear habitat and contains a small population (low density) of grizzly bears in an area that favors black bears.

Use of habitat-based occupancy models to estimate population size is based upon a number of important assumptions. First is that the population demography (birth rates and survival rates, life span, etc.) are similar between the different units. It is also important that the units being compared are similar in terms of habitat types and conditions and that the levels and types of human use. For example, we recognize ecological differences between the various population units. We believe that habitat and other ecological conditions of the most northern population (Alberta North unit) differs significantly from all other population units. We suggest that a different data-driven approach be used to provide population estimates for this unit for future management needs as habitat-occupancy methods using reference populations are unlikely to satisfy assumptions used in the model.

6. Literature cited

- Alberta Grizzly Bear Inventory Team. 2009. Grizzly bear population size and density estimates for the 2008 DNA Inventory of the Grande Cache Bear Management Area (BMA 2). Alberta Sustainable Resource Development, Fish and Wildlife Division.
- Boulanger, J., M. Proctor, S. Himmer, G. Stenhouse, D. Paetkau, and J. Cranston. 2006. An empirical test of DNA mark-recapture sampling strategies for grizzly bears. *Ursus* 17:149-158.
- Boulanger, J., G. Stenhouse, and R. Munro. 2004. Sources of heterogeneity bias when DNA mark-recapture sampling methods are applied to grizzly bear (*Ursus arctos*) populations. *Journal of Mammalogy* 85:618-624.
- Boulanger, J., G. C. White, M. Proctor, G. Stenhouse, G. MacHutchon, and S. Himmer. 2008. Use of occupancy models to estimate the influence of past live captures on detection probabilities of grizzly bears using DNA hair snagging methods. *Journal of Wildlife Management* 72:589-595
- Boyce, M. S., and L. L. McDonald. 1999. Relating populations to habitats using resource selection functions. *Trends in evolution and ecology* 14:268-272.
- Boyce, M. S., P. R. Vernier, S. E. Nielsen, and F. K. A. Schmeigelow. 2002. Evaluating resource selection functions. *Ecological Modelling* 157:231-300.
- Burnham, K. P., and D. R. Anderson. 1998. *Model selection and inference: A practical information theoretic approach*. Springer, New York.
- Fielding, A. H., and J. F. Bell. 1997. A review of methods for the assessment of predictive errors in conservation presence/absence models. *Environmental Conservation* 24:38-49.
- Gessler, P.E., I.D. Moore, N.J. McKenzie, and P.J. Ryan. 1995. Soil-landscape modeling and spatial prediction of soil attributes. *International Journal of GIS*. Vol 9, No 4, 421-432.
- Johnson, C.J., and D. R. Seip. 2008. Relationship between resource selection, distribution, and abundance for woodland caribou: a test with implications to theory and conservation. *Population Ecology* 50:145-157.

- Linke, J., and S. E. Franklin. 2006. Interpretation of landscape structure gradients based on satellite image classification of landcover. *Canadian Journal of Remote Sensing* 32:367-379.
- MacKenzie, D. I., J. D. Nichols, J. A. Royle, K. H. Pollock, L. L. Bailey, and J. Hines. 2006. *Occupancy estimation and modeling: Inferring patterns and dynamics of species occurrences*. Academic Press, New York.
- Manly, B. F. J., L. L. McDonald, and D. L. Thomas. 1993. *Resource Selection by Animals: Statistical Design and Analysis for Field Studies*. Chapman & Hall, London.
- McDermid, G., J. 2005. *Remote Sensing for large area multi-jurisdictional habitat mapping*. PhD, University of Waterloo, Waterloo.
- Nielsen, S.E., C. Johnson, D.C. Heard, & M.S. Boyce. 2005. Can models of presence-absence be used to scale abundances? Two case studies considering extremes in life history. *Ecography* 28: 197-208.
- Nielsen, S. E., M. S. Boyce, and G. Stenhouse. 2006. A habitat-based framework for grizzly bear conservation in Alberta. *Biological Conservation* 130:217-229.
- Nielsen, S. E., S. Herrero, M. S. Boyce, R. D. Mace, B. Benn, M. L. Gibeau, and S. Jevons. 2004. Modeling the spatial distribution of human-caused grizzly bear mortalities in the Central Rockies ecosystem of Canada. *Biological Conservation* 120:101-113.
- Riley, S. J., S. D. DeGloria and R. Elliot (1999). A terrain ruggedness index that quantifies topographic heterogeneity, *Intermountain Journal of Sciences*, vol. 5, No. 1-4, 1999.

