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An assessment and review of potential impacts of timber extraction  
from harvest blocks around Pete Lake in the Knight East Landscape  
Unit on the population of brown bears (*Ursus arctos*) in the Glendale-  
Tom Browne drainage

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## Executive summary

This report has been prepared in response to the proposed sale by BC Timber Sales of harvest blocks around Pete Lake in the Knight East Landscape Unit. These blocks fall within the range of the brown bear (*Ursus arctos*) population in the neighboring Glendale-Tom Browne drainage which has been the subject of ongoing scientific investigation since 1997 by research teams from Utah State University, the University of Central Lancashire and the University of Cumbria.

The report addresses spatial movement, connectivity and habitat use using both genetic tools and telemetry data. Telemetry data was collected at 30 minute intervals and is therefore highly auto-correlated; an innovative jack-knife randomization and multivariate statistical draws meaningful results from a rich but challenging dataset.

Genetic analysis has established that the Glendale population is currently well connected with populations further North on the coast. Genetic comparison to populations at the heads of Knight and Bute Inlets should be considered to establish whether gene flow is occurring between Glendale and these populations.

Telemetry data reveals that the Blind Creek drainage is the most important of the neighboring drainages for bears in the Glendale-Tom Browne system and that the Pete Lake pass is the most often used link between the systems. 1/3 of the Glendale population uses, or passes through, the proposed cutblocks each season. All identified den sites fall within the habitat type of the proposed cut – they are between 600m and 900m, in mature forest and on steep slopes.

If harvest goes ahead, the proximity of good natural edge habitats to block APbd004 makes it a good candidate for trials of innovative harvest regimes. If sufficient structural integrity can be retained in the forest denning habitat may be maintained while increasing summer habitat value by opening up the forest structure enhancing berry growth.

For both blocks APbd001 and APbd004, fall harvest is likely to be the lowest impact harvest option; however, harvest of blocks should not coincide.

As long as habitat connectivity is maintained and spring/summer harvest is avoided, a well planned harvest of blocks APbd001 and APbd004 should have only short term impacts on the Glendale bear population. It should be noted however, that in a region with a diminishing area of old forest there are biodiversity and opportunity costs beyond those associated with bear population productivity. It should also be noted that even short term disturbance can have profound impacts on the spatial and temporal distribution, and viewability of bears (Nevin et al. 2001; Nevin and Gilbert 2001); this may have serious impacts on businesses reliant on site-specific bear-viewing activities.

# 1. Introduction

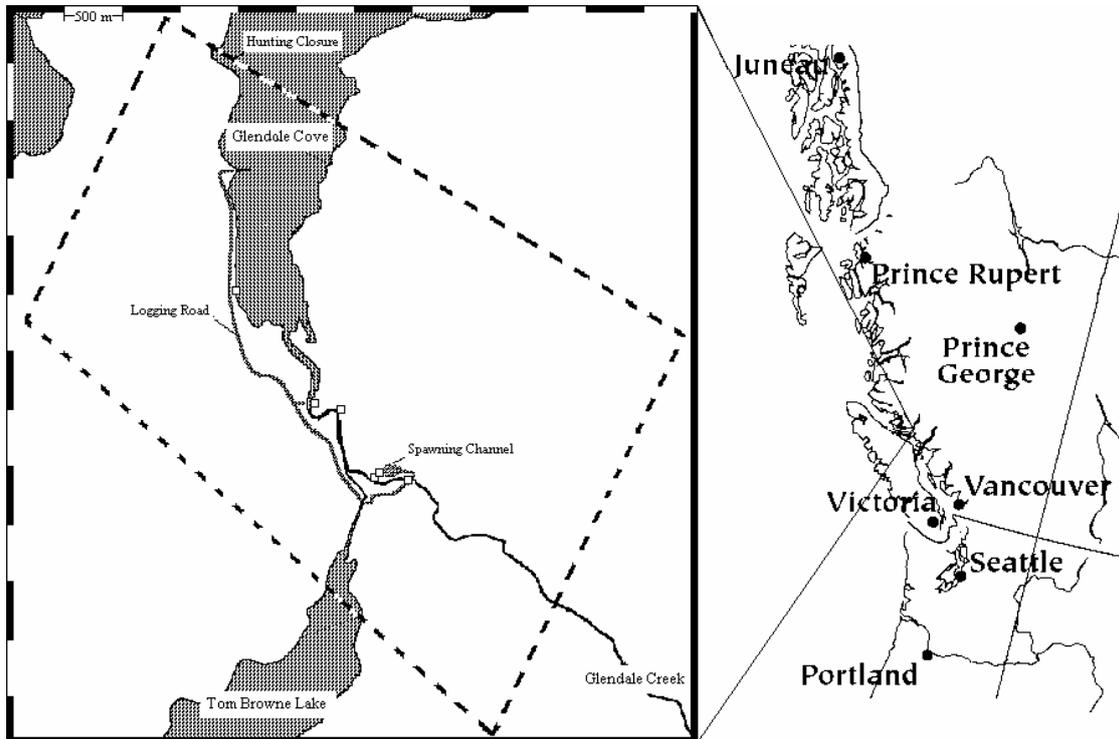
This report has been prepared in response to the proposed sale by BC Timber Sales of harvest blocks around Pete Lake in the Knight East Landscape Unit. These blocks fall within the range of the brown bear (*Ursus arctos*) population in the neighboring Glendale-Tom Browne drainage which has been the subject of ongoing scientific investigation since 1997 by research teams from Utah State University, the University of Central Lancashire and the University of Cumbria. This report draws on both published and unpublished data collected in these investigations which have been conducted and/or directed by the author.

The objective of the study is to assess potential impacts of both harvest operations and habitat alteration on the brown bear population.

## 1.1. Study area

Glendale Cove (N 50°41' W 125°44') is located on Knight Inlet in the Pacific mid-coast region of British Columbia, Canada (Fig. 1). It has a mild, hypermaritime climate with biological productivity in the range of tropical rainforests. The low elevation river valleys are characterized by rich alluvial soils, further enriched annually by upstream nutrients flooding over the stream banks of the floodplains and distributing rich silt to the roots of Sitka spruce and Western hemlock forests (Krajina 1965; Alaback & Juday 1989; Alaback & Pojar 1997).

The Glendale drainage has been subject to intensive logging, leading to the siltation of spawning gravel and the collapse of the river's salmon population. In 1986 the Department of Fisheries and Oceans Canada began construction of a 1000m x 15m spawning bed for pink salmon. This spawning bed is designed to accommodate 80,000 fish and has been one of the most successful on the coast.



**Figure 1: Site map. Glendale Cove is located on Knight Inlet in the Pacific mid-coast region of British Columbia (N 50°41' W 125°44'). The map shows the location of viewing structures (□) and spawning channel.**

Drawn by the abundant salmon, more than 40 bears now use the spawning channel as a primary fall feeding site. Many of these bears remain in the area for the whole active period of the year and are highly visible on the estuarine sedge meadows and inter-tidal zone during spring and summer.

Bear viewing tours operate in Glendale Cove from early May through mid October. Spring and summer tours mainly consist of boat-based viewing in the cove. During the salmon run, bears are observed from four permanent viewing structures.

The Glendale-Tom Browne drainage which flows into Glendale Cove is adjacent to the Blind Creek Drainage in which lies Pete Lake lies. The proposed cut blocks (APbd001 and APbd004) which lie on the shores of Pete Lake are both within 5km of areas previously identified as the key spring (breeding) and fall

(salmon-feeding) habitats (Nevin and Gilbert 2000, 2001, 2005a, b, c; Nevin et al. 2001; Nevin 2003).

Young forest habitat (forest under 140 years old), recently logged areas (harvested in the past twenty years) and old forest growth (140 years or older) make up the majority of the surrounding habitat. These habitats are spread throughout the area (Fig. 2); further to the Northeast are areas of alpine (no trees at high elevations) and sub-alpine (herb / shrub covered due to snow avalanches) habitat.

