

CORTEX CONSULTANTS INC.
CANADIAN FOREST PRODUCTS LTD.

MODELING

**Caribou Habitat Assessment and Supply
Estimator (CHASE)
Modifications and Sensitivity Analysis for the CHASE Spatially
Explicit Population Model for Northern Caribou**

Draft Not for Distribution

DAN O'BRIEN¹, GLENN SUTHERLAND¹, R. SCOTT MCNAY²

APRIL 2004

¹Cortex Consultants Inc., Victoria, BC, V8W 1W2, gsutherland@cortex.ca, danobrien99@shaw.ca.

²Canadian Forest Products Ltd., PO Box 310, Mackenzie, BC, V0J 2C0, mcnays@mackenzie.slocan.com

Prepared for Canadian Forest Products Ltd., Mackenzie Operations

CITATION: O'Brien, D., G. Sutherland, R. S. McNay. 2004. Caribou Habitat Assessment and Supply Estimator (CHASE) Modifications and Sensitivity Analysis for the CHASE Spatially Explicit Population Model for Northern Caribou Draft Not for Distribution. WII Report No. 130.



Omineca Northern Caribou Project

Caribou Habitat Assessment and Supply Estimator (CHASE)

Modifications and Sensitivity Analysis for the CHASE Spatially Explicit
Population Model for Northern Caribou

DRAFT

NOT FOR DISTRIBUTION

by

Dan O'Brien MSc., RPBio¹, Glenn Sutherland PhD, RPBio¹

and

R. Scott McNay PhD²

for:

the CHASE Modeling Team

April 2004

¹ Cortex Consultants Inc. Suite 3a - 1218 Langley Street. Victoria, BC, Canada. (250) 360 - 1492

² SLOCAN Forest Products. Mackenzie, BC.

Table of Contents

Table of Contents	2
List of Figures	3
List of TablesIntroduction	4
Introduction.....	5
Core Model Assumptions	5
Objectives.....	6
Description and Rationale for Additional Model Modifications	7
Density Dependant Distribution	7
Partitioned Predation Risk	7
Migration Corridors.....	8
Agents as Groups.....	8
Real time graphical output.....	8
Sensitivity Analysis/ Decision Analysis Framework	9
Description of Model Structure and Key Behaviours	10
Model Components	10
Description of Model Behaviour.....	10
Instructions for Running Model Scenarios and Interpreting Results	15
Input Requirements	15
Scenario Setup and Execution	15
Results Post Processing.....	16
Example Output.....	16
Sensitivity Analysis.....	17
References	Error! Bookmark not defined.
Acknowledgements	18

List of Figures

Figure 1.	Logistic function predicting the probability that a resident caribou group will split as a function of the number of individuals in the group ($b_1 = 10$, $b_2 = 0.8$).....	13
Figure 2.	Probability of groups merging modeled as a logistic of the number of individuals in the new group ($b_1 = 7$, $b_2 = 0.8$).....	14
Figure 3.	Annual mean population size ($n = 8$) in response to the projected seasonal ranges and predation risk. Black line indicates the mean; error bars indicate the standard deviation; and red dashed lines indicate the maximum and minimum values at each time step.	16

List of Tables

Table 1.	User specified model parameters.	11
Table 2.	Early and late winter range selection order.	12

Introduction

This report describes a series of updates and modification to a prototype habitat/population model for assessing risks of seasonal range management options on Northern Caribou herds, originally completed in October 2003 (Sutherland et al. 2003). The model is a spatially explicit, stochastic, age-structured population projection model implemented in SELES using its' individual-based modeling capability (called 'landscape agents').

Preliminary results for the prototype model indicated that the model responds as expected to systematic changes in vital rates, and that it was sensitive the spatial structure of the landscape. At a review meeting in November 2003, a number of improvements to the initial prototype were identified that would more accurately capture the key biological relationships in the Northern Caribou system. These include: modifying how caribou are distributed in each habitat preference category based on density at carrying capacity; integrating risk within the migration corridors; implementing the agent as a group individual caribou; a sensitivity analysis; and incorporating real time graphical output to display position and attributes of each group in relation to habitat on the seasonal range maps. During the course of the work, other necessary improvements were identified and implemented including: new logic for allowing caribou to switch between PLWR and HEWR based on availability during early and late winter seasons; reassessment of the assumptions about and methodology for computing predation risk as a function of the proportion of the landscape in each preference/ risk category.

