

BAP REPORT #8: BAP PROGRAM DOCUMENTATION

**Prepared for Millar Western Forest Products'
Biodiversity Assessment Project**

Prepared by:

A. Rudy

**KBM Forestry Consultants Inc.,
Thunder Bay, Ontario**

May 2000

Table of Contents

8.1 INTRODUCTION	1
8.2 MODEL OVERVIEW	1
8.2.1 Habitat Classification	1
8.2.2 Coarse- and Fine-filter Biodiversity Models	2
Coarse-Filter Biodiversity Analyses	2
Fine-Filter Biodiversity Models	3
8.3 PROGRAM STRUCTURE	3
8.3.1 Program Environment Variables	4
8.4 PROGRAM FLOW	5
8.4.1 Harvest Projection	5
Database and Spatial Files	6
Program/Model Description	6
Coverage and Grid Set-up	6
Habitat reclassification	7
Habitat filtering	7
8.4.2 Natural Disturbance Regime (NDR)	10
Habitat reclassification	10
Habitat Preparation	11
Habitat filtering	11
Age Grid Preparation	11
8.5 COARSE-FILTER BIOINDICATORS	12
8.5.1 Landscape Configuration Models	12
Adjacency	12
Patch Size and Shape (Mean Patch Fractal Dimension)	13
Core Area	14
Contrast Weighted Edge Length	15
Mean Edge Contrast Index (MECI)	15
Mean Nearest Neighbour	16

8.5.2	Ecosystem Diversity Models	17
	Area-weighted Age	17
	Developmental Stage Proportion	17
	Habitat Distribution	17
	Habitat Diversity Index	18
	Species Presence	19
	Species Dominance	19
8.6	FINE-FILTER BIOINDICATORS	20
	Model Input	20
	General HSM Description	20
	Habitat Supply Models	22
	General Program Files	24
8.7	BAP USER MENU INTERFACE	25
8.7.1	Menus: Coarse-filter Biodiversity Models	25
	Harvest Projection Analysis	25
	Set Up Button	26
	Harvest Projection Analysis	27
8.7.2	Menus: Fine-filter Biodiversity Models	33
8.8	LITERATURE CITED	38
APPENDIX 1: LANDSCAPE AND ECOSYSTEM ASCII FILE DESCRIPTIONS AND PARAMETERS		A1
APPENDIX 2: LANDSCAPE AND ECOSYSTEM EXAMPLES.....		A11

List of Tables

Table 8.1.	Coarse-filter biodiversity models used in BAP.	2
Table 8.2.	Wildlife species modelled in BAP.	3
Table 8.3.	Environment variables used in BAP.	4
Table 8.4.	Required files of the harvest projection analysis program.	5
Table 8.5.	General model arguments used by BAP.	6
Table 8.6.	Forested habitat codes.	8
Table 8.7.	Reclassification age class.	8
Table 8.8.	Specific habitat age class description for pure aspen stands.	8
Table 8.9.	General model arguments used by NDR.	10
Table 8.10.	The structure and format of a sample adjacency table.	12
Table 8.11.	Programs, inputs, and outputs related to the bioindicator, adjacency.	12
Table 8.12.	Adjacency codes by broad habitat type.	13
Table 8.13.	Programs, inputs, and outputs related to the bioindicators, patch size and shape. ...	13
Table 8.14.	Specific developmental stage adjacency combinations and their associated buffer distances.	14
Table 8.15.	Programs, inputs, and outputs related to the bioindicator, core area.	14
Table 8.16.	Example of the format and partial content of for-for, nfor-for, and nfor-nfor files.	15
Table 8.17.	Programs, inputs, and outputs related to the bioindicators, contrast-weighted edge length and mean edge contrast index.	15
Table 8.18.	Programs, inputs, and outputs related to the bioindicator, mean nearest neighbour. .	16
Table 8.19.	Programs, inputs, and outputs related to the bioindicator, area-weighted age.	17
Table 8.20.	Programs, inputs, and outputs related to the bioindicator,developmental stage proportion.	17
Table 8.21.	Programs, inputs, and outputs related to the bioindicator,habitat distribution.	17

Table 8.22. Sample diversity file.	18
Table 8.23. Programs, inputs, and outputs related to the bioindicator,habitat diversity.	18
Table 8.24. Programs, inputs, and outputs related to the bioindicator,species presence.	19
Table 8.25. Programs, inputs, and outputs related to the bioindicator,species dominance.	19
Table 8.26. General HSM models arguments.	22
Table 8.27. Programs, inputs, and outputs related to the fine-filter bioindicators.	23
Table 8.28. Programs, inputs, and outputs called by specific fine-filter bioindicators.	24

List of Figures

Figure 8.1. BAP directory structure.	3
Figure 8.2a. Grid of forested habitat types prior to filtering.	9
Figure 8.2b. Grid of forested habitat types after filtering.	9



8.1 INTRODUCTION

The Biodiversity Assessment Project (BAP) is a suite of models designed to quantify changes in landscape configuration, ecosystem diversity, and wildlife habitat supply. The models have been structured for Millar Western's Forest Management Agreement (FMA) area and are intended to predict the potential impacts of alternative forest management strategies on forest biodiversity within the FMA area.

BAP is constructed around ArcInfo's Arc Macro Language (AML). It requires the Windows NT operating system running ArcInfo Version 7.2. ArcInfo modules necessary for operating and maintaining the models include Arc, AML, ArcEdit, and Grid. Other software considerations include the relational database INFORMIX using INFORMIX 7.3.TC7 (running on the Windows NT operating system). Where advantageous, the tabular calculations are performed using the aforementioned software. In addition, an "in-house" C-program is used for calculation of area and shape quartiles.

8.2 MODEL OVERVIEW

BAP analyses present and future forest conditions under various forest management scenarios and natural disturbance regimes using data from simulation models. The timber supply projection data were generated using GISCOMPLAN and WOODSTOCK/STANLEY (Millar Western 2000) and are referred to as the Harvest Projection Analysis within BAP. The natural disturbance regime data were generated using LANDIS (see BAP Report #4: Natural Disturbance Regime Simulation Using LANDIS, Doyon 2000) and are referred to as Natural Disturbance Regime (NDR) data within BAP.

8.2.1 Habitat Classification

Depending on the bioindicator, BAP statistics are reported at various scales of resolution with regards to species composition and developmental stage. These scales of resolution are referred to as broad and specific levels. The broad species composition classification separates the forest into pure hardwood stands, hardwood-dominated mixedwoods, softwood-dominated mixedwoods, and pure softwood stands. These broad species composition types are further subdivided into 19 specific species composition levels that indicate the tree species that are dominant within the stand. Developmental stages subdivide the forest according to stand age. Each stand is classified into one of four broad developmental classes: opening, developing, forested, or old. The broad developmental stage of opening is further subdivided into clearcut and burned areas. Developing stands are classified as regenerating or young stands. Regenerating stands are struggling to gain ascendancy over competing vegetation and young stands have reached the free-to-grow stage but have not yet reached merchantable size. The forested class is comprised of the specific stages: immature and mature. Both immature and mature stands contain trees of merchantable size. They are distin-



guished by age and diameter. The old broad developmental class is not subdivided; the specific stage is also referred to as old. The reader is referred to BAP Report #3: Habitat Classification (Doyon 2000) for more detailed information on habitat classification.

Many bioindicators are described in terms of habitat type: a combination of species composition and developmental stage. When using the broad composition and broad developmental classes to describe a stand, the resulting habitat type is referred to as a broad habitat type. When working at the specific species composition and specific developmental stage levels, BAP refers to this level of classification as a specific habitat type.

The terrestrial habitat types described above are used only for land that is capable of supporting a viable source of commercial timber. In BAP, we refer to these areas as non-forested habitat types. Although it is well known that all habitats change with natural succession, for the purposes of BAP, non-forested habitat types are considered static. It is assumed that within the timeframe set out for the simulations, aquatic habitats, anthropogenic landscapes (e.g. roads and urban areas), barren and scattered land, treed muskeg, farms, shrub thickets, marshes, and meadows will not change to the extent that they are able to produce commercial timber.

8.2.2 Coarse- and Fine-filter Biodiversity Models

Included within BAP are coarse-filter and fine-filter biodiversity assessment models. Coarse-filter analyses make use of bioindicators that analyse ecosystem diversity and landscape configuration. The fine-filter analysis uses species-specific Habitat Supply Models (HSMs) to predict the suitability of the forest as habitat for each of the selected species throughout the simulation (see BAP Report #1: The Biodiversity Assessment Project, Duinker *et al.* 2000 and BAP Report #6: Habitat Supply Models, Higgelke *et al.* 2000). Together, the coarse- and fine-filter analyses assist forest managers in determining the potential long-term effects of alternative management strategies on forest biodiversity and wildlife habitat. As well, they help to set priorities for research and monitoring to reduce the uncertainty associated with biodiversity conservation. Relevant coarse-filter biodiversity models are shown in Table 8.1.

Table 8.1. Coarse-filter biodiversity models used in BAP.

Coarse-filter Bioindicators	
Ecosystem Diversity	Landscape Configuration
Area-weighted Age	Patch Area
Habitat Distribution	Patch Shape
Habitat Diversity	Core Area
Species Presence	Mean Edge Contrast Index
Species Dominance	Contrast-weighted Edge Length
	Adjacency Length
	Mean Nearest Neighbour

Coarse-Filter Biodiversity Analyses

The ecosystem diversity and landscape configuration analyses are considered coarse-filter bioindicators since they predict the condition of a set of forest features thought to broadly consider the basic habitat requirements of all forest-dwelling species. The bioindicators included within these analyses are summarised in Table 8.1. Please refer to BAP Report #7: Ecosystem Diversity and Landscape Configuration Models (Doyon 2000) for detailed information on the calculation of coarse-filter statistics.



Fine-Filter Biodiversity Models

Seventeen HSMs comprise the fine-filter biodiversity models (see BAP Report #2: Species Selection Procedure, Doyon and Duinker 2000 and BAP Report #6: Habitat Supply Models, Higgelke *et al.* 2000). Models were developed for the wildlife species shown in Table 8.2.

Table 8.2. Wildlife species modelled in BAP.

Birds	Mammals
Barred Owl	Canada Lynx
Brown Creeper	Elk
Least Flycatcher	Marten
Northern Goshawk	Moose
Pileated Woodpecker	Northern Flying Squirrel
Ruffed Grouse	Snowshoe Hare
Spruce Grouse	Southern Red-backed Vole
Three-toed Woodpecker	Woodland Caribou
Varied Thrush	

8.3 PROGRAM STRUCTURE

The BAP program adheres to a specific directory structure (Figure 8.1). The directory structure consists of four subdirectories below the main BAP directory: HARVPROJECT, NDR, MENU, and SPECIES. The HARVPROJECT subdirectories contain all of the models required for the harvest projection analysis. The NDR subdirectory contains all of the models required for the NDR computations. The MENU subdirectory contains the user interface menus and their associated AMLs for both the harvest projection and NDR programs. The SPECIES subdirectory contains all of the HSMs. The AMLs subdirectories below HARVPROJECT and NDR hold the specific BAP models for both landscape and ecosystem level models. The FILES subdirectories contain all of the ASCII input files. The GENERAL subdirectories are ArcInfo workspaces that contain all of the input coverages and grids.

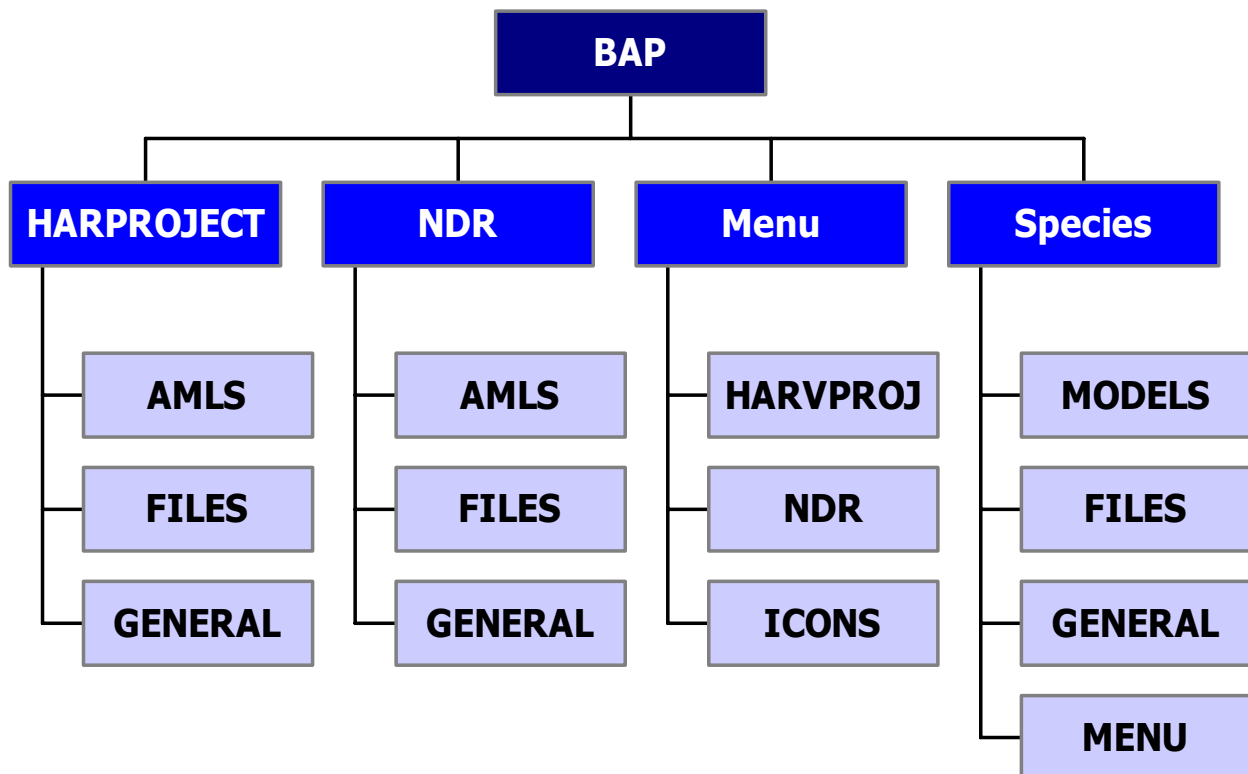


Figure 8.1. BAP directory structure.