## ***1.2. Home ranges and population density***

Home ranges in brown bears are dependent on the sex of the individual and the geographic location of the population in which they are found. In North America brown bear home ranges are on average between 80 – 280 km<sup>2</sup>. Female ranges vary from 6 – 2655 km<sup>2</sup> and male territory ranges from 24.4 – 1054 km<sup>2</sup>, although the upper limits of these ranges are extremes and depend on habitat and population numbers (Macdonald & Barrett 1993). Across the continent populations vary widely in their densities; this variation has been attributed to differences in food base. Alaskan population densities vary from a maximum of 550 bears /1000 km<sup>2</sup> in Katami National Park, where salmon are available for most of the active period, to less than 5 bears /1000 km<sup>2</sup> for mountain bears of the Eastern Brooks Range on a marginal food base (Miller et al. 1997). Typically, the home range of males is 2 to 4 times that of females in the same habitat (Dahle & Swenson 2003).

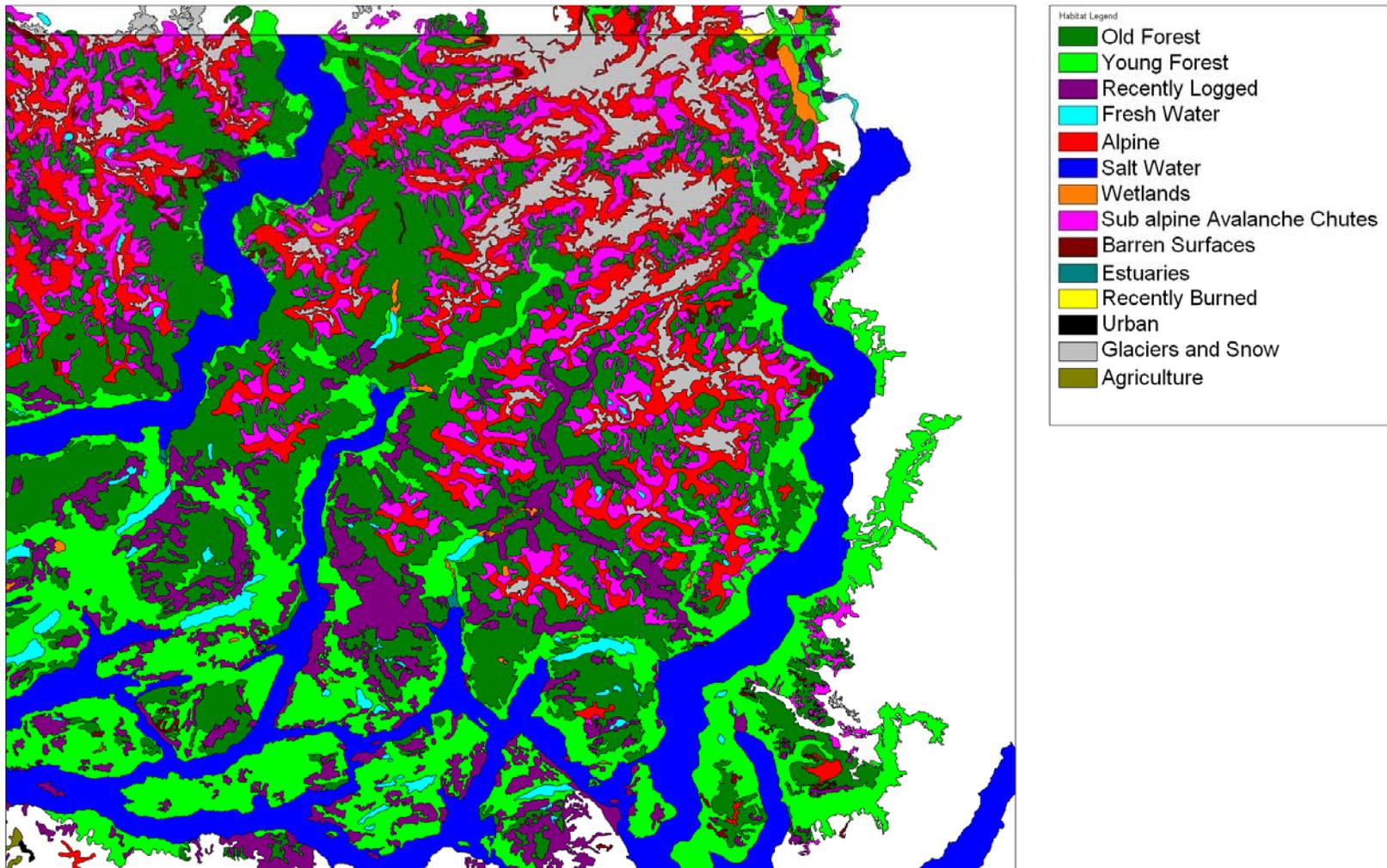
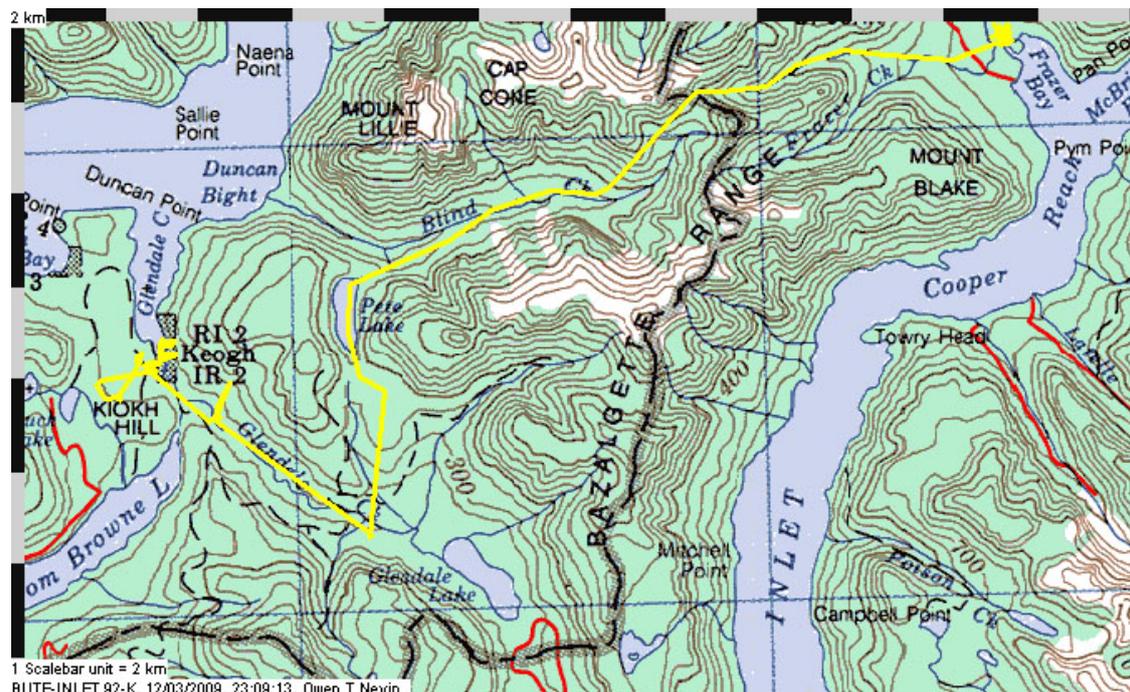


Figure 2: Land cover types. Habit defined (BTM present land use version 1) map of the area surrounding Knight Inlet, British Columbia. Coordinate range 234,400 x 5,656,700 to 371,000 x 5,580,000 – UTM Zone 9/10; NAD27 for Canada.