The improved model builds on the prototype, utilizing functionality for dynamically loading decadal seasonal range maps output by the CHASE range management model and calculating indicators of herd status and trend. At initiation, a specified number of replicate 'herds' (populations) of caribou groups (agents) are randomly located on the landscape and assigned life attributes such as age and sex. The model cycles through five time steps per year, corresponding to the five seasonal range types used by Northern Caribou: pine lichen winter range (PLWR), high elevation winter range (HEWR), corridors (CORR), and calving summer range (CSR). At the onset of each time step, predation risk is determined for each caribou based on the habitat and risk attributes associated with spatial location occupied by that individual for that range type. Survival is evaluated, and if the individual survives it then moves to another location within the range map specified for the subsequent time step. The replicate populations give an indication of the likelihood of different outcomes, given stochastic variation in environmental conditions, population rates, and uncertainty in model parameters.

Core Model Assumptions

A spatially explicit population model combines a population model with a representation of the spatial configuration of landscape features. By explicitly incorporating the spatial location of habitat, predation risk, individual animals and other features of interest, the effect of changing landscape features on population dynamics can be evaluated. The goal of the spatially explicit caribou population model is therefore to test hypotheses about how the spatial distribution of habitat and regions of high predation risk will potentially affect the viability of the population. This can be accomplished through an assessment of the risk of reaching some threshold, such as extinction, or of the projected growth of the population, either under current conditions or those predicted for proposed management.

Underlying the spatially explicit population model is a core set of assumptions that govern the behaviour of the model. These assumptions represent hypotheses about how the spatial configuration of the landscape influences the structure and demographics of the population. This model was explicitly designed to simulate a caribou population operating under the following assumptions.

The first assumption is that the distribution of population is dependant on carrying capacity. That is, for a given range type, the population will be distributed in preferred and equivocal habitat at densities no higher than the carrying capacity for that habitat type. For example, in an unchanging landscape, with the population densities in preferred habitat at carrying capacity, as the population increases more and more individuals will be forced into equivocal and avoided habitat. The number of caribou in each habitat preference category is therefore a function of the carrying capacity, the area of habitat in each category, and the size of the population.

The second core assumption is that within a given habitat preference class, caribou distribution is not dependant on predation risk. The third core assumption is that caribou will distribute themselves randomly within available habitat. Thus for a given habitat preference category, the expected number of individuals subjected to each level of predation risk will be approximately equal to the proportional area of each risk class in that habitat category.

In addition to the core model assumptions, a number of assumptions about the structure and behaviour of the population are included for capturing key behaviours that are assumed to be of key importance for influencing population dynamics. As such, these additional model assumptions should have a significant influence on the outcome of the model. It is therefore important to underline that we should first have a clear understanding about how the model behaves under variation in the core model assumptions, before interpreting the influence of more specific assumptions about individual behaviour.

Objectives

The objectives of this report are:

1. To outline the implementation of these modifications,
2. To provide a detailed description of the structure and behaviour of the model,
3. To provide detailed instructions for running model scenarios and interpreting results,
4. To discuss implications of model assumptions

Description and Rationale for Additional Model Modifications

Density Dependant Distribution

Underlying the model is the core assumption that caribou are distributed based on the availability of habitat, and that availability is limited when the population is at carrying capacity. Hence, we assume that caribou are excluded from habitat when densities in that habitat type are at carrying capacity. In order to implement this assumption, the model requires the ability to reduce the probability of a caribou moving into preferred habitat to zero, once density in that habitat type have exceeded carrying capacity (i.e. behavioural exclusion). We assume the distribution of caribou is independent of predation risk, and therefore, without other limitations on movement, the distribution within a given habitat preference category is random.

Implementation involved developing a submodel for computing the area of the landscape in each habitat preference/predation risk category for each seasonal range map. Code to compute the maximum number of individuals that can move into each habitat category by multiplying these areas by the carrying capacity is implemented. As caribou are sequentially processed during population simulation, they first select for preferred habitat, followed by equivocal and then avoided as densities in each habitat type exceed carrying capacity. We also included logic for allowing caribou to move back and forth between PLWR and HEWR during both early and late winter seasons.

Partitioned Predation Risk

The core model assumption is that the distribution of caribou are excluded from preferred habitat when density reaches carrying capacity, and that distribution within a given habitat preference class is not dependant on predation risk. In other words, we assume caribou do not perceive predation risk.