8.3.1 Program Environment Variables

BAP utilises environment variables for executing programs and setting workspace environments. Environment variables must be set for proper execution of BAP. A complete list of environment variables and their descriptions are listed in Table 8.3.

Table 8.3. Environment variables used in BAP.

Variable	Environment Name	Example Path
Harvest Projection Variables		
Main Path	BAPHOME	E:\BAP\HARVPROJ
Menu Programs	BAPMENU	E:\BAP\MENU
Ecosystem Diversity Models	ECOSYS	E:\BAP\HARVPROJ\AMLS\ECOSYSTEM
Landscape Configuration Models	LAND	E:\BAP\HARVPROJ\AMLS\LANDSCAPE
Natural Disturbance Regime (NDR)		
Main Path	NDRHOME	E:\BAP\NDR
Menu Programs	BAPMENU	E:\BAP\MENU
Ecosystem Diversity Models	NDRECO SYS	E:\BAP\NDR\AMLS\ECOSYSTEM
Landscape Configuration Models	NDRLAND	E:\BAP\NDR\AMLS\LANDSCAPE
Habitat Supply Models		
HSM Models Main Path	BAPSPECIES	E:\BAP\SPECIES
Barred Owl	BARREDOWL	E:\BAP\SPECIES\MODELS\BARREDOWL
Brown Creeper	CREEPER	E:\BAP\SPECIES\MODELS\CREEPER
Canada Lynx	LYNX	E:\BAP\SPECIES\MODELS\LYNX
Elk	ELK	E:\BAP\SPECIES\MODELS\ELK
Least Flycatcher	FLYCATCHER	E:\BAP\SPECIES\MODELS\FLYCATCHER
Marten	MARTEN	E:\BAP\SPECIES\MODELS\MARTEN
Moose	MOOSE	E:\BAP\SPECIES\MODELS\MOOSE
Northern Flying Squirrel	SQUIRREL	E:\BAP\SPECIES\MODELS\SQUIRREL
Northern Goshawk	GOSHAWK	E:\BAP\SPECIES\MODELS\GOSHAWK
Pileated Woodpecker	PILEATED	E:\BAP\SPECIES\MODELS\PILEATED
Ruffed Grouse	RUFFEDGROUSE	E:\BAP\SPECIES\MODELS\RUFFEDGROUSE
Snowshoe Hare	HARE	E:\BAP\SPECIES\MODELS\HARE
Southern Red-backed Vole	VOLE	E:\BAP\SPECIES\MODELS\VOLE
Spruce Grouse	SPRUCEGROUSE	E:\BAP\SPECIES\MODELS\SPRUCEGROUSE
Three-toed Woodpecker	THREETOED	E:\BAP\SPECIES\MODELS\THREETOED
Varied Thrush	THRUSH	E:\BAP\SPECIES\MODELS\THRUSH
Woodland Caribou	CARIBOU	E:\BAP\SPECIES\MODELS\CARIBOU



8.4 PROGRAM FLOW

The following section describes the program flow. These steps must be taken prior to execution of biodiversity models. Although the program structure for the harvest projection models is similar to that of the NDR programs, differences exist in the input data file structure and content. The development of two separate sets of programs was, therefore, necessary.

Harvest projection data describe the species composition of the stand as well as the management activities conducted within it (e.g. timing of harvesting or thinning activities). These data are housed in INFORMIX tables. Each record within the table is linked to the initial landbase through a unique identification value called a BAPKEY. It is this connection that maintains a spatial link between the database files and the landbase coverage. Tables exist for each ten-year time period, covering the 200-year planning horizon for each forest management scenario. As described in BAP Report #1: Background and Structure (Duinker *et al.* 2000), the potential impacts of eight management scenarios were predicted through BAP's coarse-filter analysis.

LANDIS generates disturbance and individual tree species raster maps for every ten-year time step over a 500-year simulation. An individual species file (e.g. aspen) contains age class values for that particular species. Eight common tree species encountered in west-central Alberta's boreal forest were defined within LANDIS. BAP combines these eight separate species files to determine each cell's habitat type. To facilitate processing within LANDIS, it was necessary to partition the FMA

area into three sections based on administrative boundaries. Where required, processing was performed on the individual sections and later combined for input into the coarse-filter analysis.

A key distinction between the harvest projection and NDR data is the basic unit tracked through the simulation period. The basic unit for the harvest projection data is the stand or polygon defined within the initial landbase coverage. Stand boundaries are fixed, in that, they do not change over time. Although BAP processing occurs within a raster environment, and several raster cells may define a stand or patch, the basic unit tracked is the whole stand or patch. In contrast, the NDR data are raster-based. Therefore, an individual raster cell is treated as the basic unit.

Harvest projection analysis and NDR files are stored within separate directories and use different environment variables (Table 8.3).

8.4.1 Harvest Projection

The following section describes the harvest projection analysis program flow.

The program, batchrun.mwi, controls the coarse-filter BAP programs and sets all required environments and arguments for the individual models. It uses several ASCII files located within the \$BAPHOME/files directory. These required files are listed in Table 8.4 and described in Appendix 1.

Once all of the ASCII files have been loaded as variables, an external AML called prep-outfiles.aml is called. This program automati-

Table 8.4. Required files of the harvest projection analysis program.

File Name	Purpose
Dbconnect.bap	Database connection and workspace information
User-inventory.lis	List of inventory files to be processed
User-files.lis	List of ASCII user files required by the various biodiversity models
User-models.lis	List of biodiversity models to be processed



cally generates empty ArcInfo INFO data files within the user-defined workspace. Data files are created for all models listed within the user-models.lis file. New data files replace any existing data files.

Each model listed in the user-models.lis file is executed and all inventory time steps listed within the user-inventory.lis file are processed. All spatial statistics generated by BAP are stored within the appropriate INFO data file created during the program start-up.

Database and Spatial Files

Data for each scenario are stored within separate INFORMIX databases. Each database contains the individual inventory files and all associated tables for that particular scenario. An individual inventory table is spatially linked to a forest grid (called FORESTG) based on the BAPKEY column. As mentioned above, BAPKEY is a unique identifier that links each record within a table to the forest grid or landbase coverage. This common link allows for the creation of grids based on any attribute contained within the inventory tables (e.g. habitat type or stand age). Then, if required, spatial analysis can be performed and statistics can be generated.

BAP maintains a common naming convention system. Thus, it expects the BAPKEY column within the inventory tables and a grid called FORESTG (stored within \$BAPHOME/general directory) whenever an association between the tabular database and spatial files is required. The FORESTG grid is based on the Alberta Vegetation Inventory (AVI) vector coverage.

Program/Model Description

The following section gives a brief description of the main programs within BAP and the required input files, program usage, and arguments. Syntax follows standard ArcInfo format.

We attempted to use a common variable naming convention for all models within BAP. Some of the commonly used model arguments are described in Table 8.5. Model arguments that are model-specific are described within each model description.

Input files must be located within the appropriate directory. All user-defined input files must reside within the \$BAPHOME/files directory. All spatial input files (e.g. grids) must reside within the \$BAPHOME/general workspace.

Table 8.5. General model arguments used by BAP.

Argument	Description
<infile>	INFORMIX inventory file name
<forestgrid>	FORESTG grid containing BAPKEY values. To create, execute the \$BAPHOME/AMLS/FMA.MWI program.
<baptable>	INFORMIX inventory habitat table. To create, execute the \$BAPHOME/AMLS/BAPCOVTYPE.MWI program.
<scenario>	Scenario name
<year>	Scenario year

Coverage and Grid Set-up

Program Name: \$BAPHOME/AMLS/
FMA.MWI

Called by: \$BAPHOME/
BATCHRUN.MWI

Usage: <for_cov> <cellsize>

Arguments:

<for_cov> Forest inventory coverage containing an attribute column called BAPKEY, which contains unique polygon ID values

<cellsize> Grid output cell size (m).
Grid cell size resolution is
25 m

Description:

This program prepares the spatial files required by the various BAP models. It creates a copy of the <for_cov> input coverage, called FMA, and generates a raster grid called FORESTG based on the required BAPKEY attribute data from the <for_cov> coverage. The BAPKEY column must contain a unique



polygon identification number for each stand within the <for_cov>. The newly created FMA coverage and FORESTG grid are stored within the \$BAPHOME/general directory. This program must be run whenever the initial input <for_cov> is altered.

Habitat reclassification

Program Name: \$BAPHOME/amls/
bapcovtype.mwi

Called by: \$BAPHOME/batchrun.mwi

Usage: <infile> <covtypefile>
<outfile>

Arguments:

<covtypefile> ASCII file defining age
class groupings

<outfile> Output INFORMIX table

Description:

The model assigns a four-digit habitat classification code to each forested habitat type. The reclassification is based on the species composition and developmental stage combinations shown in Table 8.6 and age class grouping listed in Table 8.7.

Age class groupings define the developmental stages for each specific habitat type. Age class groupings are defined within the <covtypefile> file. A partial listing of the <covtypefile> is shown in Table 8.7. In this table, each line describes the age class breakdown for a specific habitat type. Values listed after the habitat groupings define the age class range. Table 8.8 describes the age class groupings by specific developmental stage for a pure aspen. See Appendix 1 for file format.

Habitat filtering

Program Name: \$BAPHOME/amls/
habitat.mwi

Called by: \$BAPHOME/batchrun.mwi

Usage: <forestgrid> <baptable>
<outgrid>

Arguments:

<outgrid> Grid created by the habitat
filtering process

Description:

The filtering program generates a filtered habitat grid based on the INFORMIX inventory table <baptable>. The filtering process removes individual forested habitat patch types less than 16 cells (1 ha) in size but maintains non-forested habitat patches less than 16 cells in size. Non-forested habitat types include water (habitat code 64), anthropogenic clearings (103), barren and scattered land (105), treed muskeg (106), farmland (107), shrub thickets (203, 204), marsh (205), and meadows (206, 207).

Filtering of non-forested habitats

To filter non-forested habitats, a grid containing habitat values must first be produced from the <baptable> INFORMIX table. The program then initiates a search for small patches of forested habitat (*i.e.*, less than 16 cells in size) that are surrounded by non-forested habitats. Identified patches are removed and replaced by the non-forested habitat type that surrounded them. The replacement process uses an iterative approach by which the surrounding cells "grow" into the cells to be replaced. Only one surrounding cell is replaced during each pass. The process is repeated until all identified cells have been replaced. The result is a filtered non-forested grid, called NONFOREST, which contains no forested island patches less than 16 cells. The NONFOREST output grid is stored within the \$BAPHOME/general directory. Since the non-



Table 8.6. Forested habitat codes.

Broad	Specific	Opening	Developing		Forest		Old
		Clearcut/Burn	Regenerating	Young	Immature	Mature	Old
Hardwood	Aspen	1111	1122	1123	1134	1135	1146
	Poplar	1211	1222	1223	1234	1235	1246
	White birch	1311	1322	1323	1334	1335	1346
Hardwood-dominated Mixedwood	Aspen-Pine	2111	2122	2123	2134	2135	2146
	Aspen-White spruce	2211	2222	2223	2234	2235	2246
	Aspen-Black spruce	2311	2322	2323	2334	2335	2346
	Poplar-Pine	2411	2422	2423	2434	2435	2446
	Poplar-White spruce	2511	2522	2523	2534	2535	2546
	Poplar-Black spruce	2611	2622	2623	2634	2635	2646
Softwood-dominated Mixedwood	Pine-Poplar	3111	3122	3123	3134	3135	3146
	Pine-Aspen	3211	3222	3223	3234	3235	3246
	White spruce-Poplar	3311	3322	3323	3334	3335	3346
	White spruce-Aspen	3411	3422	3423	3434	3435	3446
	Black spruce-Poplar	3511	3522	3523	3534	3535	3546
	Black spruce-Aspen	3611	3622	3623	3634	3635	3646
Conifer	Pine	4111	4122	4123	4134	4135	4146
	White spruce	4211	4222	4223	4234	4235	4246
	Black spruce	4311	4322	4323	4334	4335	4346
	Larch	4411	4422	4423	4434	4435	4446

Table 8.7. Reclassification age class.