### 1.3. Seasonality in behavior and habitat requirements

Brown bear usually mate between May and July; this period sees an increase in male movement patterns with frequent, rapid medium to long range movements between sites (Fig. 3). These movements can be characterized as a form of trap-lining with males repeatedly covering circuits of likely spring habitat in the search for estrous females and breeding opportunities (Nevin unpublished data).



**Figure 3: Male trap-lining behavior.** Yellow line shows the movement of an adult male over a period of 10 days during the spring breeding season; the first 5 days are spent in the Glendale estuary, followed by a rapid movement (18 hours) to similar habitat in Frazer Bay. Note that this individual traveled through the area of the proposed timber harvest.

Summer sees bears disperse through a range of habitats with the dense spring aggregations in the estuarine sedge meadows no-longer in evidence. The high productive bear populations of coastal British Columbia and Alaska are highly dependent on salmon (Gilbert & Lanner 1995; Miller et al. 1997; Hilderbrand et al. 1999; Nevin 2003) and the densest aggregations of the year occur on salmon rivers in the fall. This is especially true for Glendale bears

which gain more than 75% of their annual assimilated energy from salmon (Nevin 2003).

After fall hyperphagia winter denning occurs. Older forest stands at higher elevations are preferred, partly because the more developed forest trees have deeper root formations making for more stable dens (Ciarniello et al. 2005).

#### **1.4. *Conservation status of the brown bear***

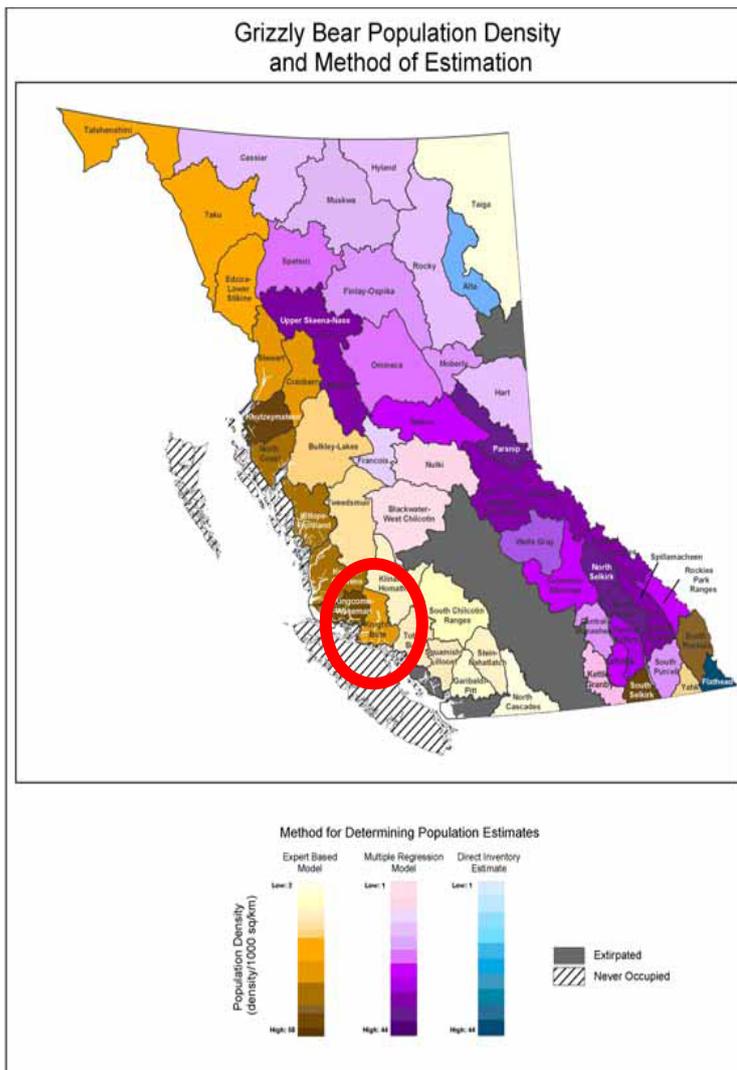
Brown bear populations worldwide have declined due to overexploitation and habitat loss. British Columbia has a population last estimated at 16, 887 and is classified as vulnerable (Hamilton et al. 2004); within the Province the Knight-Bute management unit is considered to have a medium population level (Fig. 4).

#### **1.5. *Impacts of development***

Brown bear habitat can be adversely impacted by the construction of road systems, forestry plantations and logging operations. These may reduce habitat availability or quality thereby supporting smaller populations (Ciarniello et al. 2005, Nellemann et al. 2007). These activities can also cause population isolation and cut off populations genetically, leading to a weaker gene pool (Posillico et al. 2004).

#### **1.6. *Studies of habitat use***

Brown bear habitat use has been studied by many scientists all over the world. Their early methods included surveying signs left by brown bears such as paw prints, tree damage and scats. Trapping and gathering hair from bait stations are techniques that have also been previously performed to gain more insight as brown bears are wary of humans and have generally low population numbers in vast home ranges making locating individuals difficult (Ward & Kynaston 1999; Herrero et al. 2000; Posillico et al. 2004; Nams et al. 2006).



**Figure 4: Brown bear population estimate in British Columbia (Hamilton et al. 2004). The Knight-Bute management unit is circled in red.**

Telemetry studies have greatly advanced our knowledge of brown bear habitat preferences and behavior. Collars can now be tracked by satellite giving researchers data on dispersal patterns, seasonal activities and home ranges over long periods of time (Ward & Kynaston 1999; Stevens 2002; Kansas et al. 2003). This can be merged with GIS packages for further study (Kobler & Adamic 2000). Current standard habitat use studies involve comparison of the telemetry data against a null hypothesis model where no habitat selection takes places. The results of these are taken as proof for random habitat use or whether a preference exists (Heithaus et al. 2006,

Martin et al. 2008). These uninformed-null models do not account for the auto-correlation which may arise in satellite derived telemetry data; i.e. as the interval between locations becomes shorter the probability that the animal will remain in the same habitat type becomes higher and so even an animal moving purely at random will appear to be acting non-randomly in traditional analysis.

A new methodology for the analysis of auto-correlated habitat use data was outlined by Heithaus et al. (2006) in their study of tiger shark (*Galeocerdo cuvier*). Heithaus et al. (2006) utilized a jack-knife randomization procedure to generate simulated random movement patterns from observed data which were both biologically feasible and retained the same level of auto-correlation as the telemetry data. This procedure effectively generates an informed-null which allows for a more powerful and reliable analysis of datasets in which relocations are frequent. The carnivore research team within the National School of Forestry's Centre for Wildlife Conservation has been developing this methodology and here present its first application to a terrestrial carnivore.