The vital rates estimated from observed telemetry data represent the current level of mortality being experienced by the population operating on the current configuration of the landscape. Based on our assumptions of random distribution with available habitat, simply distributing individuals into each habitat / risk category in proportion to the area of each category on the landscape, and then applying mortality rates modified for predation risk, should yield the same overall rate of mortality in the population.

In order to capture the relationship between predation rates and the area of the landscape in each habitat/risk category, we divide the proportion of the landscape in each category at a given time step by the proportion at time = 0. Thus, the ratio of the proportion of the landscape in each habitat/risk category at any given time, to the proportion for the current landscape (t=0), are applied as weights to mortality. At time = 0, all weights are equal to one. However if the proportion for any category increases in the future, then the ratio is > 1, and < 1 if it decreases.

Thus, realized mortality (M_s^*) for life stage s is computed as:

$$M_s^* = M_{rs} \times PR_i \times \frac{pHab_{ijt_0}}{pHab_{ijt}}, \quad \text{[Equation 1]}$$

Where:

M_{rs} = Partitioned range specific mortality for life stage s ;

PR_i = Predation risk multiplier for risk category i ;

$pHab_{ij0}$ = Proportion of landscape in risk class i , habitat class j , at time zero;

$pHab_{ijt}$ = Proportion of landscape in risk class i , habitat class j , at current time.

Migration Corridors

Some Northern Caribou populations are composed of both resident and migratory types of caribou, and the seasonal movement of resident caribou between available habitat from each seasonal to the next is restricted by some maximum distance. Migratory caribou are not restricted in movement, and can potentially move between any two locations of available habitat within the entire study area. Migratory caribou also utilize movement corridors during spring migrations between HEWR and CSR and during the fall migration between CSR and PLWR, whereas residents do not.

Once in a corridor, migratory caribou move through the corridor, and are subjected to the cumulative predation risk for the entire corridor. Thus, rather than compute predation risk based on the habitat and risk attributes associated with a static spatial location occupied by that individual, we determine predation risk from the average predation risk for all hectares in the corridor. Essentially, this integrates predation risk across the entire corridor, and represents the overall expected predation risk encountered by caribou as they move through the corridor.

Implementation in the model involved enabling functionality for identifying the individual corridors, calculating their area and cumulative predation risk, and then assigning the mean to each individual corridor.

Agents as Groups

Caribou tend to aggregate and move in small groups. As a result, the individuals within a group will be subjected to the same predation risk as determined from the group's position on the landscape. If a group happens to move into a high risk area, then a greater number of individuals would be subjected to higher mortality than if each individual in the group were allowed to move independently throughout the landscape. Grouping caribou provides a more realistic representation of how caribou are distributed on the landscape. However, we predict that the grouping will increase variability in population mortality as a disproportionate number of individuals will be subjected to higher or lower mortality rates than the mean, and this effect will increase with increasing group sizes.

Implementation required extensive restructuring of most of the model. First code was implemented to compute the size and composition of each group during initiation of the population. New tracking variables were also required to store information about the attributes of each individual within the group, in addition to code for accessing each individual in the group for evaluation of survival and reproduction. During movement individual caribou move as a group. If the group grows too large, a smaller group can split off, and if this splinter groups encounters another other group, the two groups can merge together.

Real time graphical output

A series of dynamic layers are created at each time step that display the locations of individual caribou/groups on the landscape. Circular clusters are created around each agent at each time step. For agents representing groups, the relative size of cluster will relate to number of individuals in that group. Individual agents are differentiated by separate colours. These layers

are then superimposed over a grayscale habitat map and updated at each time step to display the position and relative size of each caribou group.

Sensitivity Analysis/ Decision Analysis Framework

Sensitivity analysis first requires a systematic exploration of the core model assumptions. This will provide baseline information about the sensitivity of the vital rates to changes in the proportion of the landscape in each habitat/risk category. The parameter set for a steady state population can then be identified and used as a base for introducing additional model behaviours. Systematically increasing model complexity provides foundation for interpreting the response of the model to the influence of additional model behaviours. The set of parameter states and associated outcomes are then used to populate a Bayesian Belief Network, where each node in the network represents a different parameter or outcome indicator. The resulting BBN will function as a decision analysis framework that can be used to assess the impact of different scenarios on the outcome of the population.