<COVTYPE>
AW 0 2 10 20 50 100
PO 0 2 10 20 50 110
BW 0 5 10 25 60 90
AW_PL 0 4 10 20 50 115
AW_SW 0 5 13 25 65 120
AW_SB 0 5 13 25 70 130
PO_PL 0 4 10 20 55 120
PO_SW 0 5 13 25 65 125
PO_SB 0 5 13 25 70 135
PL_PO 0 6 10 20 55 110
PL_AW 0 6 10 20 60 115
SW_PO 0 7 13 25 75 130
SW_AW 0 7 13 30 71 125
SB_PO 0 7 13 25 75 140
SB_AW 0 7 13 30 70 140
PL 0 5 10 20 60 120
SW 0 8 15 30 80 150
SB 0 8 15 30 90 160
LT 0 4 10 25 50 150

Table 8.8. Specific habitat age class description for pure aspen stands.

Specific Habitat type	Clearcut/Burn	Regenerating	Young	Immature	Mature	Old
Aw	0 - 1	2 - 9	10 - 19	20 - 49	50 - 99	100+

forested habitat patches do not change over time, the filtered NONFOREST grid is only generated once. Whenever the habitat.mwi program is run, the \$BAPHOME/general is checked to determine if the NONFOREST grid exists. If it is absent, the grid will be automatically generated.

Other non-forested habitat types cannot replace small patches of non-forested habitat. This constraint was added to keep non-forested habitat types (e.g. lakes or rivers) from increasing in size through the filtering process.

Filtering of forested habitats

Similar to the process described above, a habitat grid is first generated from the <baptable>. The grid is then merged with the non-forested habitat grid, which updates the forested habitat grid with the filtered non-forested grid. The filtering process begins by setting up a nested loop program. The program first identifies all forested habitat patches that are one cell in size. Identified patches are then removed and replaced by the habitat value of the forested stand adjacent to it. Once all of the single-celled patches have been replaced, the process is repeated for habitat patches that are equal to two cells in size. The replacement process uses an iterative approach by which the surrounding cells "grow" into the cells to be replaced. Only one surrounding cell is replaced during each pass. The process is repeated until all identified cells have been replaced. The program continues to loop through the steps until patches equal to 15 cells in size have been replaced. The <outgrid> is stored within the \$BAPHOME/general/habitat workspace.

Figures 8.2a and 8.2b illustrate sample results of the forested habitat filtering process. A small patch has been identified and marked with a circle in Figure 8.2a. In Figure 8.2b, we see the result of the filtering process. Both brown and green habitat types have replaced the smaller blue patch. Because the majority of the surrounding cells are green, green replaces more blue cells than brown.



Figure 8.2a. Grid of forested habitat types prior to filtering.



Figure 8.2b. Grid of forested habitat types after filtering.



8.4.2 Natural Disturbance Regime (NDR)

The following section describes the NDR program flow. Process flow for NDR is similar to those listed within the Harvest Projection section discussed above. However, since different input file structures are used, separate programs are required. In this section, we only discuss differences between the Harvest Projection and NDR programs. Where there is no description of the program process given, it can be assumed to be identical to that described in the Harvest Projection section above.

NDR programs are controlled by the LANDIS-BATCH.MWI AML. All input files must be located within the appropriate directory. User-defined input files must reside within the \$NDRHOME/files directory. All input spatial files (e.g. grids) must reside within the \$NDRHOME/general workspace, unless otherwise stated. File descriptions are provided in Appendix 1.

We attempted to use a common variable naming convention for all NDR models within BAP. In order to avoid redundancy, some of the commonly used model arguments are described in Table 8.9. Model arguments specific to only one or two models are described within each model description.

Habitat reclassification

Program Name: \$NDRHOME/amls/
bapcov.mwi

Called by: \$NDRHOME/landis-
batch.mwi

Usage: <totyears> <timestep>
<covtypefile>
<landismap> <section>
<zipfile>

Description:

Assigns a four-digit habitat classification value to all forested cells. This program generates a combined species grid from the individual species LANDIS files. The combined grid's value attribute table (VAT) is then transferred to INFORMIX for processing. An individual table is generated for each time step. File names consist of the key word ndr_ followed by the year. A table called, ndr_200, for example, represents an inventory file for the 200th year of the 500-year LANDIS simulation. Habitat values are stored within the HABITAT column.

LANDIS predicts only species presence and stand age. Therefore, the species composition component of the habitat classification can only be predicted by determining the two oldest species present within the stand. Based on the assumption that two species with similar ages are likely to both occupy the upper canopy of a stand, the determination of pure or mixedwood status is accomplished through a comparison of the ages of the two oldest tree species. The greater the difference in ages, the more likely the second species is to be an understory species. Mixedwood stands

Table 8.9. General model arguments used by NDR.

Argument	Description
<totyears>	Total number of years to process
<timestep>	Time period between each time step
<landismap>	LANDIS input file
<section>	Key word indicating which section of the FMA area will be processed
<zipfile>	Name of the compressed file containing the LANDIS output
<habgrid>	Filtered habitat grid
<year>	Simulation year



are those in which the ratio between the ages of the two oldest species is greater than 0.66. Pure stands are defined as those in which the ratio between the ages of the two oldest species is less than 0.66.

Consider an example in which a stand is composed of lodgepole pine and aspen. The aspen trees are 60 years old and the lodgepole pine trees are 56 years old. The species composition assigned to this cell would be an aspen-dominated mixedwood (aspen/pine) since the ratio between the aspen (2nd oldest) and the pine (oldest) trees is 0.93. If the pine component were 39 years old, however, a ratio of 0.65 would result, placing it into a pure aspen species composition type.

Habitat Preparation

Program Name: \$NDRHOME/aml/prep-habitat.mwi

Called by: \$NDRHOME/ landis-batch.mwi

Usage: <totyears> <timestep>

Requirements: INFORMIX inventory files
(e.g. ndr_10)
Combined species grids

Description:

Generates a single habitat grid of the whole FMA area. This program generates separate habitat grids for each section and combines them into a single grid. Output grids are stored within a user-specified workspace.

Habitat filtering

Program Name: \$NDRHOME/aml/habitat.mwi

Called by: \$NDRHOME/ landis-batch.mwi

Usage: <totyears> <timestep>

Description:

Generates a filtered habitat grid. A complete discussion on the filtering process is provided in the Habitat Filtering section above. Filtered habitat grids are stored within a user-defined workspace. File names consist of the key word ndr_hab followed by the simulation year. A grid called, ndr_hab200, for example, represents the filtered habitat grid for the 200th year of a 500-year LANDIS simulation.

Age Grid Preparation

Program Name: \$NDRHOME/aml/prep-age.mwi

Called by: \$NDRHOME/ landis-batch.mwi

Usage: <totyears> <timestep>

Requirements: INFORMIX inventory files
(e.g. ndr_10)
Combined species grids
(e.g. year_10)

Description:

Prepares the age grids required for area-weighted age determination. Age grids are generated for each section and combined to form a single age grid of the entire FMA area. The age grid is based on the oldest species age (AGE1 column within the INFORMIX data files).



8.5 COARSE-FILTER BIOINDICATORS

The following subsections describe the programs used to execute the coarse-filter biodiversity models. Examples of all coarse-filter landscape configuration and ecosystem diversity bioindicators are shown in Appendix 2. Please refer to BAP Report #7: Ecosystem Diversity and Landscape Configuration Models for more detailed information on associated calculations.

8.5.1 Landscape Configuration Models

Adjacency

Adjacency tables describe the total edge length between each combination of adjacent broad habitat types. There are 325 possible adjacency combinations. These tables are used to describe the total adjacency lengths expected under various forest management scenarios and under the natural disturbance regime. In addition, the tables are used as

inputs to the mean edge contrast index and contrast-weighted edge length indices.

The habitat grid is converted to a vector coverage in order to calculate edge length and habitat adjacency. The newly created polygon attributes table (PAT) and arc attributes table (ATT) are then exported to INFORMIX for processing.

Each table lists the arcs for each habitat polygon, defines its adjacent broad habitat type, and the arc length in meters. Table 8.10 illustrates the structure and format of an adjacency table. Column ARCID represents the arc's internal identification number. LHAB and RHAB represent the two digits of the broad habitat type code. LENGTHL and LENGTHR represent the length of the arc. These two values are always equal.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.11.

Table 8.10. The structure and format of a sample adjacency table.

ARCID	LUNIT	RUNIT	LHAB	RHAB	LENGTHL	LENGTHR
10	2	2	22	24	25	25
18	2	2	22	103	50	50
27	1	1	23	43	50	50
29	1	1	23	43	100	100
30	1	1	23	24	375	375
33	1	1	43	23	150	150
38	1	1	24	23	525	525

Table 8.11. Programs, inputs, and outputs related to the bioindicator, adjacency.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$LAND/prep-adjacency.mwi	\$NDRLAND/prep-adjacency.mwi
Called By	\$NDRHOME/batchrun.mwi	\$NDRHOME/batchrun.mwi
Calls		
Usage	<habgrid>	<habgrid> <year>
Output	Informix adjacency table	Informix adjacency table



BAP Report #8: BAP Program Documentation

The required ASCII file, <adjacency-file>, defines all possible broad habitat type and non-forested adjacency combinations and the associated code value. Table 8.12 is an example of the format and partial content of an <adjacency-file> file. As previously mentioned, a total of 325 possible adjacency code combinations exist.

Table 8.12. Adjacency codes by broad habitat type.

<ADJACENCY-FILE>
11,12,1
11,13,2
11,14,3
11,21,4
11,22,5
11,23,6
.
.
.
.
205,206,323
205,207,324
206,207,325

Each line within the file (e.g. 11, 12, 1) contains a single broad habitat combination and/or non-forested habitat (e.g. 11, 12) and the associated code value (e.g. 1). A comma separates all values. A complete list of all adjacency combinations and assigned code values can be found in Appendix 1.

Adjacency lengths are written to the EDGE-FMA.ADJACENCY INFO data file. This file contains a scenario and year column, indicating the scenario name and inventory year. In addition, a column exists for each combination code value. These column names consist of the key word CODE followed by a combination code value. A column name of CODE1, for example, represents the habitat adjacency between 11 and 12, as defined within <adjacency-file>.

If a habitat combination does not exist within the current time step, a value of zero is assigned to that habitat combination.

Patch Size and Shape (Mean Patch Fractal Dimension)

These bioindicators reveal the expected patch size and shape (mean patch fractal dimension index) descriptive statistics. The following statistics are calculated at both broad and specific species composition levels: frequency, total area (area statistic only), mean, standard deviation, minimum, maximum, 25th quartile, 50th quartile, and 75th quartile. For each quartile, the number of records from the last quartile is also recorded.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.13.

Table 8.13. Programs, inputs, and outputs related to the bioindicators, patch size and shape.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$LAND/patch-stats.mwi	\$NDRLAND/patch-stats.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls	C-program \$BAPHOME/aml/quartiles/quartiles	C-program \$NDRHOME/aml/quartiles/quartiles
Usage	<habgrid> <scenario> <year>	<habgrid> <year> <scenario>
Output	land-fma.area and land-area.shape INFO database files	land-fma.area and land-area.shape INFO database files



Core Area

Calculates mean core area descriptive statistics. Statistics are calculated at both broad and specific species composition levels.

The core area program determines core area habitat by removing cells within a specified distance between two edge adjacency habitat types. Patch size statistics are then calculated on the remaining core areas. Buffer distances for all possible edge type combinations are defined in the <core-codes> ASCII file. An example of a <core-codes> file is presented in Table 8.14.

In the example below, each line describes the adjacency combination between two specific developmental stage habitat types and

the associated buffer distance (expressed in metres). The first record, 1,2,50, for example, assigns a 50 m buffer distance to an edge between a patch with the developmental stage of opening (value of 1) and a patch with the developmental stage of developing (value of 2).

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.15.

Table 8.14. Specific developmental stage adjacency combinations and their associated buffer distances.

<CORE-CODES>
1,2,50
1,3,100
1,4,75
1,64,0
1,103,0
1,105,0
1,106,25
1,107,0
1,203,25
1,204,25
1,205,0
1,206,0
1,207,0

Table 8.15. Programs, inputs, and outputs related to the bioindicator, core area.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$LAND/patch-core.mwi	\$NDRLAND/patch-core.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls	C-program \$BAPHOME/aml/quartiles/quartiles	C-program \$NDRHOME/aml/quartiles/quartiles
Usage	<habgrid> <scenario> <year> <core-codes>	<habgrid> <year> <scenario> <corecodes>
Output	land-fma.core INFO database file	land-fma.core INFO database file



Contrast Weighted Edge Length

Calculates the contrast-weighted edge length (km). Output is a single value stored under the CWEL column within the LAND-FMA.CONTRAST INFO data file.