## **2. Methodology**

### **2.1. Data collection**

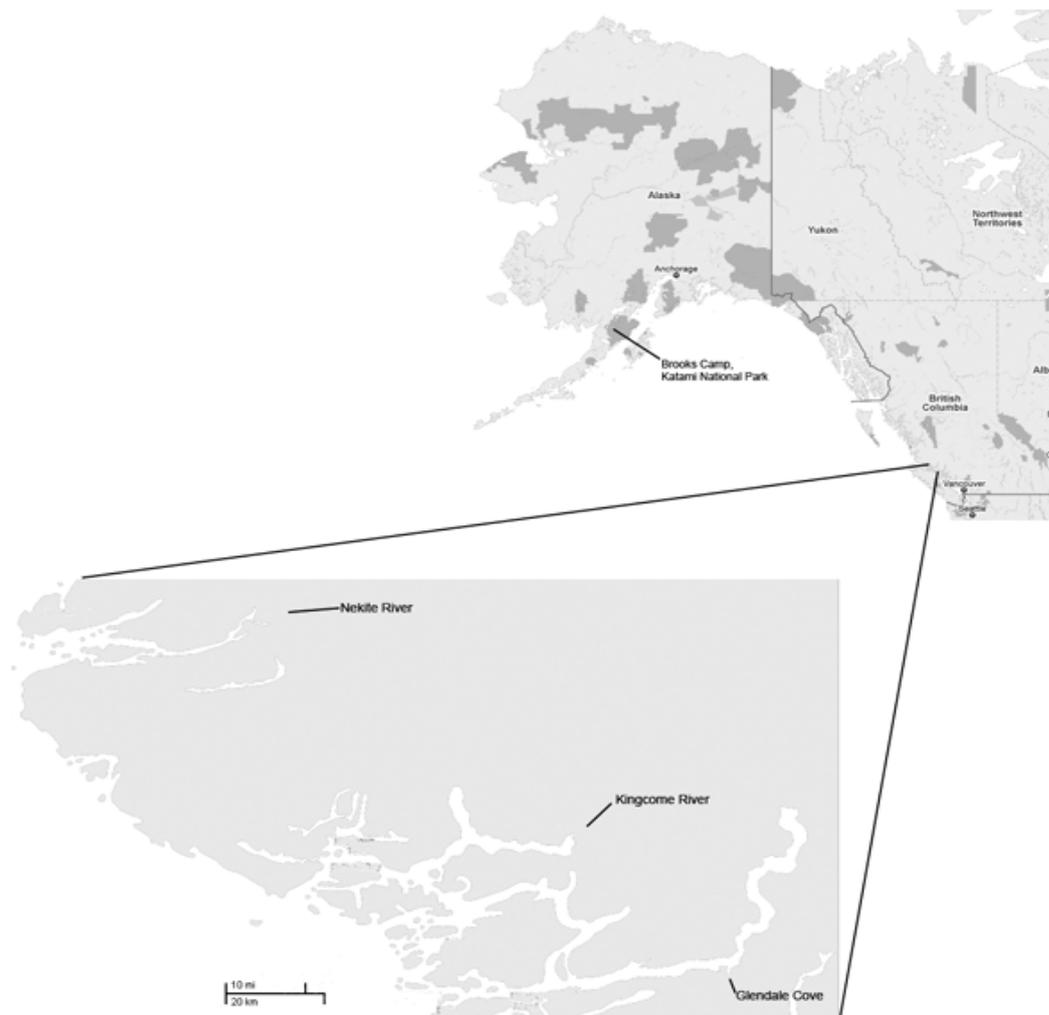
The data presented in this report have been collected in various studies in the period from 1997 to 2007 in the Glendale Cove area of Knight Inlet (N 50°41' W125°44') in British Columbia.

#### **2.1.1. Genetic samples**

Between August 1997 and September 2006 hair samples utilized in this study were collected (Nevin 2003; unpublished data) via a combination of invasive and non-invasive techniques. Non-invasive sampling included collection of hair from baited scent traps, trail hair traps and opportunistic collection; invasive sampling was conducted through live dart capture of bears for the purpose of GPS tracking, collar fitting and ear tagging. Hair samples were

removed using forceps or needle-nose pliers and protected in plastic sample vials.

Glendale samples were compared to samples collected non-invasively in the Nikite River (N 51° 25' W 127° 7') area of British Columbia with Southern Alaskan (N 58° 33' W 155° 46') samples included as an outgroup (Fig. 5).



**Figure 5: Locations of brown bear hair collection, 1997-2006. Glendale Cove, British Columbia; Nikite River, British Columbia and Brooks Camp, Alaska.**

### **2.1.2. Telemetry data**

Between June 2005 and November 2006, 12 bears from the Glendale population were fitted with Televilt GPS-Satlink collars signal. This system logged GPS locations for the collared animals every 30 minutes during the non-denning period and reported these locations once daily via satellite

modem. Not all collars were deployed and/or active for the whole study period however more than 12,300 locations were successfully logged. This full data set has been used to assess use and importance of the Blind Creek drainage while a subset of the data (collected over the period of 15/09/2005 to 6/10/2006 for one adult male brown bear) has been used in the jack-knife randomization procedure (Heithaus et al. 2006) and subsequent analysis. This subset of 1448 locations was chosen for analysis prior to the request to conduct this assessment.

A similar methodology has been applied recently (Martin et al. 2008) in a study of Scandinavia brown bears. The study differed from the methodology applied here in that individual points were randomized rather than the simulation of movement tracks applied here. Martin et al. (2008) showed that an uninformed null was more likely to be rejected than an informed (simulated) null.

### **2.1.3. Genetic analysis**

Wildlife Genetics International (WGI), Nelson, British Columbia performed all DNA extraction and genotyping on hair samples collected. DNA extraction, marker selection and microsatellite genotyping were conducted. DNA extraction was carried out using QIAGEN's DNeasy Tissue Kits (following standard protocols). Further details are available in Clapham et al. (*In review*).

### **2.1.4. Spatial data processing**

Data were uploaded from the collars via satellite and transferred into a Geographical Information System for mapping against topographic and habitat layers. A unique data layer was created for each individual bear; these were created in the Universal Transverse Mercator projection in zone 9 / 10 (Canada). Data was cleansed to remove points with insufficient satellites visible to acquire a 3-dimensional fix, after this process the subsample selected for jack-knifing had 1287 data points remaining.

The data was then divided into seasonal categories: spring (defined as April to June), summer (July to August) and autumn (September to November).

Tracks were then created from these different seasons.

### 2.1.5. Creation of habitat layers

Habitat maps were obtained from the base mapping and geometric service in the Integrated Land Management Bureau of the British Columbian government at a scale of 1:250000. These maps were geo - coded and provided in vector format which was preferential for this study. The habitat maps were later color coded for visual representation. Habitats were classified into 12 categories (Table 1).

<b>Habitat type</b>	<b>Habitat description</b>
Alpine	Areas which are virtually devoid of trees at high elevations.
Barren surfaces	Rock barrens, badlands, sand and gravel flats, dunes and beaches where un-vegetated surfaces predominate.
Estuaries	Salt water mud flats and inter-tidal areas at the mouth of rivers and creeks where the vegetation is influenced by frequent flooding at least once a year.
Fresh Water	Bodies of water with low salt / dissolved solid concentrations.
Glaciers and snow	Glaciers and permanent snow.

Old Forest	Forest greater than or equal to 140 years old and greater than 6 meters in height.
Recently Burned	Areas which are virtually devoid of trees due to fire within the past 20 years. Forest cover less than or equal to 15%.
Recently logged	Timber harvesting taken place within the past 20 years, or older if tree cover is less than 40% and under 6 meters in height.
Salt water	Inter – tidal zones / oceanic waters
Sub-alpine avalanche chutes	Areas below the tree line that are devoid of forest growth due primarily to snow avalanches. Usually herb or shrub covered.
Wetlands	Wetlands including swamps, marshes, bogs or fens. This excludes lands with evidence or knowledge of haying or grazing in drier years.
Young Forest	Forest less than 140 years old and greater than 6 meters in height. Areas defined as Recently Logged and Selectively Logged land uses are excluded.

**Table 1: Habitat classification. BTM present land use version 1 (1995).**

This data (provided by the Integrated Land Management Bureau) was used to create the habitat layer (Fig. 2) for the study area onto which bear location data was added.

#### **2.1.6. Random habitat representation (the uninformed null)**

A random data set was created for the purpose of statistical comparison; this consisted of 250 randomly assigned points within zones 9 and 10 of the National Canadian UTM coordinate system (coordinates 234,400 by 5,656,700 and 371,000 by 5,580,000) in a separate GIS layer. These zones and coordinates encompassed all of the observed bear locations.

#### **2.1.7. Creating simulated movement sets (the informed null)**

In total ten tracks were used from each season (spring / summer / fall) of differing lengths depending on data that was recorded. Each of these tracks was used as a base to create ten more 'simulated' tracks. Simulated data in this study refers to using actual brown bear movement distances and a real starting location but using a random order of these movements by reorganizing the X and Y coordinates. This random order was created by taking the horizontal and vertical distance between each point on a 90 degree vector, leaving a set of real distances that could be randomized through a jack-knife process to create a simulated brown bear movement. Starting positions used for each observed track remained the same for the simulated data sets. These coordinates for simulated brown bear movements were then transferred into GIS layers and mapped onto the habitat base map as for the observed data.