Description of Model Structure and Key Behaviours

Model Components

`HabitatManagement.lse` - Increments seasonal range type for scheduling loading of seasonal range maps each decade.

`HabitatLocation.lse` - Identifies and counts cells in each habitat preference/ risk class category and stores locations of each cell in list variables to be used by the population model for selecting move locations.

`PartitionMortality.lse` - Computes area and proportion of the landscape in each habitat preference/ risk class category for each seasonal range map. Computed ratio of current proportions to proportions at initial time. These are used to weight mortality * predation risk. Identifies individual movement corridors and computes area-weighted predation risk.

`PopulationModel.lse` - SELES landscape agent definition for a spatially-explicit, stage based caribou population model. Agents are initiated as groups of individual caribou, which are then distributed on the landscape within each habitat preference class. At each time step, individual are evaluated for survival and reproduction. If an agent survives, it then moves to available habitat in the range map corresponding to the subsequent time step. The population model tracks a number of demographic variables, including population size, numbers of individuals in each life stage, number of offspring, number of deaths, number of individuals in each habitat/ risk class category etc.

`RealTimeGraphics.lse` - Creates a circular buffer around the location of individual groups of caribou. The radius of the circle is directly related to group size. By default, residents are coloured blue and migratory caribou are coloured yellow.

`Reporting.lse` - Summarizes and writes population tracking variables to output file at each time step.

Description of Model Behaviour

Initiation

At initiation the model loads up the range maps for the current decade and schedules future range maps to be loaded in subsequent decades. The area and proportion of the landscape in each habitat preference/ risk class category is then computed and the locations of cells in each habitat preference class are stored in list variables.

The population model then initiates by first dividing the initial population into resident and migratory individuals using the parameter $pPropMigratory$, which specifies proportion of the population that is migratory selected from a normal distribution with a specified mean and standard deviation (Table 1). The number of caribou in each life stage is then computed for each group using the parameter $pInitDemographics$, which specifies the proportion of the population in each life stage (Table 1). Following this, the number of individuals in each habitat preference category is determined by multiplying the area in each habitat preference class by the carrying capacity for that class specified in $dRangeCCbyHP$ (Table 1). The number of caribou in the migratory group is then computed by multiplying the proportion of migratory caribou, selected from a normal distribution with a mean and standard deviation specified in

pGroupSizeDistribution (Table 1), by the initial population size. Initiation locations are then assigned to each agent group by randomly selecting a location from available habitat cells. Caribou groups select preferred habitat first. Carrying capacity is met when the density of caribou initiating in preferred habitat exceeds the maximum allowed. The caribou groups then select for equivocal habitat locations, followed by avoided once equivocal habitat is used up.

Individual caribou are then assigned to each caribou group. Adults are first distributed randomly into each caribou group. If an adult female is created in a group, then a calf is automatically assigned to that group if there is still room available in the group, and if there are still calves left to be distributed. Yearlings and juveniles are then assigned randomly to groups with space available. Attributes of each individual such as its sex, stage and age are stored and maintained in agent list variables.

Table 1. User specified model parameters.

Key Spatial Population Model Parameters

Parameter	Description	Variable Name [array dimensions]	Source
Proportion Migratory	Proportion of the population that is migratory	<i>pPropMigratory</i> [1,2]	estimated
Initial demographics	Proportion of the population in each life stage.	<i>pInitDemographics</i> [1,4]	Estimated for steady state population.
Carrying Capacity	Habitat carrying capacity for each range type.	<i>dRangeCCbyHP</i> [3,5]	(Sutherland et al 2003)
Group Size Distribution	Mean and standard deviation for number of individuals in groups of resident and migratory caribou.	<i>pGroupSizeDistribution</i> [2,2]	estimated
Mean mortality rates	Mean stage specific mortality rates by seasonal range type	<i>pStageMortBySR</i>	(Sutherland et al 2003)
Variance in mortality rates	Standard deviation of stage specific mortality rates by seasonal range types.	<i>pStageMortSDBySR</i>	estimated
Maximum movement distance	Maximum movement distance for resident caribou groups	<i>maxMoveDistance</i> [1,2]	estimated
Fecundity	Probability of reproduction	<i>pFecundity</i> [1,2]	(Sutherland et al 2003)
Logistic Function Constants	Constants specifying the shape of the logistic function used to estimate the likelihood that a caribou group will either split, or merge.	<i>logisticConstants</i> [4,2]	estimated
Splinter Group Size	Mean and standard deviation for the size of the new group when a caribou group splits.	<i>pSplinterGrpSizeDist</i> [2,2]	estimated
Minimum group transfer distance.	Distance within which other groups can be considered for merging with splinter groups.	<i>minTransferDistance</i> [1,2]	estimated