The three required ASCII files (<for-for-file>, <nfor-for-file>, and <nfor-nfor-file>) define the broad habitat adjacency weighted contrast values. More specifically, the <for-for-file> defines the forested to forested habitat adjacency combinations, <nfor-for-file> defines the non-forested to forested adjacencies and <nfor-nfor-file> defines the non-forested habitat adjacencies. Forested habitats are based on broad habitat types. Listed in Table 8.16 are examples of the format and partial content of each of the required files.

Each line within the file (e.g. 11, 12, 0.4) contains a single broad habitat adjacency combination (e.g. 11, 12) and its contrast weight value (e.g. 0.4). Contrast values range from

zero (low contrast between two adjacent habitat types) to one (high contrast between two adjacent habitat types). A comma separates all values. A complete list of all contrast weight values can be found in Appendix 1.

Mean Edge Contrast Index (MECI)

Calculates the mean edge contrast index.

The three required ASCII files (<for-for-file>, <nfor-for-file>, and <nfor-nfor-file>) are described within the Contrast Weighted Edge Length program description section.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.17.

Table 8.16. Example of the format and partial content of for-for, nfor-for, and nfor-nfor files.

<FOR-FOR-FILE>	<NFOR-FOR-FILE>	<NFOR-NFOR-FILE>
11,12,0.4	64,11,0.1	207,206,0.0
11,13,1.0	64,12,0.3	207,205,0.4
11,14,0.8	64,13,1.0	207,204,0.4
11,21,0.0	64,14,0.8	207,203,0.4
11,22,0.4	64,21,0.1	207,107,0.2
11,23,1.0	64,22,0.3	207,106,0.5
11,24,0.8	64,23,1.0	207,105,0.5
11,31,0.2	64,24,0.8	207,103,0.2
11,32,0.6	64,31,0.1	207,64,0.5
11,33,1.0	64,32,0.3	206,205,0.4
11,34,0.8	64,33,1.0	206,204,0.4
11,41,0.2	64,34,0.8	206,203,0.4
11,42,0.6	64,41,0.1	206,107,0.2

Table 8.17. Programs, inputs, and outputs related to the bioindicators, contrast-weighted edge length and mean edge contrast index.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$LAND/edge-contrast.mwi	\$NDRLAND/edge-contrast.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls		
Usage	<scenario> <year> <for-for-file> <nfor-for-file> <nfor-nfor-file>	<year> <scenario> <for-for-file> <nfor-for-file> <nfor-nfor-file>
Output	land-fma.contrast INFO database file	land-fma.contrast INFO database file



Mean Nearest Neighbour

Mean nearest neighbour patch statistics include mean nearest patch distance (m), patch frequency, and standard deviation. Statistics are calculated at the broad habitat type level.

Mean nearest neighbour calculates the average nearest distance between similar patches for each habitat type. Nearest neighbour statistics are only calculated for habitat types with more than one patch. A maximum distance of 5,000 m has been set when determining a patches closest neighbour. Thus, any patch with a nearest patch distance greater than 5,000 m is assigned a patch distance of 5,000 m.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.18.

Table 8.18. Programs, inputs, and outputs related to the bioindicator, mean nearest neighbour.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$LAND/config-nearest.mwi	\$NDRLAND/config-nearest.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls		
Usage	<habgrid> <scenario> <year>	<habgrid> <year> <scenario>
Output	land-fma.near INFO database file	land-fma.near INFO database file



8.5.2 Ecosystem Diversity Models

Area-weighted Age

Calculates the area-weighted age of the FMA area based on the STAND_AGE column within the INFORMIX <baptable> table. This program generates an age grid (based on the STAND_AGE attribute column) from which patch areas are determined. The calculated weighted-age is stored within the ECO-FMA.AGE data file.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.19.

Developmental Stage Proportion

Determines the proportion of each specific developmental stage by broad habitat class within the FMA area. Habitat type is based

on the values stored within the INFORMIX <baptable>.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.20.

Habitat Distribution

Calculates total area (ha) by specific habitat type. The required ASCII file, <habcodes>, contains a list of all forested habitat types. A list of all habitat types can be found in Appendix 1.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.21.

Table 8.19. Programs, inputs, and outputs related to the bioindicator, area-weighted age.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$ECOSYS/eco-age.mwi	\$NDRECOYS/eco-age.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls		
Usage	<baptable> <scenario> <year>	<agegrid> <year> <scenario>
Output	eco-fma.age INFO database file	eco-fma.age INFO database file

Table 8.20. Programs, inputs, and outputs related to the bioindicator,developmental stage proportion.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$ECOSYS/eco-standstage.mwi	\$NDRECOYS/eco-standstage.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls		
Usage	<forestgrid> <baptable> <scenario> <year>	<habgrid> <year> <scenario>
Output	eco-fma.standstage INFO database file	eco-fma.standstage INFO database file

Table 8.21. Programs, inputs, and outputs related to the bioindicator,habitat distribution.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$ECOSYS/eco-distrib.mwi	\$NDRECOYS/eco-distrib.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls		
Usage	<forestgrid> <baptable> <scenario> <year> <habcodes>	<habgrid> <year> <scenario> <habcodes>
Output	eco-fma.distrib INFO database file	eco-fma.distrib INFO database file



Habitat Diversity Index

Calculates a single diversity index value for the entire FMA area. Habitat diversity index is based on broad habitat types and user-defined contrast weight values. The user-defined contrast weight file, <diversity-file>, contains the contrast weight values assigned to each forested broad habitat type combination. Table 8.22 provides a partial listing of a <diversity-file> file.

Each line of the file (e.g. 11, 12, 1) contains a single broad habitat type combination (e.g. 11, 12) and the associated contrast value (e.g. 0.4). Contrast values range from 0 (low

contrasting edge between habitat types) to 1 (high contrasting edge between habitat types). A comma separates all values. A complete list of all adjacency combinations and assigned contrast values can be found in Appendix 1.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.23.

Table 8.22. Sample diversity file.

<DIVERSITY-FILE>		
11,12,0.4		
11,13,1.0		
11,14,0.8		
11,21,0.0		
11,22,0.4		
11,23,1.0		
11,24,0.8		
11,31,0.2		
11,32,0.6		
11,33,0.1		
11,34,0.8		
11,41,0.2		
11,42,0.6		

Table 8.23. Programs, inputs, and outputs related to the bioindicator, habitat diversity.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$ECOSYS/eco-diversity.mwi	\$NDRECO SYS/eco-diversity.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls		
Usage	<forestgrid> <baptable> <scenario> <year> <diversity-file>	<habgrid> <year> <scenario> <diversity-file>
Output	eco-fma.diversity INFO database file	eco-fma.diversity INFO database file



Species Presence

Determines the presence of a species within a stand. Species presence is calculated for white spruce, black spruce, lodgepole pine, fir, larch, aspen, poplar, and white birch. For the harvest projection analysis, species presence is based on the species attributes, held within the INFORMIX <baptable>. The <baptable> contains eight species columns (SP1...SP8) along with the associated percentages (PER1...PER8). The percentage values held within the PER# columns represent the percentage of volume for a particular species within a stand.

For the natural disturbance regime analysis, species presence within each cell is based on the species age ratio between the two oldest species. As explained above, a stand is only considered a mixedwood (*i.e.*, having more than one species present in the overstorey) if the ratio of the ages of the two oldest species is greater than 0.65.

The species presence statistics only reveal whether or not a species is present within a stand. They do not consider species dominance.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.24.

Species Dominance

Determines species dominance weighted by area. For the harvest projection analysis, species dominance is based on a stand's species attributes held within the INFORMIX <baptable>. The <baptable> contains eight species columns (SP1...SP8) and the associated percentages (PER1...PER8). The percentage values held within the PER# columns represent the percentage of volume for that particular species within the stand.

Species dominance could not be calculated for the natural disturbance regime analysis because the LANDIS data only provide species presence and age. They do not provide any information with regards to the dominant species occupying a particular cell.

Details regarding program inputs and outputs specific to the harvest projection and natural disturbance regime analyses can be found in Table 8.25.

Table 8.24. Programs, inputs, and outputs related to the bioindicator, species presence.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$ECOSYS/eco-tree.mwi	\$NDRECOYS/eco-tree.mwi
Called By	\$BAPHOME/batchrun.mwi	\$NDRHOME/landis-batch.mwi
Calls		
Usage	<baptable> <scenario> <year>	<year> <scenario>
Output	eco-fma.diversity INFO database file	eco-fma.diversity INFO database file

Table 8.25. Programs, inputs, and outputs related to the bioindicator, species dominance.

	Harvest Projection	Natural Disturbance Regime
Program Name	\$ECOSYS/eco-tree.mwi	N/A
Called By	\$BAPHOME/batchrun.mwi	N/A
Calls		
Usage	<baptable> <scenario> <year>	N/A
Output	eco-fma.dominance INFO database file	N/A



8.6 FINE-FILTER BIOINDICATORS

The following section outlines the programs used when running the Habitat Supply Models (HSMs). All models follow the same format and file naming conventions. The individual HSMs are located within separate directories below the `bap\species\models` sub-directory. Any associated reclassification or weight files are stored within the individual species directory. Required spatial input files must be stored within the `$BAPSPECIES\general` workspace.

Model Input

The full suite of HSMs utilises data from a variety of sources. The primary data source is the harvest projection inventory tables. The Special Habitat Element (SHE) models (e.g. percentage of the forest floor covered with shrubs), ecological classification (e.g. site productivity) data, and Alberta's provincial database files (e.g. digital elevation models) may also be drawn upon as source data.

The harvest projection data files contain information related to the projected species composition and management activities within each stand. SHE models provide additional information not available from the inventory data. The suite of SHE models developed for BAP is structured around the format of the harvest projection files.

All SHE variables are stored within the individual inventory tables. Each SHE model creates a new column (e.g. `canopy_closure`) within the inventory table, which contains the SHE variable value. Values are first determined for conditions under natural stand development. They are, then, adjusted to reflect the variable's response to certain management activities (e.g. a reduction in canopy closure is applied to stands recently thinned).

General HSM Description

The HSMs subdivide results by habitat use. For example, a model would reveal predicted suitability throughout the FMA area for hiding cover separately from foraging habitat. A suitability rating for a habitat use (e.g. hiding cover) is drawn from calculation of a suitability index (SI) equation in which one or more habitat elements considered important to the species for a particular habitat use are combined. From published scientific literature and consultation with biologists, SI curves were created for each important habitat element such that the preferred condition (e.g. heavy shrub cover) is associated with a high suitability rating. Please refer to BAP Report #6: Habitat Supply Models (Higgelke *et al.* 2000) for detailed information on HSM development.

The method used to standardise a variable to a SI value is dependent on the data type (refer to BAP Report #5: Special Habitat Element Model Development, Doyon and MacLeod 2000 for detailed information on SHE variable data types). For continuous data type variables, such as canopy closure, the reclassification is performed in GRID, based on a SI curve. For discrete variables, such as habitat types, the reclassification is performed using an INFORMIX-based reclassification table.

The way in which suitability ratings are applied to several habitat elements involves a distance-dependent relationship. In these cases, suitability is determined based on the distance of a cell from a particular feature. Distance related suitability calculations are all performed within GRID. For example, a pixel located proximate to a major road may be less suitable as nesting habitat. To take this into account, a suitability curve is applied to the measured distance of a cell to a major road as a distance-dependent suitability grid.

As explained in BAP Report #6: Habitat Supply Models (Higgelke *et al.* 2000), the process of home range smoothing is intended to provide an indication of the potential suitability



ity of each cell as the centre of a home range. Depending on the home range size of the species in question, the home range smoothing process used may vary. In addition, a slightly different smoothing process may be utilised for species that only require a certain percentage of suitable habitat within its chosen home range.

In general, home range smoothing involves averaging or 'smoothing' the suitability ratings of all cells within a circular area comparable to the expected home range size. The circle or 'window' moves across the grid and assigns an average SI value to the centre cell of the circular window. Each cell within the grid receives an averaged SI value.

For species with small home range sizes (e.g. Southern Red-backed Vole), all grid cells are smoothed (*i.e.*, each cell on the entire grid acts as the centre of a home range circle). For species with larger home range sizes, the home range smoothing process systematically samples the landscape. By this process, the window moves over the grid in such a way that its centres are located one full radius apart. Thus, if the radius for a home range is 1,000 m, the average suitability rating is calculated within a circular window of radius 1,000 m, located 1,000 m apart. This results in an output grid with smoothed values every 1,000 m.