## **2.2. *Statistical analysis proposed***

### **2.2.1. Gene flow and relatedness**

Fisher's exact test for Hardy Weinberg Equilibrium (HWE) (Fisher 1935) was chosen for initial analysis of data using GENEPOP on the web (Raymond and Rousset 1995). Initial indications of genetic variability were obtained through assessments of allele diversity and expected ( $H_e$ ), as well as observed ( $H_o$ )

heterozygosity at each of the 8 sampled microsatellite loci using Microsatellite Analyzer (MSA) 4.05 (Dieringer and Schlotterer 2003). As a measure of relatedness, cluster analysis was performed using the data-mining program XLMiner (3.3.2) on the kinship coefficient and proportion of shared alleles distance data. Further details of the analysis of genetic data are available in Clapham et al. (*In review*).

### **2.2.2. Use and importance of the Blind Creek drainage**

This is mainly supported by descriptive statistics with the analysis of bears departing the Glendale-Tom Browne drainage being conducted using a Pearson chi – square goodness-of-fit test ( $\chi^2$ ).

### **2.2.3. Habitat use (uninformed null)**

Data from the observed and random data sets was analyzed using the Pearson's chi – square goodness-of-fit test ( $\chi^2$ ) for each season to determine whether distributions show any significant differences.

### **2.2.4. Habitat use (informed null)**

Data was analyzed using a General Linear Model (GLM) to assess any significance differences between the observed and simulated data tracks. This is a complex factorial analysis but other forms of analysis were inadequate given the structure of the data. The GLM allows a univariate analysis of variance to take place analyzing potentially both covariance and regression. Factors may be fixed or random and data sets balanced or unbalanced.

Therefore, general linear modeling allows for the analysis of multiple factors and multiple responses. The GLM test can also compensate for unbalanced data sets where observations are replicated. In this study the GLM will create a design matrix for the 'track' and 'season' factors and analyze the multiple responses and levels of these factors (where a level for factor 'season' would be for example 'summer') (Zar 1996).

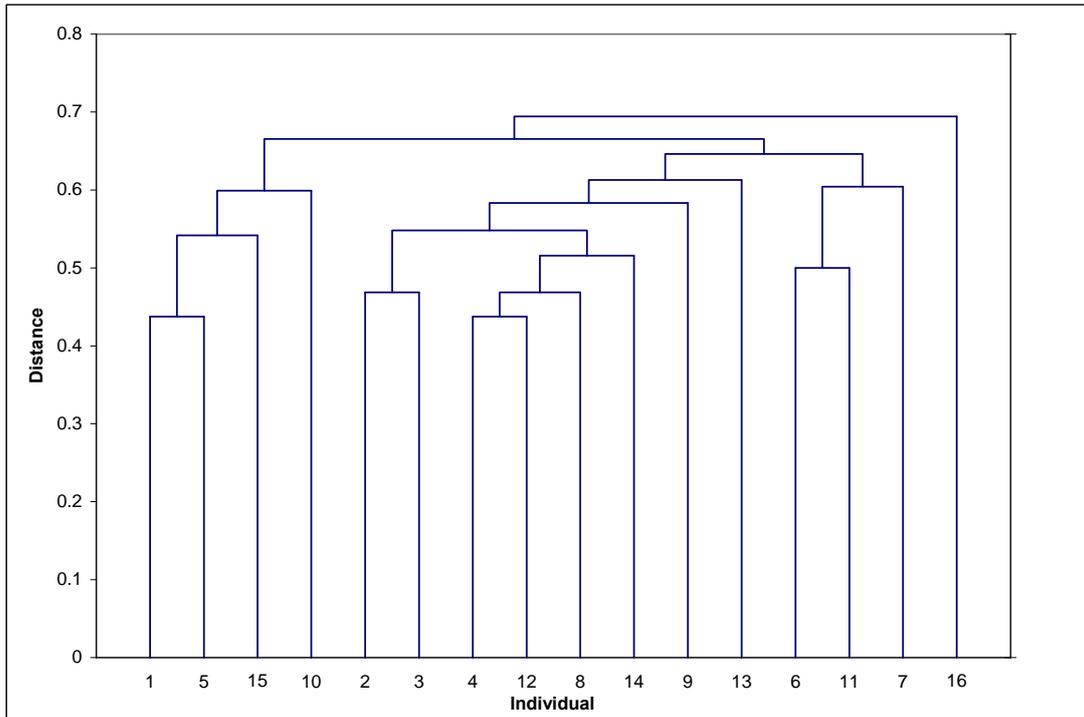
### 3. Results

#### 3.1. *Genetic Analysis*

Individuals sampled from the Glendale population were tested for Hardy-Weinberg Equilibrium. From the 8 microsatellites only locus G10J held a  $p$ -value close to 0.05 ( $p = 0.06$ ); therefore, none of the loci displayed significant departures from Hardy-Weinberg proportions.

The pairwise distance measure of kinship coefficient was run for both individual distances and population distances. The Glendale Cove and Nekite River bears were the two regions with the least kinship distance between them ( $D_{kf} = 0.69$ ), with both being almost equally distant from the Brooks Camp region bear ( $D_{kf} = 0.90$  and  $0.91$  respectively).

Using XLMiner, the initial run to assess hierarchical clustering between all individuals used the kinship coefficient data as a distance matrix. Using the dendrogram (Fig. 6) as a visual representation of results, two main clusters have emerged from the kinship data. Individuals 1, 5, 15 and 10 correspond to 3 individuals from the Glendale Cove area and 1 individual from Nekite River, and together form one cluster of kinship. The other individuals from the Glendale Cove region are grouped together in the second cluster, with the Brooks Camp individual (16), isolated on the far right of the graph. Individuals 4 and 12, as well as 1 and 5 had the lowest inter-cluster distance, with individual 16 being the most distant. Individual 15 (Nekite River) shared a high level of relatedness to individuals 1, 5, and 10, from the Glendale Cove region.