Parameter	Description	Variable Name [array dimensions]	Source
Maximum group size.	Maximum number of individuals in resident and migratory groups	<i>maxInGroup</i> [1,2]	estimated

Evaluation for Survival

Once group composition has been determined, each group is sequentially initiated at the selected spatial location on the landscape. This represents the beginning of the first time step. Caribou are first evaluated for survival. As the groups are processed off the cue, each individual in the group is evaluated for survival. The probability of dieing (mortality) is selected from a normal distribution with a mean and standard deviation corresponding to the life stage of the individual and the current seasonal range type (*pStageMortBySR*, *pStageMortSDBySR*, Table 1). The predation risk multiplier is then determined from the habitat preference category and the risk class at the location of the caribou group (*pPredRiskMult*, Table 1). The product of the mortality rate and the predation risk multiplier is then multiplied by the portioned mortality area weights corresponding to the habitat preference category and the risk class. If the current range type is movement corridors, then the probabilities of dieing are obtained from the area weighted corridor risk layers (see above). The derived mortality rate represents the probability that the individual will die in this time step. If this value is greater than a random number selected from a uniform distribution ranging from zero and one, the individual dies. If the individual survives, and it is currently in the last seasonal range map for the year, then it ages one year and transitions life stages.

Movement

Once all individuals in the group have been evaluated, and if there are still individuals alive in the group, the group then moves to a new location in the subsequent range map. During winter months caribou can select habitat in either pine lichen winter range (PLWR) or high elevation winter range (HEWR) depending on availability (Table 2). During early winter, caribou select first for preferred and equivocal habitat in PLWR. If none is available, they select preferred and equivocal habitat in HEWR. During late, winter months the selection order is reversed, with caribou selecting first for preferred and equivocal habitat in HEWR, followed by PLWR. In early winter, caribou groups are first distributed into preferred PLWR. Between winter and summer seasons, migratory groups randomly select a location within the movement corridors. However, resident caribou remain in their current location, and are subjected to mortality rates for that season and do not move until the subsequent time step. Both migratory and resident caribou groups move to available habitat in calving summer range (CSR).

Table 2. Early and late winter range selection order.

Preference	Early winter	Late Winter
First	PLWR – Preferred	HEWR – Preferred
Second	PLWR – Equivocal	HEWR – Equivocal
Third	HEWR – Preferred	PLWR – Preferred
Fourth	HEWR – Equivocal	PLWR – Equivocal
Fifth	PLWR – Avoided	PLWR – Avoided
Sixth	HEWR – Avoided	HEWR – Avoided

Besides difference in group size, resident caribou groups differ from migratory groups in their movement behaviour. Where migratory groups can select locations to move to from within the entire study area, movement by resident groups is restricted to the area within the maximum movement distance for residents. Resident groups move to a randomly selected cell of available habitat within this area. However, if there is no available habitat within the search area, then the location of nearest available habitat cell is selected.

Reproduction

Following movement, female juvenile and adult caribou are evaluated for reproduction by evaluating a value for fecundity selected from a normal distribution with mean and standard deviation specified in the parameter *pFecundity*. If this parameter evaluates true, then a single offspring is produced and assigned the attributes of a calf.

Group Splitting/Merging

Following reproduction, each caribou group is evaluated to determine if one or more individuals will leave the group. These splinter groups can either merge with other nearby groups or remain on their own. The likelihood that a group will split is modeled as a logistic function (Figure 1), where the probability increases with the number of individuals in the group,

$$pGrpSplit = \left(\frac{1}{1 + \exp(-1(GrpSize - b_1)/b_2)} \right), \quad \text{[Equation 2]}$$

where, *GrpSize* is the number of individuals in the caribou group, and *b₁* and *b₂* are logistic constants specified in the parameter *logisticConstants*. The shape of the logistic function is controlled by these 2 parameters, and *b₁* specifies the group size where there is a 50% chance that a group will split off. Separate constants are specified for residents and migratory groups.