Generally the home range smoothing process considers all values within the window. However, in some cases, only the highest SI values are averaged. For example, it is thought that the Northern Goshawk requires only four suitable nesting sites within its home range. Therefore, it is only necessary to average the highest four nesting suitability ratings within the circle. To accomplish this, all values within a window are ranked, from highest SI to lowest SI. The average value is then calculated using only the top four values. This process always generates a sampled output grid, which is based on the radius of the home range size, as described above.

It is difficult to interpret sampled HSM output grids because the grids are not continuous. Therefore, for display purposes only, empty cells (where no home range value was calculated) are assigned a value equal to the closest sampled cell. This technique "fills" in the areas not smoothed.



Habitat Supply Models

We attempted to use a common variable naming convention for all HSMs. To avoid redundancy, some of the commonly used model arguments are described in Table 8.26.

All models are called by batchspecies.aml. Details regarding program inputs and outputs for each of the HSMs can be found in Table 8.27.

Table 8.26. General HSM models arguments.

Argument	Description
<bapinv>	INFORMIX inventory file name
<scenario>	Scenario name
<year>	Scenario year
<species.lis>	ASCII file name defining a model's input parameters. The file name usually contains the wildlife species name with which it is associated (e.g. barredowl.lis)
<proportion>	Value defining the proportion of the suitability ratings to be sampled within a smoothing window

Table 8.27. Programs, inputs, and outputs related to the fine-filter bioindicators.

Species	Program Name	Calls ²	Usage	Programs required to be executed prior to running the HSM ³
Birds				
Barred Owl	\$BARREDOWL/barredowl.aml	sicurve.aml and home-smooth-avg.aml	<bapinv> <scenario> <year> <barredowl.lis>	home-smooth-zones.aml
Brown Creeper	\$CREEPER/creeper.aml	sicurve.aml	<bapinv> <scenario> <year> <creeper.lis>	
Least Flycatcher	\$FLYCATCHER/flycatcher.aml		<bapinv> <scenario> <year> <flycatcher.lis>	
Northern Goshawk	\$GOSHAWK/goshawk.aml	sicurve.aml, home-smooth-top4.aml and home-smooth-avg.aml	<bapinv> <scenario> <year> <goshawk.lis>	home-smooth-zones.aml and block.aml
Pileated Woodpecker	\$PILEATED/pileated.aml	sicurve.aml, home-smooth-avg.aml and home-smooth-pro.aml	<bapinv> <scenario> <year> <pileated.lis> <proportion>	home-smooth-zones.aml
Ruffed Grouse	\$RUFFEDGROUSE/ruffedgrouse.aml	sicurve.aml and home-smooth-avg.aml	<bapinv> <scenario> <year> <ruffedgrouse.lis>	home-smooth-zones.aml
Spruce Grouse	\$SPRUCEGROUSE/sprucegrouse.aml	sicurve.aml and home-smooth-avg.aml	<bapinv> <scenario> <year> <sprucegrouse.lis>	home-smooth-zones.aml
Three-toed Woodpecker	\$THREETOED/threetoed.aml	sicurve.aml and home-smooth-pro.aml	<bapinv> <scenario> <year> <threetoed.lis> <proportion>	home-smooth-zones.aml
Varied Thrush	\$THRUSH/thrush.aml	sicurve.aml	<bapinv> <scenario> <year> <thrush.lis>	
Mammals				
American Marten	\$MARTEN/marten.aml	sicurve.aml and home-smooth-avg.aml	<bapinv> <scenario> <year> <marten.lis> <proportion>	home-smooth-zones.aml
Canada Lynx	\$LYNX/lynx.aml	sicurve.aml	<bapinv> <scenario> <year> <lynx.lis>	
Elk	\$ELK/elk.aml	sicurve.aml	<bapinv> <scenario> <year> <elk.lis>	
Moose	\$MOOSE/moose.aml	sicurve.aml	<bapinv> <scenario> <year> <moose.lis>	
Northern Flying Squirrel	\$SQUIRREL/squirrel.aml	sicurve.aml	<bapinv> <scenario> <year> <squirrel.lis>	
Snowshoe Hare	\$HARE/hare.aml	sicurve.aml	<bapinv> <scenario> <year> <hare.lis>	
Southern Red-backed Vole	\$VOLE/vole.aml	sicurve.aml	<bapinv> <scenario> <year> <vole.lis>	
Woodland Caribou	\$CARIBOU/caribou.aml	sicurve.aml and home-smooth-avg.aml	<bapinv> <scenario> <year> <caribou.lis>	\$CARIBOU/home-smooth-zones.aml

¹ files reside within the \$BAPSPECIES directory² files reside within the \$BAPSPECIES/models/common directory³ files reside within the \$BAPSPECIES/ models/common directory unless a full directory path is indicated



General Program Files

Several general programs used by the various HSMs are outlined below. These programs are stored within the \$BAPSPECIES/models/common sub-directory.

The programs, inputs, and outputs associated with these model requirements are outlined in Table 8.28.

Table 8.28. Programs, inputs, and outputs called by specific fine-filter bioindicators.

Program Name	\$BAPSPECIES/models/common/sicurve.aml
Called By	Various HSMs
Calls	
Usage	<reclass-grid> <si> <remapfile>
Output	suitability index grids (e.g. sf2)
Program Name	\$BAPSPECIES/models/common/home-smooth-zones.aml
Called By	Various HSMs
Calls	
Usage	<radius>
Output	zonal grids required for home-range smoothing
Program Name	\$BAPSPECIES/models/common/home-smooth-avg.aml
Called By	Various HSMs
Calls	
Usage	< sigrid> <outgrid>
Output	grid representing averaged (smoothed) habitat based on habitat values found within a species home-range.
Program Name	\$BAPSPECIES/models/common/home-smooth-pro.aml
Called By	Various HSMs
Calls	
Usage	<sigrid> <outgrid> <proportion>
Output	grid representing averaged (smoothed) habitat based on the top portion of highest values found within a home-range.
Program Name	\$BAPSPECIES/models/common/home-smooth-top4.aml
Called By	\$GOSHAWK\goshawk.aml
Calls	
Usage	< sigrid> <outgrid>
Output	grid representing averaged (based on the four highest) SI values within a nesting block.
Program Name	\$BAPSPECIES/models/common/block.aml
Called By	\$GOSHAWK\goshawk.aml
Calls	
Usage	< blocksize>
Output	grid of non-overlapping nesting areas (blocks).



8.7 BAP USER MENU INTERFACE

The following section describes the BAP menus that have been developed to assist the user in accessing the landscape configuration and ecosystem diversity models and HSMs.

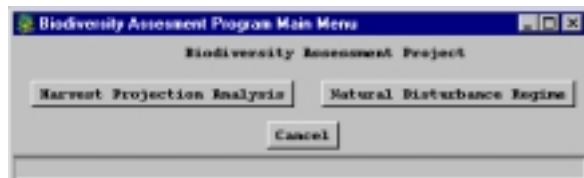
8.7.1 Menus: Coarse-filter Biodiversity Models

The following menus are an interface to the batchrun.mwi. It is designed to allow the user to enter the required information and execute the appropriate models. User supplied information is written to the appropriate user-files listed in Table 8.4 (Harvest Projection Section). Once the required information has been entered, the batchrun.mwi program can be invoked to execute the desired models.

The BAP menu system is started at the arc prompt using the following command:

Arc> **&r \$BAPMENU/bap.aml init**

This command opens the main BAP menu, which appears in the upper left corner of the screen.

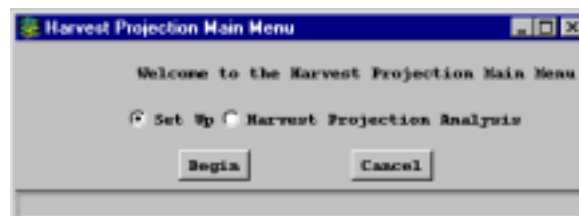


The **Harvest Projection Analysis** or **Natural Disturbance Regime** selection buttons direct the user to the appropriate menus for that selection. The **Cancel** button will close the menu and return control back to the command window.

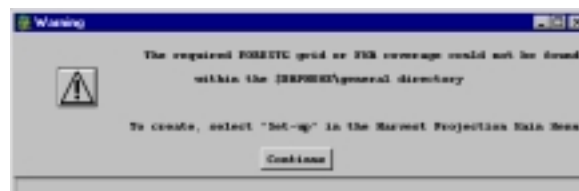
Harvest Projection Analysis

The following section describes the Harvest Projection Analysis menus.

Selecting the **Harvest Projection Analysis** button opens the **Harvest Projection Main Menu**.



The BAPHOME/general directory is checked during start up to determine the presence of a coverage called FMA and a grid called FORESTG. If absent, the following message appears, indicating these files are missing and need to be created using the Set Up Button. These files are required for several biodiversity models.

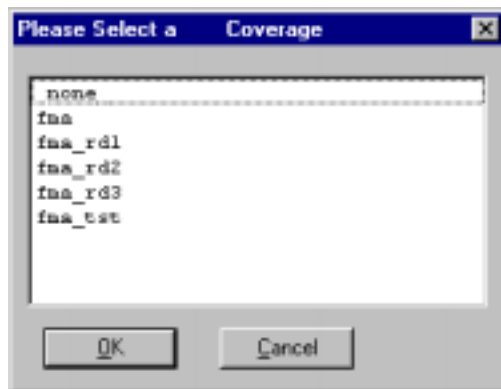




Set Up Button

The Set Up menu controls input into the \$BAPHOME/aml/fma.aml program. This program copies the selected forest coverage to a new coverage called FMA. The input forest coverage must reside within the \$BAPHOME/general directory. A new grid, called FORESTG, is then generated based on the BAPKEY column within the FMA coverage.

The BAPKEY column should contain unique polygon id values. The **Raster Output Cell Size** controls the FORESTG grid output grid cell size. The default output value is 25 m. This procedure must be performed whenever the initial forest coverage is altered.





Harvest Projection Analysis

The **Harvest Projection Analysis** button opens the Harvest Projection’s main menu.



Specify Inventory File Input

Edit

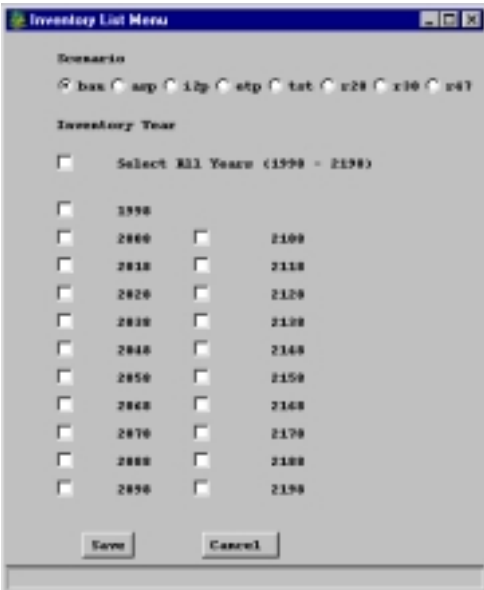
The Edit button displays the Inventory List Menu. Users select the scenario and inventory years to be processed. Input is written to the \$BAPHOME/files/user-inventory.lis file using the Save button. Changes must be saved in order to update the \$BAPHOME/files/user-inventory file.

View File Button This button displays the content of the \$BAPHOME/files/user-inventory file.

General Model Environment Settings:

View / Edit Model Environment Button

This button displays the Model Environment Settings menu. The user must specify the name of an existing INFORMIX database, the name of the database connection file,





and the path to an existing workspace. All model INFO data output files are stored within the defined workspace. Input is written to the \$BAPHOME/files/dbconnect.bap file using the **Save Settings** button. Changes must be saved in order to up date the \$BAPHOME/files/ dbconnect.bap file.

The INFORMIX database must already exist. The database connection file contains information required by ArcInfo for establishing a connection to INFORMIX. The connection file is a simple text file stored within the \$ARCHOME/database directory. The file must contain the following two lines:

ARC/INFO 7.2 - INFORMIX Server

\$ARCHOME/bin/dbi_INFORMIX

A connection file is required for each database. The file must have a .dbs extension (e.g. etp.dbs).

View / Edit User Files Button

This button displays the Harvest Projection Model User Files menu. The specified files must reside within the \$BAPHOME/files directory. Files may be viewed using the **View File** button. Input is saved to the \$BAPHOME/files/user-files.lis file using the **Save Settings** button. Changes must be saved in order to update the \$BAPHOME/files/user-files.lis file.



Inventory Reclassification and Filtering Programs

Cover Type Reclassification Button

Evokes the \$BAPHOME/aml/bapcovtype.mwi program.

Habitat Filtering Button

Evokes the \$BAPHOME/aml/habitat.mwi program

Biodiversity Assessment Programs

BAP Model Selection List Button

Displays the Harvest Projection Model Selection Menu. The selected models to be processed are written to the \$BAPHOME/files/user-models.lis file using the **Save Model Selections** button.

Selections button.