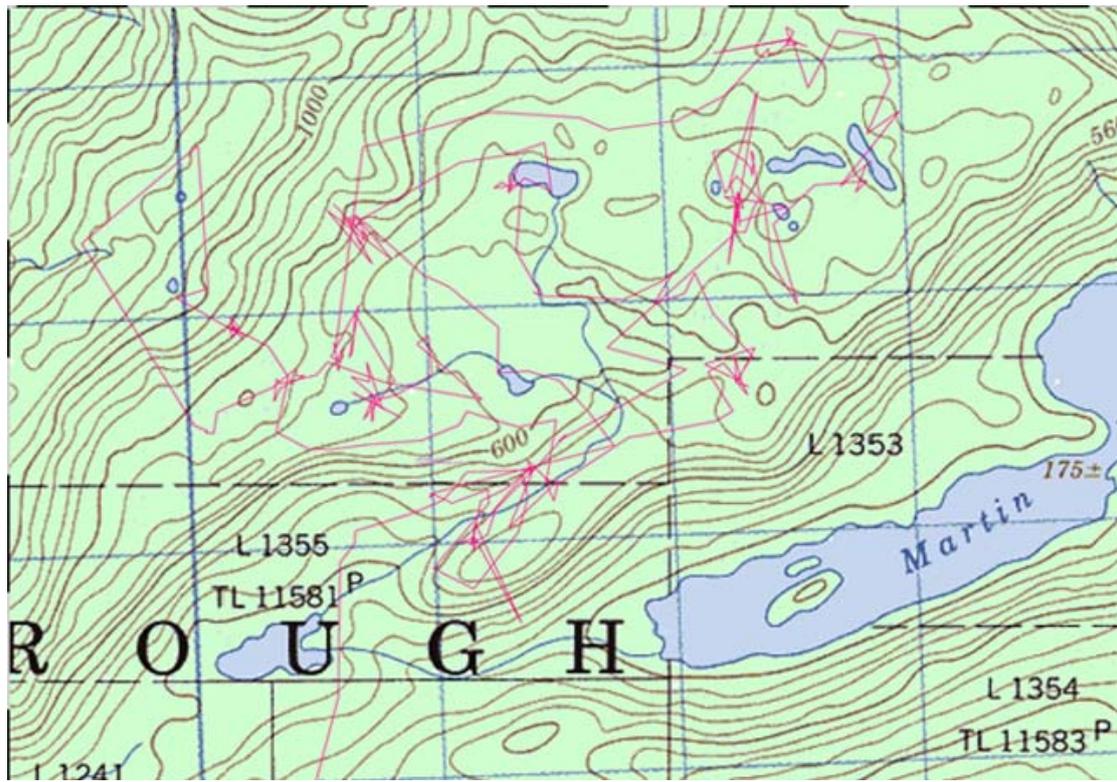


**Figure 6: Dendrogram showing hierarchical clustering of individual brown bears by kinship analysis. Individuals 1-14 Glendale Cove, individual 15 Nekite River, and individual 16 Brooks Camp (outgroup).**

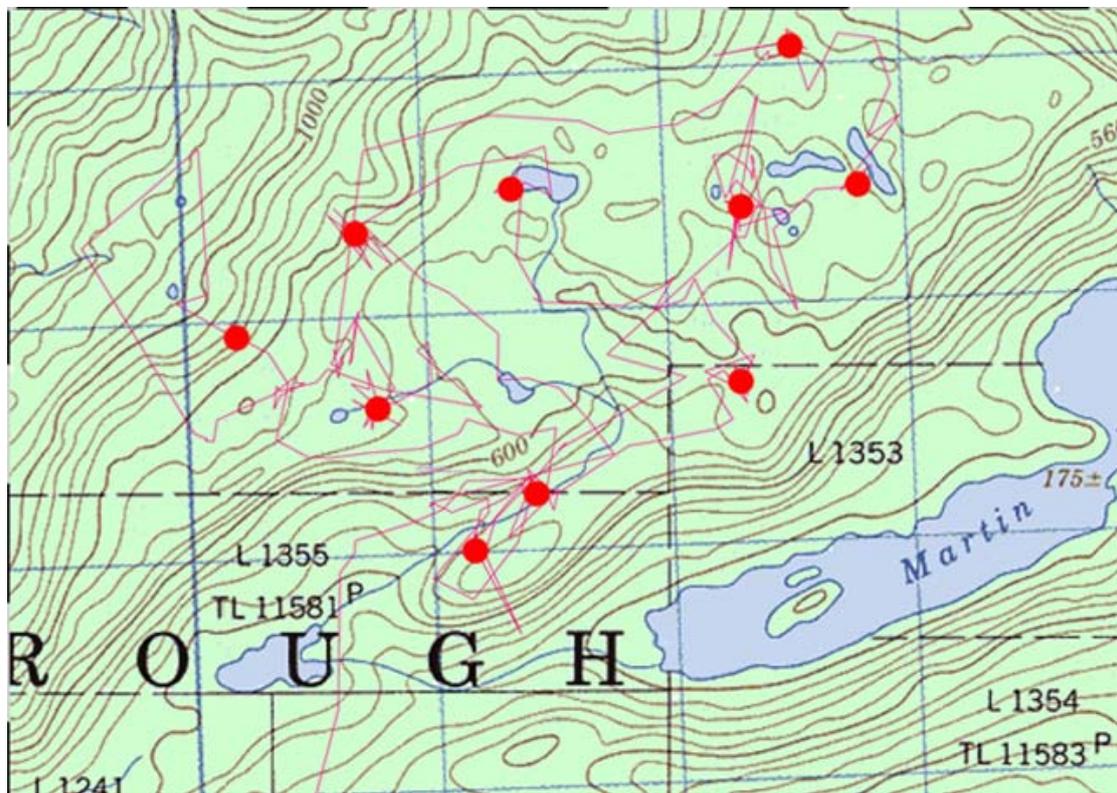
### ***3.2. Use and importance of the Blind Creek drainage***

During the telemetry study collared bears were using the area around Pete Lake in both spring and summer with the peak usage of the area occurring in July; 80% of all activity in the proposed cuts blocks was seen in July. July habitat use has been assessed habitats similar to the block just to the west of APbd004. The pink line in Figure 7a and b shows where the bear went with the red dots (Fig. 7b, c) marking clusters of activity. Satellite imagery reveals that these activity clusters occur in edge habitats. It is likely that the bear is feeding on berry growth at these natural and man-made edges; however, it is not using the center of the cut blocks for either foraging or travel.

7a



7b





**Figure 7: July habitat use. The pink line in *a* and *b* shows where the bear went with the red dots (*b* and *c*) marking clusters of activity. Satellite imagery reveals these activity clusters to be on edges – lake/stream banks, cutblocks and land slips (dark greens are old trees, light greens are young trees).**

Among collared bears, 33% used the area impacted by the proposed cuts; since collared bears were a stratified random sample (i.e. they represented all age/sex classes proportionately) it is reasonable to conclude that 1/3 of all bears in the Glendale-Tom Browne drainage make use of the area impacted by the proposed cuts. While none of the collared bears denned in the habitat surrounding Pete Lake, all for these bears denned between 600m and 900m, in mature forest on steep slopes. This would adequately describe the habitat within the proposed cut blocks.

The Blind Creek drainage is an important neighboring drainage to the Glendale-Tom Browne drainage; on 12 of the 48 occasion when bears were tracked leaving the Glendale-Tom Browne drainage they entered the Blind Creek drainage, this is significantly more than the other neighboring drainages

( $p=0.03$ ). Of all bears entering the Blind Creek drainage 50% did so through the area impacted by the proposed cuts.

### **3.3. *Habitat use (uninformed null)***

In each season habitat use was shown to be non-random (Spring  $X^2=351.317$ ,  $p<0.001$ ; Summer  $X^2=12504.4$ ,  $p<0.001$ ; Fall  $X^2=1544.50$ ,  $p<0.001$ ). While these results are statistically significant they are not unexpected due to the high levels of auto-correlation inherent in a dataset where subjects are relocated every 30 minutes. To draw any biologically meaningful or useful management conclusions we must look at this data in another way.

### **3.4. *Habitat use (informed null)***

The data was examined using a General Linear Model. Three features were tested; whether the habitat use in each data set were significantly different from each other, whether the habitat use by season showed any significant difference and if an interaction between the data set and the season showed any significance.

#### **3.4.1. General Linear Model- Observed vs. Simulated**

<b>General Linear Model: H1, H2, ... versus Track, Season</b>			
Factor	Type	Levels	Values
Track	Fixed	2	o, s
Season	Fixed	3	spring, summer, autumn

Analysis of Variance for h8 (recently logged)						
Source	DF	Seq ss	Adj ss	Adj ms	F	P
Track	1	442.8	442.8	442.8	0.86	0.358
Season	2	21384.8	21384.8	10692.4	20.72	0.000
Track * Season	2	963.5	963.5	481.7	0.93	0.399
Error	54	27859.7	27859.7	515.9		
Total	59	50650.8				
S = 22.7139		R-sq = 45%		R-sq(adj) = 39.90%		
Analysis of Variance for h9 (salt water (inter – tidal))						
Source	DF	Seq ss	Adj ss	Adj ms	F	P
Track	1	87.9	87.9	87.9	0.17	0.678
Season	2	12669.1	12669.1	6334.5	12.58	0.000
Track * Season	2	696.9	696.9	348.4	0.69	0.505
Error	54	27193.2	27193.2	503.6		
Total	59	40647.0				
S = 22.4405		R-sq = 33.10%		R-sq(adj) = 26.90%		

These are the results of importance for the general linear model test for the observed and simulated data sets; the full general linear model output can be found in Appendix I.