7. **Appendix 1: Unstandardized logistic regression coefficients (β) for models listed in Table 4.**

Model	Parameter	β	StdErr (β)	CI (β)	χ^2	$P(\beta=0)$	
MS-1	Intercept	-4.429	3.479	-11.248	2.391	1.620	0.203
MS-1	P6RDDNS_6M	-0.617	0.383	-1.367	0.133	2.600	0.107
MS-1	s10k_wet	-14.792	8.650	-31.746	2.162	2.920	0.087
MS-1	s10k_regen	-7.943	3.433	-14.672	-1.215	5.350	0.021
MS-1	s10k_rege*s10k_regen	13.953	6.740	0.743	27.164	4.290	0.038
MS-1	UPTREE16p9	-7.372	1.348	-10.014	-4.730	29.910	<.0001
MS-1	s10k_tri	0.311	0.123	0.069	0.552	6.350	0.012
MS-1	s10k_tri*s10k_tri	-0.011	0.004	-0.018	-0.004	8.460	0.004
MS-1	s300_cti	1.352	0.650	0.079	2.626	4.330	0.037
MS-1	s300_cti*s300_cti	-0.066	0.033	-0.130	-0.002	4.020	0.045
MS-4	Intercept	-5.778	3.244	-12.136	0.580	3.170	0.075
MS-4	P6RDDNS_6M	-1.160	0.303	-1.753	-0.567	14.710	0.000
MS-4	s395_wet	-8.366	5.372	-18.895	2.164	2.420	0.119
MS-4	UPTREE16p9	-6.463	1.082	-8.582	-4.343	35.710	<.0001
MS-4	s10k_tri	0.387	0.097	0.197	0.577	15.920	<.0001
MS-4	s10k_tri*s10k_tri	-0.012	0.003	-0.018	-0.006	14.830	0.000
MS-4	s300_cti	1.242	0.635	-0.003	2.487	3.820	0.051
MS-4	s300_cti*s300_cti	-0.058	0.032	-0.121	0.004	3.360	0.067
L-9	Intercept	1.026	0.906	-0.749	2.802	1.280	0.257
L-9	P6RDDNS_6M	-1.200	0.301	-1.789	-0.610	15.910	<.0001
L-9	s10k_wet	-12.551	8.025	-28.280	3.178	2.450	0.118
L-9	UPTREE16p9	-6.372	1.091	-8.510	-4.234	34.110	<.0001
L-9	s10k_tri	0.325	0.120	0.090	0.560	7.330	0.007
L-9	s10k_tri*s10k_tri	-0.010	0.004	-0.018	-0.003	7.900	0.005
MS-5	Intercept	0.720	0.835	-0.917	2.356	0.740	0.389
MS-5	P6RDDNS_6M	-1.226	0.301	-1.816	-0.636	16.590	<.0001
MS-5	s395_wet	-7.171	5.109	-17.185	2.843	1.970	0.161
MS-5	UPTREE16p9	-6.684	1.040	-8.722	-4.647	41.340	<.0001
MS-5	s10k_tri	0.386	0.097	0.196	0.576	15.900	<.0001
MS-5	s10k_tri*s10k_tri	-0.012	0.003	-0.018	-0.006	14.910	0.000
MS-3	Intercept	-6.301	3.273	-12.717	0.115	3.710	0.054
MS-3	P6RDDNS_6M	-0.943	0.347	-1.623	-0.263	7.390	0.007
MS-3	s395_wet	-9.774	5.685	-20.918	1.369	2.960	0.086
MS-3	UPTREE16p9	-5.801	1.172	-8.097	-3.505	24.520	<.0001
MS-3	s10k_tri	0.338	0.102	0.139	0.538	11.060	0.001
MS-3	s10k_tri*s10k_tri	-0.010	0.003	-0.017	-0.004	9.220	0.002
MS-3	s300_moose	0.756	0.634	-0.486	1.999	1.420	0.233
MS-3	s300_cti	1.256	0.644	-0.006	2.517	3.800	0.051
MS-3	s300_cti*s300_cti	-0.061	0.032	-0.124	0.002	3.610	0.058