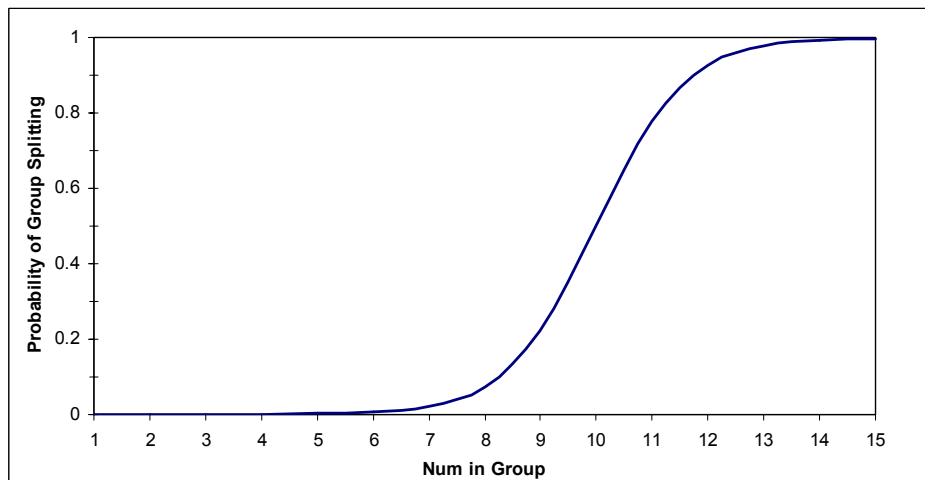


Figure 1. Logistic function predicting the probability that a resident caribou group will split as a function of the number of individuals in the group (*b₁* = 10, *b₂* = 0.8).

If a group splits, then the size of the splinter group is determined by selecting a value from a normal distribution with mean and standard deviation specified in the parameter

pSplinterGrpSizeDist. Separate splinter group size parameters are specified for resident and migratory groups. Individuals are selected randomly for placement in the new splinter group.

When a group splits, other nearby groups are identified, and the splinter group is then evaluated to determine if it will merge with one of these groups. The minimum distance for groups to be considered in merging is specified by selecting a value from a normal distribution with mean and standard deviation specified in the parameter *minTransferDistance*. If there are groups within the minimum transfer distance, then one is randomly selected. The probability that a group will merge is modeled as a logistic function of the combined number of individuals in the two groups (Figure 2), with constants specified in the parameter *logisticConstants*. Thus, the likelihood of a group merging decreases logistically with the number of individuals in the group. All individuals in the merging group are transferred to the splinter group, and the merging group is removed in the following time step. For groups to be considered for merging, they must have already been evaluated for survival and reproduction. If a group were to merge before it was evaluated for survival and reproduction, then the individuals in this group would skip being evaluated in the current time step, because group splitting/merging occurs after survival and reproduction.