Among all the habitats there are two statistically significant findings. First, for recently logged habitat there is significant difference in use between seasons. A similar result is evident with salt water (inter-tidal) habitat.

## **4. Discussion**

### **4.1. *Genetic Analysis***

Gene flow was only assessed between Glendale and populations to the North. Relatedness tests between individuals suggested gene flow between the sampled individuals at Glendale Cove and Nekite River; this indicates connectivity over a large range on the along the coast. This genetic evidence of connectivity is supported by telemetry data from a dispersing sub-adult male brown bear recorded moving more than 50km north from Glendale Cove into the Kingcome River drainage (Nevin unpublished data). Dispersal movements of this type and the trap-lining seen in breeding males highlight the potential impacts of habitat degradation in areas which form corridors connecting high density aggregations of bears. This is especially important where the topography channels bear movement through narrow or constricted passes as in the case at Pete Lake.

### **4.2. *Use and importance of the Blind Creek drainage***

The Blind Creek drainage is used by Glendale bears significantly more often than any of the other 9 drainages which border the Glendale-Tom Browne system. With at least six distinct entry routes directly from the Glendale-Tom Browne drainage to the Blind Creek drainage, the fact that 50% of movements between the systems pass through the Pete Lake pass identify this area as a major movement corridor. Although the pass is not exceptionally narrow, the presence of the lake creates a major constriction point. With cut blocks proposed on both lake shores there is potential to restrict movement both during operations and during the regeneration phase due to the high levels of dispersed timber waste associated with heli-logging practices.

Heavy summer use of the area of the proposed cut blocks, and similar habitats elsewhere, indicates that harvesting operations during this period would negatively impact summer foraging behavior. This summer foraging is highly associated with edge habitats (Fig. 7) and post harvest habitat modification does have the potential to increase this habitat where sufficient mature forest is allowed to remain.

#### **4.3. *Habitat use (uninformed null)***

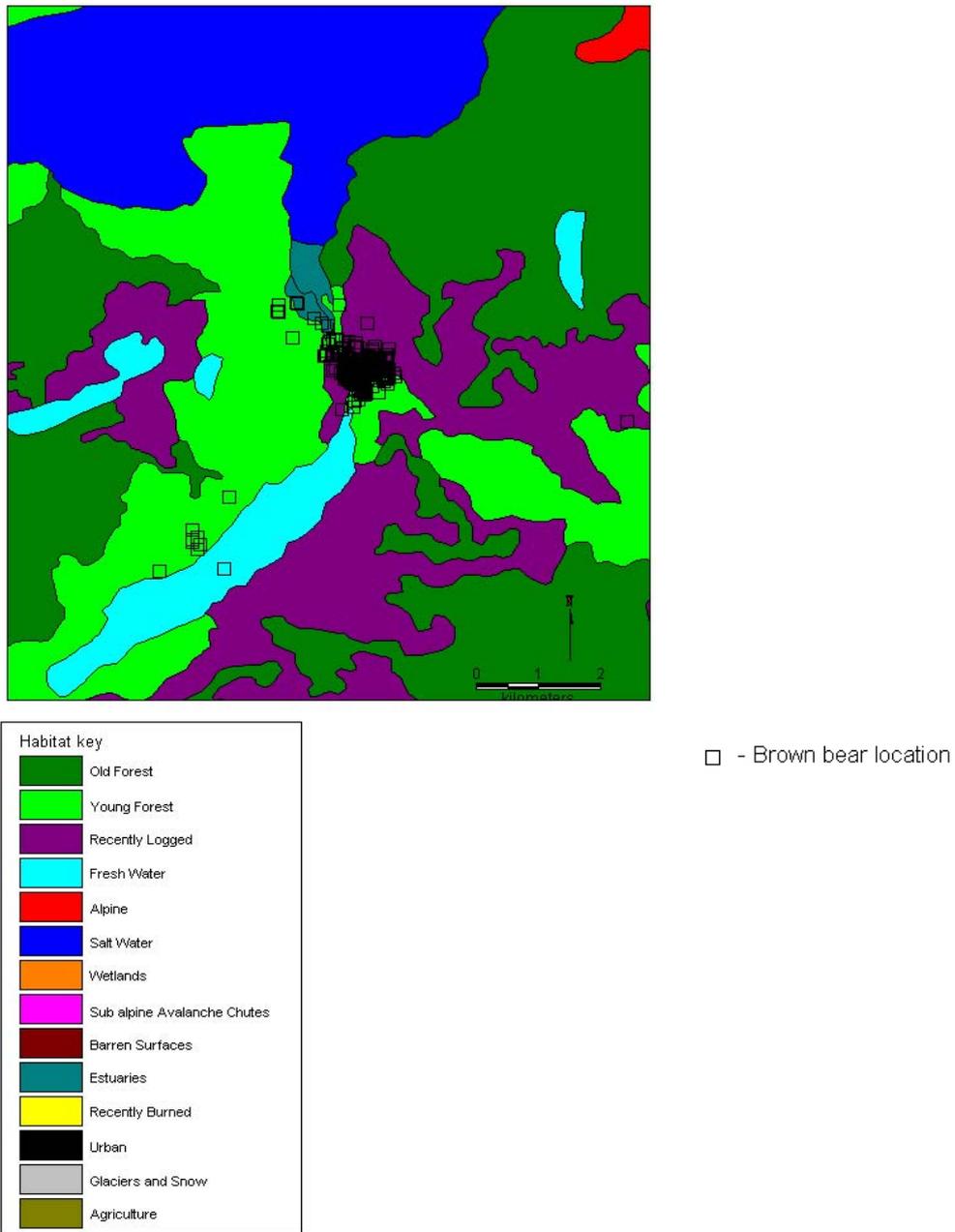
A significant difference was seen between the observed habitat use and habitat availability in the landscape. This is seen in all of the seasons analyzed (spring, summer and fall). Winter habitat use, i.e. den locations all fell in a single habitat type - forest greater than or equal to 140 years old and greater than 6 meters in height. It is an unremarkable result that bears show a habitat preference; however, this result is included to allow comparison to older studies or those restricted to simplistic data analysis. Reported  $p$ -values ( $<0.001$ ) are “deflated” by auto-correlation within the dataset thereby increasing the chance on Type I error (rejection of a null hypothesis which is in fact true). Results, however, do not lie near the boundary of true significance and this increased error probability does not therefore impact the conclusions drawn.

#### **4.4. *Habitat use (informed null)***

With a biologically feasible, informed null which retains the level of auto-correlation seen in the observed data many fewer significant differences were identified (Appendix 1). In this analysis there is no inflation of Type I error because of the internally retained consistency in auto-correlation. The unbalanced nature of the dataset would lead to increased Type II errors (failure to reject a null hypothesis which is in fact not true) if a 2-way analysis of variance [2-way ANOVA] had been performed; however, General Linear Modeling is a more flexible technique and unbalanced data can be accounted for in the design of the analysis.

Significant differences were seen in the seasonal use of recently logged habitats and salt water/inter-tidal habitat. While recently logged habitat is widespread in the region use of this habitat is highly localized; the driving variable appears not to be the habitat itself but rather the presence of the Glendale Salmon Enhancement Project within this habitat type. The super-abundant food resource which salmon provide, draw large numbers of bears into this otherwise low value habitat in the fall (Nevin 2003). Figure 8 shows locations for one bear during the salmon run with locations heavily concentrated in and around the Glendale spawning channel in the recently logged habitat type.