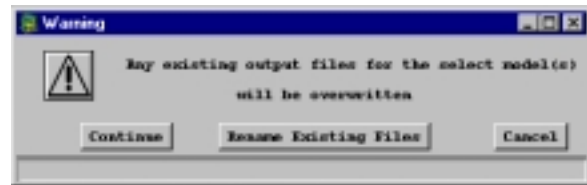


View Selected Models List Button

Displays the selected model(s) listed in the \$BAPHOME/files/user-models.lis file. The program informs the user if no models have been selected.

Run Selected Models Button

Evokes the \$BAPHOME/aml/batchrun.mwi program. A warning menu appears indicating that existing data files (only for the selected models) will be replaced. Users have the option to continue by selecting **Continue**, which will replace any existing file or to rename an existing file before continuing by selecting the **Rename Existing Files**.



Rename Existing Files

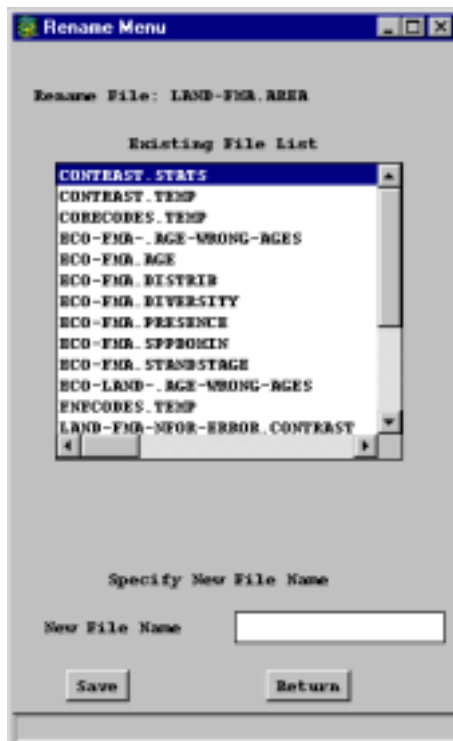
Opens a new menu displaying any existing INFO model data files. Only data files associated with models listed within the \$BAPHOME/files/user-models.lis file are displayed. Users have the option to rename a listed file by selecting the **Rename** button. The **Continue** button starts the modelling process. The **Cancel** button returns the user back to the **Harvest Project Main Menu**.





Rename

Opens a new menu that allows users to re-name the selected file.



Natural Disturbance Regime (NDR)

The following section describes the NDR menu system.

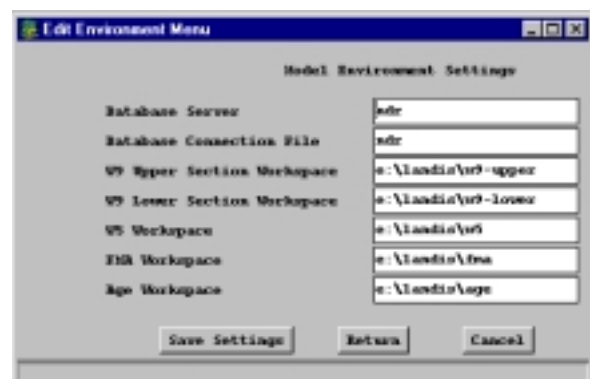
Selecting the **Natural Disturbance Regime** button from the main BAP menu opens the main NDR menu.



General Model Environment Settings

View/Edit Environment Settings

Displays the Model Environment Settings menu. The user must specify the name of an existing INFORMIX database, the name of the database connection file, and workspace locations. The W9 Upper Section, W9 Lower Section, and W5 workspaces are used to store intermediate model output. The FMA workspace stores all combined output grids and the various model INFO output data files. The age workspaces stores all age related grids. Input is written to the \$NDRHOME/files/dbconnect.bap file using the **Save Settings** button. Changes must be saved in order to update the \$NDRHOME/files/dbconnect.bap file.





BAP Report #8: BAP Program Documentation

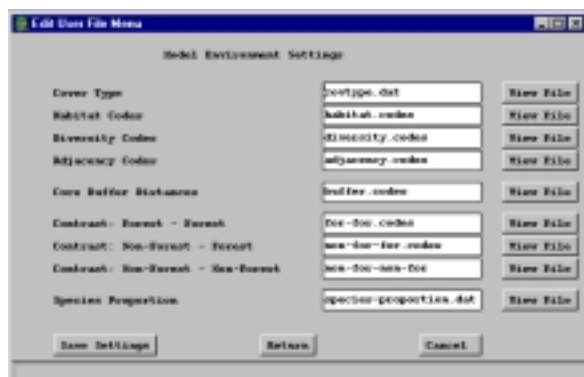
View/Edit Spatial Files

Displays the Edit User Coverage/Grid Menu. The required file names and the location of LANDIS input and output files are defined within this menu. To help reduce storage space, all LANDIS output files, by section are compressed into a single file. BAP automatically un-compresses the necessary file when required. Input is saved to the \$NDRHOME/files/NNNNN-files.lis file using the **Save Settings** button.



View / Edit User Files Button

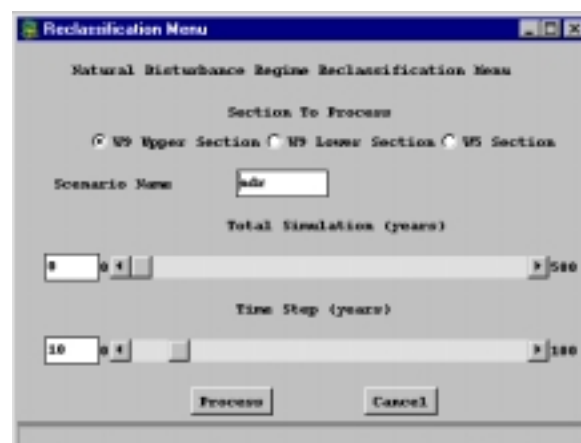
Displays the NDR Model User Files menu. All required user defined model files are entered using this menu. The specified files must reside within the \$NDRHOME/files directory. Files may be viewed using the **View File** button. Input is saved to the \$BAPHOME/files/user-files.lis file using the **Save Settings** button. Changes must be saved in order to update the \$BAPHOME/files/user-files.lis file.



Data Preparation

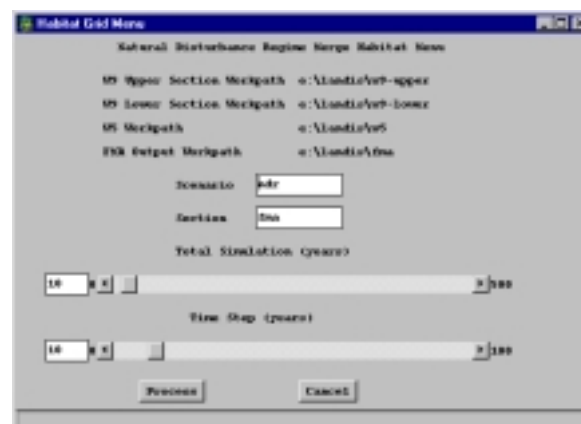
Process 1

Opens the Re-classification menu. Users select the section, scenario name, total simulation time period, and time step. The **Process** button executes the \$NDRHOME\bapcov.mwi AML.



Process 2

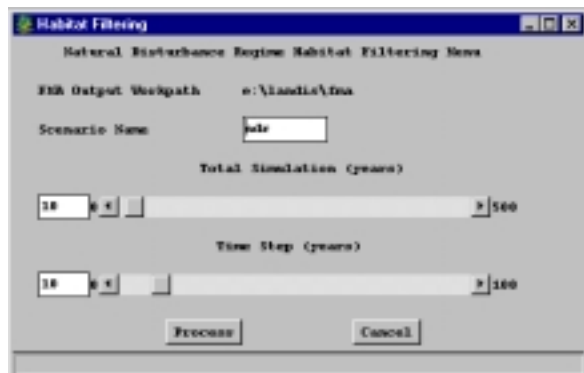
Opens a Habitat Grid Menu. Executes the \$NDRHOME/prep-habitat.mwi, which merges the individual section grids into a single grid for the entire FMA area. Workspace input and output paths are displayed. By default, combined grids are stored within the FMA section directory, as defined in the previous Edit Environment menu discussed above.





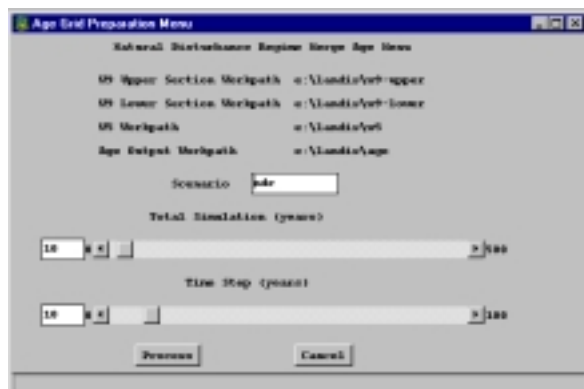
Process 3

Opens the Habitat Filtering menu. Users specify the scenario name, total simulation time period, and time step between periods. The **Process** button executes the \$NDRHOME\habitat.mwi AML that begins the filtering process.



Process 4

Opens the Age Grid Preparation menu. Users specify the scenario name, total simulation time period, and the time step between periods. The **Process** button executes the \$NDRHOME\prep-age.mwi AML which prepares the age grids for the up coming analysis.



Biodiversity Assessment Models

Before the biodiversity models are run, users must have prepared all datasets by executing the Process buttons, as discussed above.

Total Simulation (years) and Time Step (years)

Users specify the simulation time period and the number of years between time steps. This value controls the process period for the selected BAP models.

Scenario Name

Users specify the scenario name. The default scenario name is ndr.

BAP Model Selection List

Displays the NDR Model Selection Menu. Users select the models to be processed. Selected model names are written to the \$NDRHOME/files/user-models.lis file using the **Save Model Selections** button.



View Selected Model(s) List

Displays the selected model(s) listed in the \$NDRHOME/files/user-models.lis file. The program informs the user if no models have been selected.

Run Selected Model(s)

Evokes the \$NDRHOME/aml/landis-batch.mwi program.



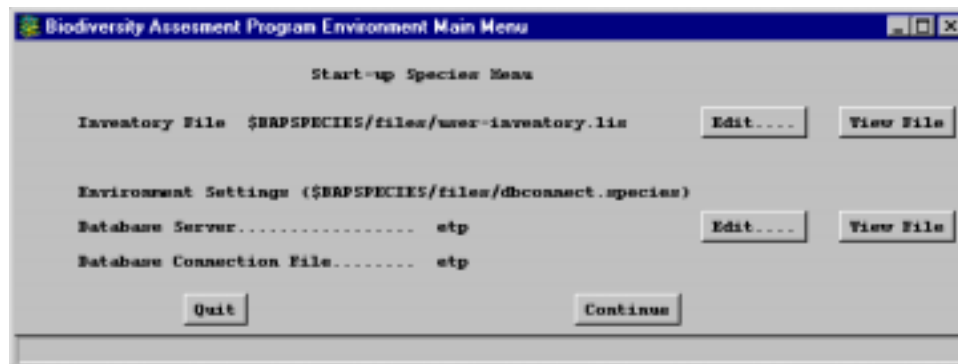
8.7.2 Menus: Fine-filter Biodiversity Models

The following menus are an interface to the batchspecies.mwi program. The menus are designed to allow the user to enter the required information and execute the appropriate HSMS. User supplied information is written to the appropriate user-files. Once the required information has been entered the batchspecies.mwi program can be invoked to execute the desired models.

The BAP species menu system is started at the arc prompt using the following command:

Arc> **&r \$BAPSPECIES/species start**

The first menu to appear is the main environment menu.

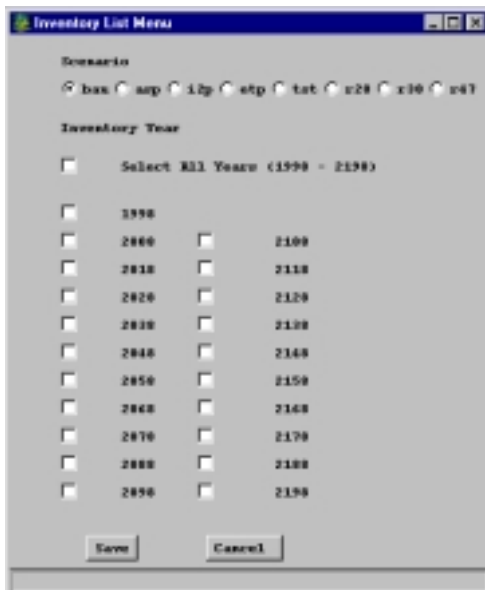




Start-up Species Menu

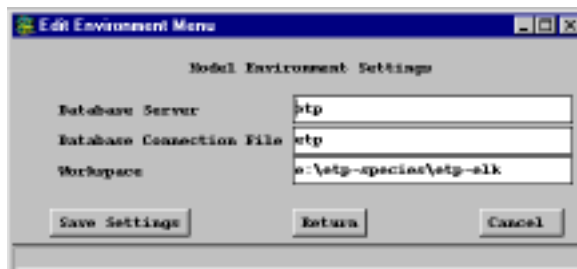
Edit (Inventory File)

Displays the Inventory List Menu. Users select the scenario and inventory years to process. Input is written to the \$BAPSPECIES/files/user-inventory.lis file using the Save button. Changes must be saved in order to update the \$BAPSPECIES/files/user-inventory file.