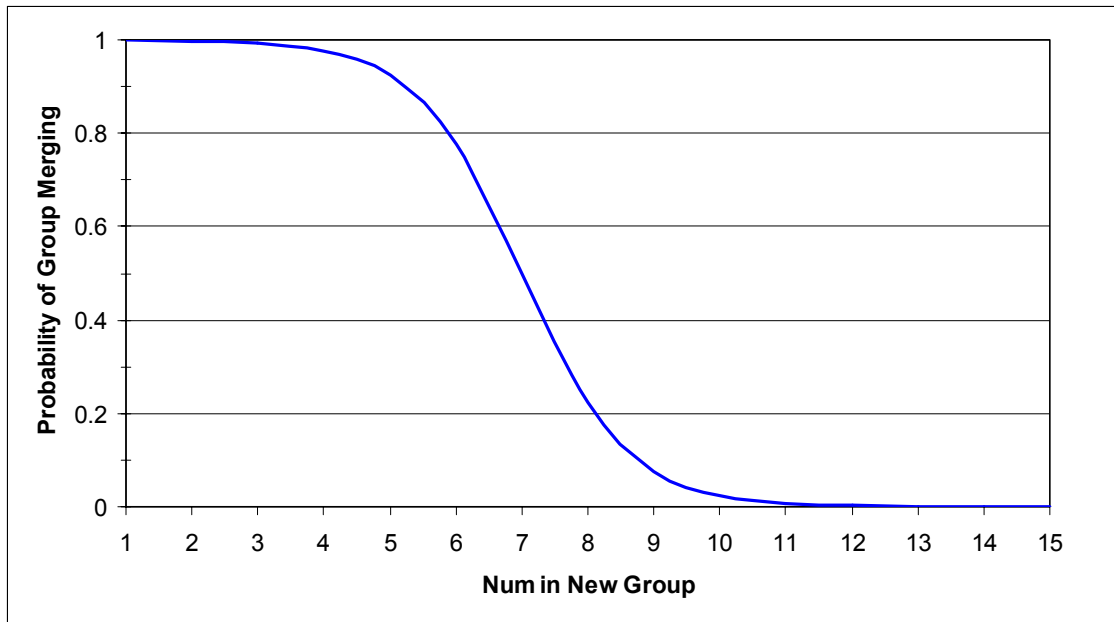


Figure 2. Probability of groups merging modeled as a logistic of the number of individuals in the new group ($b_1 = 7$, $b_2 = 0.8$).

Instructions for Running Model Scenarios and Interpreting Results

Input Requirements

The main inputs into the model are a series of text files containing values for the main model parameters (Table 1), and a time series of seasonal range maps for the projected landscape. Note that these should be habitat preference maps (independent of predation risk), as opposed to habitat value maps (habitat preference stepped down by predation risk). The parameter input files are stored in a subdirectory named `inputFiles`, and the seasonal range maps are stored in the `gisData` subdirectory. Note that the model requires that the seasonal range maps be in GRASS COMPRESSED format. A SELES script (`convertASCII2GRASS.scn`) for converting ASCII rasters into GRASS COMPRESSED format is included in the `gisData` subdirectory. To operate this script, set the correct source and output directories in the scenario file and then open this file in SELES to execute.

Scenario Setup and Execution

The model is set up to run either in single population mode or in batch mode. In single population mode, the user interface is accessible and the graphic display can be overlaid on each seasonal range map. In batch mode, multiple populations are automatically simulated over multiple scenarios, however the user interface is inaccessible.

Single Population Mode

To run the model in single population mode, edit and execute the `PopulationModel_singlPopn.scn` file located in the main directory. The model will run using input files contained within the `inputFiles` subdirectory located in the main directory.

Once the model has loaded in SELES, open the SIMULATION CONTROL dialog window in the DYNAMICMODELS pull down menu. Then specify the number of years you want the simulation to run and press SIMULATE. Once the model is running, you can then overlay the graphic display on each seasonal range map by selecting RASTER VIEW PROPERTIES in the VIEW pull down menu and selecting *graphicDisplay* as an overlay. When doing this remove the check in COLOUR DISPLAY to improve discrimination of the two layers.

The results of the model will be output into a subdirectory named `outputFiles` located in the main directory. By default, attributes of each individual agent will be output in the `AgentStats_Seasonal.txt` file as each agent is processed. Population level attributes are output to the file `PopStateOutput_Seasonal.txt` at the end of each time step.

Batch Mode

Running the model in batch mode first requires that the parameter values for each scenario be specified and stored in an input file. This is automated using a scenario setup script which reads in a spreadsheet of parameter values and then creates a series of subdirectories containing input files with the parameter values for each scenario. The model is launched and iterates automatically over the specified number of populations simulations for each scenario.

To set up a series of scenarios first open the `ScnParamVals.xls` file in excel, located in the `Experiment` subdirectory. In this spreadsheet the columns correspond to model parameters and the rows correspond to scenarios. This allows you to easily and quickly modify parameter values

while keeping others constant. Once parameter values for all scenarios have been specified, save the file as a tab delimited text file in the same directory. Then set the correct source directory in the `ScenarioSetup.scn` file and then execute it in SELES. This will create a series of subdirectories, one for each scenario. In each subdirectory you will find an `inputFiles` subdirectory containing all the required parameter input files.

Once this has been completed, you will need to set the correct path names in the `LearningScenarios.scn` file. You can also specify the initial population size, the number of simulated populations per scenario, and whether you want to output the attributes of each individual agent, although not recommended for batch runs.

Then execute the `LearningScenarios.scn` file in SELES and sit back and wait. Note that with the Wolverine data set, the model requires ~ 500MB of RAM and when running with a steady state population of approx 1000 individuals will require approximately 40 minutes per population on a machine with a 1.7 GHz processor.