Salt water/inter tidal habitat was also preferred by the brown bear in spring (defined in this study as April – end of June). This is probably due to the combination of abundant early-season food resources in this habitat and the increased breeding opportunities that the discrete spatial nature of this habitat provides. While narrow, linear shoreline is abundant and widespread in this region, broad shallow intertidal zones and estuarine habitat is patchily distributed and rather uncommon (Fig. 2). This leads to spring aggregations of bears and the trap-lining behavior of adult males foraging for mates (Fig. 3). This patchy distribution of spring and fall resources makes inter-patch connectivity of great importance.



**Figure 8: Map showing observed brown bear locations in recently logged habitat. These locations are concentrated in and around the Glendale Salmon Enhancement Project (spawning channel).**

## 5. Conclusions and recommendations

Genetic analysis has established that the Glendale population is currently well connected with populations further North on the coast. It is important that

potential impacts of timber extraction operations and subsequent habitat change on gene flow to populations east of the Glendale-Tom Browne drainage be considered. Genetic comparison to populations at the heads of Knight and Bute Inlets should be considered to establish whether gene flow is occurring between Glendale and these populations.

It has been suggested (Nevin 2003) that the Glendale population will act as a source population due to enhanced reproduction at the site resulting from positive energetic impacts of carefully managed ecotourism activity (Nevin 2003; Nevin and Gilbert 2005 a, b). Monitoring gene flow and maintaining connectivity is therefore important for surrounding populations as well as for the Glendale population.

Telemetry data reveals that the Blind Creek drainage is the most important of the neighboring drainages for bears in the Glendale-Tom Browne system and that the Pete Lake pass is the most often used link between the systems. Within a season, telemetry indicates that 1/3 of the Glendale population uses or passes through the proposed cutblocks. In addition, All identified den sites fall within the habitat type of the proposed cut – they are between 600m and 900m, in mature forest and on steep slopes.

It is noteworthy that the harvest block APbd004 lies adjacent to an area of high quality summer habitat. This wet area to the west of the proposed cut has an abundance of natural edge habitat which is indicative of good berry production. This means that summer harvest operations would negatively impact the use of this resource by bears and potentially lead to increased encounter bear rates for timber crews. If harvest does proceed, a fall harvest will have the least impact on the bear population in the long term. The selective nature of heli-logging operations and the proximity of good natural edge habitats makes block APbd004 a good candidate for trials of innovative harvest plans which retain sufficient structural integrity in the forest to maintain denning habitat while increasing summer habitat value by opening up the forest structure creating more edge and enhancing berry growth in a landscape which can be accessed by bears. For block APbd001, fall harvest

is also the least impacting harvest option; however, this should not coincide with harvest of block APbd004.

As long as habitat connectivity is maintained and spring/summer harvest is avoided, a well planned harvest of blocks APbd001 and APbd004 should have only short term impacts on the Glendale bear population. It should be noted however, that in a region with a diminishing area of old forest there are biodiversity and opportunity costs beyond those associated with bear population productivity. It should also be noted that even short term disturbance can have profound impacts on the spatial and temporal distribution, and viewability of bears (Nevin et al. 2001; Nevin and Gilbert 2001); this may have serious impacts on businesses reliant on site-specific bear-viewing activities.

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## Appendix 1: General Linear Model – Observed and Simulated Tracks

Factor	Type	Levels	Values
Track	fixed	2	o, s
Season	fixed	3	Autumn, Spring, Summer

Analysis of Variance for H1, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	0.0000000	0.0000000	0.0000000	**	
Season	2	0.0000000	0.0000000	0.0000000	**	
Track*Season	2	0.0000000	0.0000000	0.0000000	**	
Error	54	0.0000000	0.0000000	0.0000000		
Total	59	0.0000000				

S = 0    R-Sq = \*%    R-Sq(adj) = \*%

Analysis of Variance for H2, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	0.02817	0.02817	0.02817	1.00	0.322
Season	2	0.05633	0.05633	0.02817	1.00	0.375
Track*Season	2	0.05633	0.05633	0.02817	1.00	0.375
Error	54	1.52100	1.52100	0.02817		
Total	59	1.66183				

S = 0.167829    R-Sq = 8.47%    R-Sq(adj) = 0.00%

Analysis of Variance for H3, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	62.9	62.9	62.9	0.58	0.451
Season	2	266.3	266.3	133.1	1.22	0.304
Track*Season	2	102.3	102.3	51.1	0.47	0.629
Error	54	5898.7	5898.7	109.2		
Total	59	6330.2				

S = 10.4516    R-Sq = 6.82%    R-Sq(adj) = 0.00%

Analysis of Variance for H4, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	1.6667	1.6667	1.6667	2.00	0.163
Season	2	0.8333	0.8333	0.4167	0.50	0.609
Track*Season	2	0.8333	0.8333	0.4167	0.50	0.609
Error	54	45.0000	45.0000	0.8333		
Total	59	48.3333				

S = 0.912871    R-Sq = 6.90%    R-Sq(adj) = 0.00%

Analysis of Variance for H5, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	0.0000000	0.0000000	0.0000000	**	
Season	2	0.0000000	0.0000000	0.0000000	**	
Track*Season	2	0.0000000	0.0000000	0.0000000	**	
Error	54	0.0000000	0.0000000	0.0000000		
Total	59	0.0000000				

S = 0 R-Sq = \*% R-Sq(adj) = \*%

Analysis of Variance for H6, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	0.4002	0.4002	0.4002	1.56	0.217
Season	2	0.5573	0.5573	0.2786	1.08	0.345
Track*Season	2	0.5573	0.5573	0.2786	1.08	0.345
Error	54	13.8717	13.8717	0.2569		
Total	59	15.3864				

S = 0.506836 R-Sq = 9.84% R-Sq(adj) = 1.50%

Analysis of Variance for H7, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	0.0000000	0.0000000	0.0000000	**	
Season	2	0.0000000	0.0000000	0.0000000	**	
Track*Season	2	0.0000000	0.0000000	0.0000000	**	
Error	54	0.0000000	0.0000000	0.0000000		
Total	59	0.0000000				

S = 0 R-Sq = \*% R-Sq(adj) = \*%

Analysis of Variance for H8, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	442.8	442.8	442.8	0.86	0.358
Season	2	21384.8	21384.8	10692.4	20.72	0.000
Track*Season	2	963.5	963.5	481.7	0.93	0.399
Error	54	27859.7	27859.7	515.9		
Total	59	50650.8				

S = 22.7139 R-Sq = 45.00% R-Sq(adj) = 39.90%

Analysis of Variance for H9, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	87.9	87.9	87.9	0.17	0.678
Season	2	12669.1	12669.1	6334.5	12.58	0.000
Track*Season	2	696.9	696.9	348.4	0.69	0.505
Error	54	27193.2	27193.2	503.6		
Total	59	40647.0				

S = 22.4405 R-Sq = 33.10% R-Sq(adj) = 26.90%

Analysis of Variance for H10, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	0.0000000	0.0000000	0.0000000	**	
Season	2	0.0000000	0.0000000	0.0000000	**	
Track*Season	2	0.0000000	0.0000000	0.0000000	**	
Error	54	0.0000000	0.0000000	0.0000000		
Total	59	0.0000000				

S = 0 R-Sq = \*% R-Sq(adj) = \*%

Analysis of Variance for H11, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	0.0000000	0.0000000	0.0000000	**	
Season	2	0.0000000	0.0000000	0.0000000	**	
Track*Season	2	0.0000000	0.0000000	0.0000000	**	
Error	54	0.0000000	0.0000000	0.0000000		
Total	59	0.0000000				

S = 0 R-Sq = \*% R-Sq(adj) = \*%

Analysis of Variance for H12, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Track	1	444.8	444.8	444.8	0.50	0.481
Season	2	1709.9	1709.9	855.0	0.97	0.386
Track*Season	2	281.9	281.9	140.9	0.16	0.853
Error	54	47604.2	47604.2	881.6		
Total	59	50040.8				

S = 29.6911 R-Sq = 4.87% R-Sq(adj) = 0.00%