View / Edit Model Environment Button

Displays the Model Environment Settings menu. The user must specify the name of an existing INFORMIX database, the name of the database connection file, and the path to an existing workspace. All model INFO data output files are stored within the defined workspace. Input is written to the \$BAPSPECIES/files/dbconnect.bap file using the **Save Settings** button. Changes must be saved in order to update the \$BAPSPECIES/files/dbconnect.bap file.

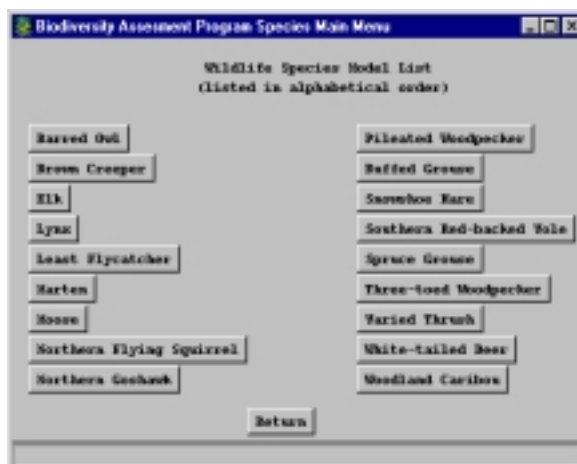


View File

Displays either the \$BAPSPECIES/files/dbconnect.bap or \$BAPSPECIES/files/user-inventory.lis files.

Continue

Opens the main species menu. Selecting a species button displays the HSM interface for the selected species. All species menus follow the same format and structure. Therefore, we will describe only the Barred Owl HSM menus.





BAP Report #8: BAP Program Documentation

Selecting the **Barred Owl** species button opens the main HSM menu.



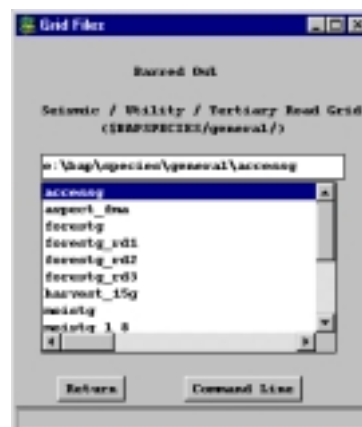
Output Workspace

The output workspace location is entered. The defined workspace stores all model outputs. The workspace may also be set in the Main Environment menu.

Grid Input (Select)

Opens the Grid selection menu. Users select the required seismic / utility and tertiary road grid. The selected grid name is written to the \$BARREDOWL\barredowl.lis file.

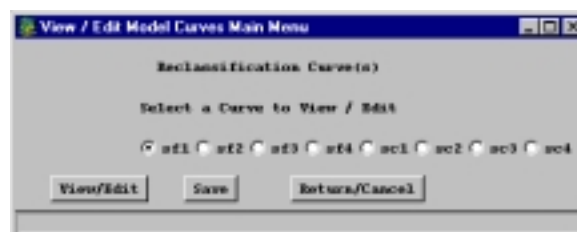
The **Command Line** provides access to the ArcInfo terminal window. To close this menu and return back to the main HSM menu, select the **Return** button.



Edit Model Input Parameters

Edit (SI) Suitability Index Graphs (SI)

Starts the View / Edit Model Curves Main menu.



Return/Cancel

Closes the SI edit menus and returns the user to the main HSM menu.

Save

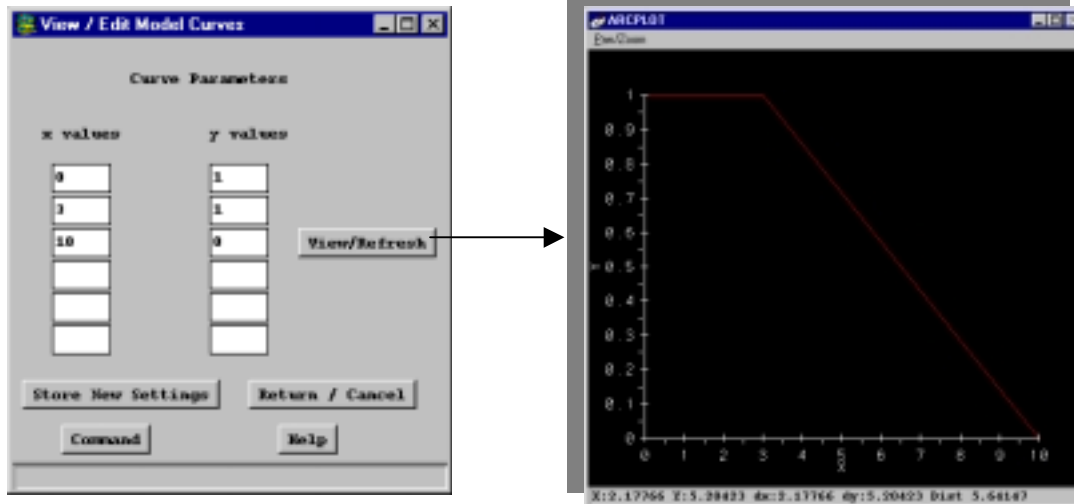
All changes made to any of the SI curves are written to a SI curve definition file called \$BARREDOWL\barredowl.rmp file.

View Edit

The View/Edit button opens an edit menu for the selected SI curve. Entering the appropriate X and Y co-ordinate values defines the SI curve. The **Store New Settings** button temporally stores all entered values as variables. To save any stored co-ordinate variables, the **Save** button in the View / Edit Model Curves Main menu must be selected. The **Return / Cancel** button closes the current window. The **Command** button provides access to the ArcInfo terminal window. The



View/Refresh button opens a display window containing the defined curve. Any further edits to the curve can be viewed by updating the window with the **View/Refresh** button.





BAP Report #8: BAP Program Documentation

Home Range Smoothing

Smoothing Window Radius (# of cells)

Sets the size of the circular window used in the home ranging smoothing process. The values are expressed in number of cells. The distance is dependent on the grid cells size. For a 25 m cell size, the defined 28 cell radius equals 700 m.

Food and Cover Proximity Kernel File

Select

Opens the Kernel File selection menu. The name of the selected file is written to the \$BARREDOWL\barredowl.lis file. The **Return** button closes the current menu and returns the user to the main HSM menu.



View Model Parameter ASCII Files

View

The various View buttons display the content of the appropriate ASCII files.

Run Model

Executes the HSM model.

Return to Species Menu

Closes the current menu and returns the user to the main species menu.



8.8 LITERATURE CITED

- Doyon, F. 2000. Habitat classification. Biodiversity Assessment Project for Millar Western Forest Products. BAP Report 3. Chair in Forest Management and Policy, Faculty of Forestry, Lakehead University, Thunder Bay, ON. 7 pp.
- Doyon, F. and P.D. Duinker. 2000. Natural disturbance regime simulation using LANDIS. Biodiversity Assessment Project for Millar Western Forest Products. BAP Report 4. Institut Quebecois d'Amenagement de la Foret Feuillue, St-Andre-Avellin, Quebec. 28 p.
- Doyon, F. and H.L. MacLeod. 2000. Ecosystem Diversity and Landscape Configuration Models. Biodiversity Assessment Project for Millar Western Forest Products. BAP Report 7. Institut Quebecois d'Amenagement de la Foret Feuillue, St-Andre-Avellin, Quebec. 5 p.
- Doyon, F. and P. Duinker. 2000. Species Selection Procedure. Biodiversity Assessment Project for Millar Western Forest Products. BAP Report 2. Thunder Bay, Ontario. Chair in Forest Management and Policy, Faculty of Forestry, Lakehead University, 11 pp.
- Doyon, F. and H. MacLeod. 2000. Special Habitat Element Modelling. Biodiversity Assessment Project for Millar Western Forest Products Ltd. BAP Report 5. Institut Quebecois d'Amenagement de la Foret Feuillue, St-Andre-Avellin, Quebec and KBM Forestry Consultants Inc., Thunder Bay, Ontario. 33 pp. + appendices.
- Duinker, P.D., F. Doyon, R. Morash, L. Van Damme, H.L. MacLeod, and A. Rudy. Background and Structure. Biodiversity Assessment Project for Millar Western Forest Products Ltd. BAP Report 1. Chair in Forest Management and Policy, Faculty of Forestry, Lakehead University, Thunder Bay, Ontario and KBM Forestry Consultants Inc., Thunder Bay, Ontario. 17 pp.
- Higgelke, P., H. MacLeod, and F. Doyon. 2000. Habitat Supply Models. Biodiversity Assessment Project for Millar Western Forest Products Ltd. BAP Report 6. Chair in Forest Management and Policy, Faculty of Forestry, Lakehead University, Thunder Bay, ON. 11 pp.

APPENDIX 1: LANDSCAPE AND ECOSYSTEM ASCII FILE DESCRIPTIONS AND PARAMETERS



To provide user flexibility, BAP utilises various ASCII files to store program set-up variables and model input variables. We attempted to use a standard formatting structure for all files. Many of the files are system-generated and are automatically created through the BAP menus. The following section presents examples of all system-generated files and their expected format. Other files are user-defined files. It is the responsibility of the user to construct these files. All user-defined files are presented below.

HARVEST PROJECTION AND NDR SYSTEM-GENERATED FILES

File: dbconnect.bap

Defines the parameters required to make a connection to an INFORMIX database and workspace path(s) required for model output file storage.

Harvest Projection

```
bapdbserver : etp
bapconnectfile : etp
workpath : e:\etp
```

NDR

```
bapdbserver : ndr
bapconnectfile : ndr
w9-upper-workpath : e:\landis\w9-upper
w9-lower-workpath : e:\landis\w9-lower
w5-workpath : e:\landis\w5
fma-workpath : e:\landis\fma
age-workpath : e:\landis\age
```

File: user-inventory.lis (harvest projection analysis only)

Contains a tabular listing of inventory file names.

```
bau_1998
bau_2008
bau_2018
bau_2028
```

File: user-model.lis

A tabular listing of the biodiversity models to be executed. For example:

```
patch-stats
patch-core
edge-adjacency
```

File: user-files.lis

Contains a listing of all ASCII file names required by the various models. The structure of the file consists of a key word identifying the file name, followed by a space, a colon (:), a space, and the user-defined file name. For example:

```
covtypefile : covtype.dat
habitatfile : habitat.codes
diversityfile : diversity.codes
adjacencyfile : adjacency.codes
corefile : bapcore.codes
for-for : for-for.codes
for-for : nf-for.codes
nfor-nfor : nf-nf.codes
```

**File: user-cover.lis (for NDR only)**

Contains a listing of all input (spatial) file names required by the various models. The structure of the file consists of a key word identifying the file name, followed by a space, a colon (:), a space, and the user-defined file name. For example:

```
w9-upper-map : e:\landis\mapgis_u.gis
w9-lower-map : e:\landis\mapgis_l.gis
w5-map : e:\landis\mapgis_w5.gis
w9-upper-zipfile : e:\landis\w9-upper.zip
w9-lower-zipfile : e:\landis\w9-lower.zip
w5-zipfile : e:\landis\w5.zip
```

SB_AW -10 7 13 30 70 140

PL -10 5 10 20 60 120

SW -10 8 15 30 80 150

SB -10 8 15 30 90 160

LT -10 4 10 25 50 150

File: habitat.codes

A single column file with each line representing a specific habitat type code value. All broad habitat codes must be listed. A complete listing of all codes can be found in Table 7.6.

**HARVEST PROJECTION AND NDR
USER-DEFINED FILES****File: covtype.dat**

```
AW -10 2 10 20 50 100
PO -10 2 10 20 50 110
BW -10 5 10 25 60 90
AW_PL -10 4 10 20 50 115
AW_SW -10 5 13 25 65 120
AW_SB -10 5 13 25 70 130
PO_PL -10 4 10 20 55 120
PO_SW -10 5 13 25 65 125
PO_SB -10 5 13 25 70 135
PL_PO -10 6 10 20 55 110
PL_AW -10 6 10 20 60 115
SW_PO -10 7 13 25 75 130
SW_AW -10 7 13 30 71 125
SB_PO -10 7 13 25 75 140
```

**File: diversity.codes**

A single column file. Each line contains a single broad habitat combination and its contrast value. A comma separates all values. A complete listing is shown in tabular form below (Table A1).

Table A1. Complete listing of diversity codes.