Results Post Processing

Output for each scenario is stored in an `outputFiles` subdirectory created in the corresponding scenario subdirectory. The population state at each timestep is recorded in the `PopStateOutput_Seasonal.txt` output file. Each population is simulated sequentially, so the results for each population are appended to the bottom of the file as they are processed. To summarize the results first open the file in EXCEL. Then sort the file by `PopNum` first, and then by `RangeType`. To obtain the mean, standard deviation, max and min values for each population at each change in `RangeType` use the Subtotals command in Excel (located in the Data pull down menu). Compress the tree by clicking the 2 in the upper right corner of the spreadsheet, select the data range, hit `ctrl+g` (or `Edit/GoTo`), press `Special` and select visible cells only. Then copy the selected range into a new spreadsheet.

Example Output

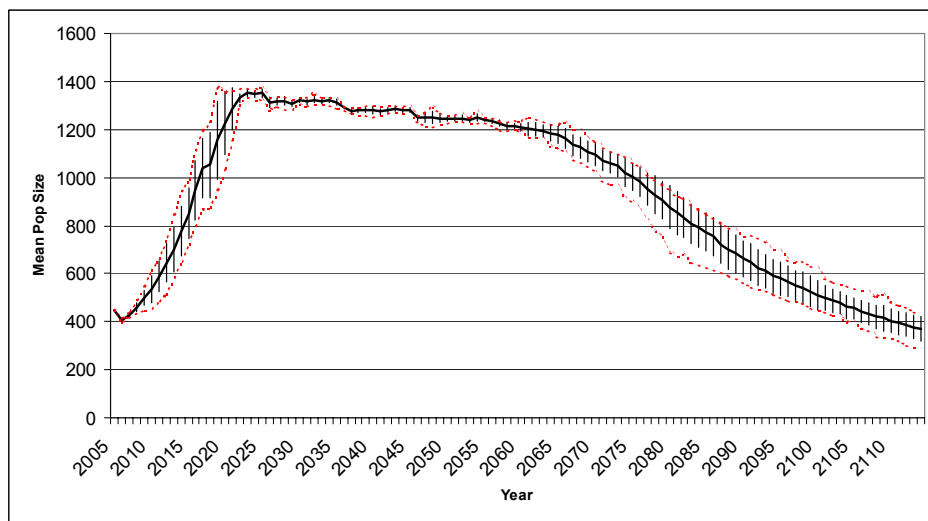


Figure 3. Annual mean population size ($n = 8$) in response to the projected seasonal ranges and predation risk. Black line indicates the mean; error bars indicate the standard deviation; and red dashed lines indicate the maximum and minimum values at each time step.

Sensitivity Analysis

The modifications to the spatial population model required extensive restructuring of the program code. The additional modifications add complexity and uncertainty to the model. Furthermore base values for these model parameters can at best be estimated from available observational data and expert opinion. In order to evaluate the influence and sensitivity of the model when run with the additional model behaviours, it is important to understand how the model behaves to variability in parameters representing the core assumptions. More specifically, how does the changing landscape influence survival and reproduction under the assumption of density dependant distributions, and random distribution within available habitat independent of predation risk.

With a clear understanding of the behaviour of a simple model that captures only the core assumptions, we can better understand how the additional behaviours, such as modeling agents as groups, effects the response of the population projections to changes in the structure of the landscape. With the additional modifications running the model has become computationally expensive. With a steady state or growing populations, the time to simulate 1 population over 100 years takes almost 45 minutes on a 1.7Ghz machine and uses in excess of 500MB of RAM.

The suggested approach should be followed for exploring model sensitivity. Limiting the model to those behaviours that represent the core model assumption, the model will run substantially faster (Table 3). Therefore, first generate population means from a large sample of populations (N=100) with the limited model behaviour . Then generate population means with smaller sample size (n=10), while systematically varying parameters specifying the complex model behaviours operating.

To be completed...

Table 3. Assumptions correponding to model parameters.

Core Parameters	Additional Behaviour Parameters
<ul style="list-style-type: none"> • Mean and standard deviation for stage specific mortality by seasonal range type. • Predation risk • Mean and standard deviation for juvenile and adult fecundity • Range specific carrying capacity for each habitat category • Initial population demographics (proportion in each life stage) 	<ul style="list-style-type: none"> • Proportion of the population that are migratory • Group size probabilities for migratory and residents • Coefficients for logistic function specifying the probability that a group of caribou will either split or merge given the group size.

Acknowledgements

This project was supported by the B.C. Ministry of Forests (Forest Practices Branch) through funding provided by the Forestry Investment Account