11,11,0.0	12,22,0.2	14,43,0.8	24,33,0.6
12,12,0.0	12,23,0.6	14,44,0.8	24,34,0.6
13,13,0.0	12,24,0.8	21,22,0.4	24,41,0.8
14,14,0.0	12,31,0.4	21,23,1.0	24,42,0.6
21,21,0.0	12,32,0.4	21,24,0.8	24,43,0.8
22,22,0.0	12,33,0.7	21,31,0.0	24,44,0.6
23,23,0.0	12,34,0.8	21,32,0.4	31,32,0.4
24,24,0.0	12,41,0.6	21,33,1.0	31,33,1.0
31,31,0.0	12,42,0.8	21,34,0.8	31,34,0.8
32,32,0.0	12,43,0.1	21,41,0.2	31,41,0.0
33,33,0.0	12,44,0.1	21,42,0.6	31,42,0.4
34,34,0.0	13,14,0.4	21,43,1.0	31,43,1.0
41,41,0.0	13,21,0.1	21,44,0.8	31,44,0.8
42,42,0.0	13,22,0.6	22,23,0.5	32,33,0.4
43,43,0.0	13,23,0.2	22,24,0.7	32,34,0.6
44,44,0.0	13,24,0.5	22,31,0.4	32,41,0.4
11,12,0.4	13,31,0.1	22,32,0.2	32,42,0.2
11,13,1.0	13,32,0.8	22,33,0.6	32,43,0.6
11,14,0.8	13,33,0.5	22,34,0.8	32,44,0.6
11,21,0.0	13,34,0.6	22,41,0.4	33,34,0.4
11,22,0.4	13,41,0.1	22,42,0.8	33,41,1.0
11,23,1.0	13,42,0.9	22,43,0.8	33,42,0.6
11,24,0.8	13,43,0.6	22,44,0.7	33,43,0.4
11,31,0.2	13,44,0.7	23,24,0.4	33,44,0.5
11,32,0.6	14,21,0.8	23,31,1.0	34,41,0.8
11,33,0.1	14,22,0.8	23,32,0.6	34,42,0.8
11,34,0.8	14,23,0.4	23,33,0.4	34,43,0.6
11,41,0.2	14,24,0.2	23,34,0.8	34,44,0.4
11,42,0.6	14,31,0.8	23,41,1.0	41,42,0.4
11,43,0.1	14,32,1.0	23,42,0.8	41,43,1.0
11,44,0.8	14,33,0.6	23,43,0.8	41,44,0.8
12,13,0.6	14,34,0.6	23,44,0.6	42,43,0.4
12,14,0.8	14,41,0.8	24,31,0.8	42,44,0.5
12,21,0.4	14,42,0.8	24,32,0.8	43,44,0.4

**File: adjacency.codes**

A single column file. A comma separates all values. A complete listing is shown in tabular form below (Table A2).

Table A2. A complete listing of adjacency codes.

11,12,1	13,31,55	21,106,109	24,64,163	33,204,217	44,64,271
11,13,2	13,32,56	21,107,110	24,103,164	33,205,218	44,103,272
11,14,3	13,33,57	21,203,111	24,105,165	33,206,219	44,105,273
11,21,4	13,34,58	21,204,112	24,106,166	33,207,220	44,106,274
11,22,5	13,41,59	21,205,113	24,107,167	34,41,221	44,107,275
11,23,6	13,42,60	21,206,114	24,203,168	34,42,222	44,203,276
11,24,7	13,43,61	21,207,115	24,204,169	34,43,223	44,204,277
11,31,8	13,44,62	22,23,116	24,205,170	34,44,224	44,205,278
11,32,9	13,64,63	22,24,117	24,206,171	34,64,225	44,206,279
11,33,10	13,103,64	22,31,118	24,207,172	34,103,226	44,207,280
11,34,11	13,105,65	22,32,119	31,32,173	34,105,227	64,103,281
11,41,12	13,106,66	22,33,120	31,33,174	34,106,228	64,105,282
11,42,13	13,107,67	22,34,121	31,34,175	34,107,229	64,106,283
11,43,14	13,203,68	22,41,122	31,41,176	34,203,230	64,107,284
11,44,15	13,204,69	22,42,123	31,42,177	34,204,231	64,203,285
11,64,16	13,205,70	22,43,124	31,43,178	34,205,232	64,204,286
11,103,17	13,206,71	22,44,125	31,44,179	34,206,233	64,205,287
11,105,18	13,207,72	22,64,126	31,64,180	34,207,234	64,206,288
11,106,19	14,21,73	22,103,127	31,103,181	41,42,235	64,207,289
11,107,20	14,22,74	22,105,128	31,105,182	41,43,236	103,105,290
11,203,21	14,23,75	22,106,129	31,106,183	41,44,237	103,106,291
11,204,22	14,24,76	22,107,130	31,107,184	41,64,238	103,107,292
11,205,23	14,31,77	22,203,131	31,203,185	41,103,239	103,203,293
11,206,24	14,32,78	22,204,132	31,204,186	41,105,240	103,204,294
11,207,25	14,33,79	22,205,133	31,205,187	41,106,241	103,205,295
12,13,26	14,34,80	22,206,134	31,206,188	41,107,242	103,206,296
12,14,27	14,41,81	22,207,135	31,207,189	41,203,243	103,207,297
12,21,28	14,42,82	23,24,136	32,33,190	41,204,244	105,106,298
12,22,29	14,43,83	23,31,137	32,34,191	41,205,245	105,107,299
12,23,30	14,44,84	23,32,138	32,41,192	41,206,246	105,203,300
12,24,31	14,64,85	23,33,139	32,42,193	41,207,247	105,204,301
12,31,32	14,103,86	23,34,140	32,43,194	42,43,248	105,205,302
12,32,33	14,105,87	23,41,141	32,44,195	42,44,249	105,206,303
12,33,34	14,106,88	23,42,142	32,64,196	42,64,250	105,207,304
12,34,35	14,107,89	23,43,143	32,103,197	42,103,251	106,107,305
12,41,36	14,203,90	23,44,144	32,105,198	42,105,252	106,203,306
12,42,37	14,204,91	23,64,145	32,106,199	42,106,253	106,204,307
12,43,38	14,205,92	23,103,146	32,107,200	42,107,254	106,205,308
12,44,39	14,206,93	23,105,147	32,203,201	42,203,255	106,206,309
12,64,40	14,207,94	23,106,148	32,204,202	42,204,256	106,207,310
12,103,41	21,22,95	23,107,149	32,205,203	42,205,257	107,203,311
12,105,42	21,23,96	23,203,150	32,206,204	42,206,258	107,204,312
12,106,43	21,24,97	23,204,151	32,207,205	42,207,259	107,205,313
12,107,44	21,31,98	23,205,152	33,34,206	43,44,260	107,206,314
12,203,45	21,32,99	23,206,153	33,41,207	43,64,261	107,207,315
12,204,46	21,33,100	23,207,154	33,42,208	43,103,262	203,204,316
12,205,47	21,34,101	24,31,155	33,43,209	43,105,263	203,205,317
12,206,48	21,41,102	24,32,156	33,44,210	43,106,264	203,206,318
12,207,49	21,42,103	24,33,157	33,64,211	43,107,265	203,207,319
13,14,50	21,43,104	24,34,158	33,103,212	43,203,266	204,205,320
13,21,51	21,44,105	24,41,159	33,105,213	43,204,267	204,206,321
13,22,52	21,64,106	24,42,160	33,106,214	43,205,268	204,207,322
13,23,53	21,103,107	24,43,161	33,107,215	43,206,269	205,206,323
13,24,54	21,105,108	24,44,162	33,203,216	43,207,270	205,207,324
					206,207,325

**File: bapcore.codes**

A single column file. A comma separates all values. A complete listing is shown in tabular form below (Table A3).

Table A3. A complete listing of core codes.

1,2,50	2,206,50
1,3,100	2,207,50
1,4,75	3,4,25
1,64,0	3,64,100
1,103,0	3,103,100
1,105,0	3,105,100
1,106,25	3,106,100
1,107,0	3,107,75
1,203,25	3,203,50
1,204,25	3,204,50
1,205,0	3,205,100
1,206,0	3,206,100
1,207,0	3,207,100
2,3,75	4,64,100
2,4,50	4,103,100
2,64,75	4,105,75
2,103,50	4,106,75
2,105,50	4,107,100
2,106,50	4,203,50
2,107,50	4,204,50
2,203,0	4,205,75
2,204,0	4,206,75
2,205,75	4,207,75



File: for-for.codes

A single column file. A comma separates all values. A complete listing is shown in tabular form below (Table A4).

Table A4. A complete listing of contrast codes between forested habitat types.

11,12,0.4	13,14,0.4	21,32,0.4	24,34,0.6	41,44,0.8	112,24,0.9
11,13,1.0	13,21,1.0	21,33,1.0	24,41,0.8	42,43,0.4	112,31,0.0
11,14,0.8	13,22,0.6	21,34,0.8	24,42,0.6	42,44,0.5	112,32,0.3
11,21,0.0	13,23,0.2	21,41,0.2	24,43,0.8	43,44,0.4	112,33,1.0
11,22,0.4	13,24,0.5	21,42,0.6	24,44,0.6	111,11,0.1	112,34,0.9
11,23,1.0	13,31,1.0	21,43,1.0	31,32,0.4	111,12,0.3	112,41,0.0
11,24,0.8	13,32,0.8	21,44,0.8	31,33,1.0	111,13,1.0	112,42,0.3
11,31,0.2	13,33,0.5	22,23,0.5	31,34,0.8	111,14,0.8	112,43,1.0
11,32,0.6	13,34,0.6	22,24,0.7	31,41,0.0	111,21,0.1	112,44,0.9
11,33,1.0	13,41,1.0	22,31,0.4	31,42,0.4	111,22,0.3	113,11,0.5
11,34,0.8	13,42,0.9	22,32,0.2	31,43,1.0	111,23,1.0	113,12,0.0
11,41,0.2	13,43,0.6	22,33,0.6	31,44,0.8	111,24,0.8	113,13,0.8
11,42,0.6	13,44,0.7	22,34,0.8	32,33,0.4	111,31,0.1	113,14,1.0
11,43,1.0	14,21,0.8	22,41,0.4	32,34,0.6	111,32,0.3	113,21,0.5
11,44,0.8	14,22,0.8	22,42,0.8	32,41,0.4	111,33,1.0	113,22,0.0
12,13,0.6	14,23,0.4	22,43,0.8	32,42,0.2	111,34,0.8	113,23,0.8
12,14,0.8	14,24,0.2	22,44,0.7	32,43,0.6	111,41,0.1	113,24,1.0
12,21,0.4	14,31,0.8	23,24,0.4	32,44,0.6	111,42,0.3	113,31,0.5
12,22,0.2	14,32,1.0	23,31,1.0	33,34,0.4	111,43,1.0	113,32,0.0
12,23,0.6	14,33,0.6	23,32,0.6	33,41,1.0	111,44,0.8	113,33,0.8
12,24,0.8	14,34,0.6	23,33,0.4	33,42,0.6	111,112,0.	113,34,0.6
12,31,0.4	14,41,0.8	23,34,0.8	33,43,0.4	111,113,0.	113,41,0.5
12,32,0.4	14,42,0.8	23,41,1.0	33,44,0.5	112,11,0.0	113,42,0.0
12,33,0.7	14,43,0.8	23,42,0.8	34,41,0.8	112,12,0.3	113,43,0.8
12,34,0.8	14,44,0.8	23,43,0.8	34,42,0.8	112,13,1.0	113,44,1.0
12,41,0.6	21,22,0.4	23,44,0.6	34,43,0.6	112,14,0.9	
12,42,0.8	21,23,1.0	24,31,0.8	34,44,0.4	112,21,0.0	
12,43,1.0	21,24,0.8	24,32,0.8	41,42,0.4	112,22,0.3	
12,44,1.0	21,31,0.0	24,33,0.6	41,43,1.0	112,23,1.0	

**File: nf-for.codes**

A single column file. A comma separates all values. A complete listing is shown in tabular form below (Table A5).

Table A5. A complete listing of contrast codes between non-forested and forested habitat types.

64,11,0.1	103,34,1.0	106,23,0.9	203,12,0.1	204,41,0.3	206,24,1.0
64,12,0.3	103,41,0.2	106,24,0.8	203,13,0.7	204,42,0.3	206,31,0.2
64,13,1.0	103,42,0.5	106,31,0.1	203,14,0.8	204,43,0.8	206,32,0.4
64,14,0.8	103,43,1.0	106,32,0.3	203,21,0.3	204,44,0.7	206,33,1.0
64,21,0.1	103,44,1.0	106,33,0.8	203,22,0.1	205,11,0.2	206,34,1.0
64,22,0.3	105,11,0.2	106,34,0.8	203,23,0.7	205,12,0.3	206,41,0.2
64,23,1.0	105,12,0.4	106,41,0.1	203,24,0.8	205,13,0.8	206,42,0.4
64,24,0.8	105,13,1.0	106,42,0.3	203,31,0.3	205,14,0.8	206,43,1.0
64,31,0.1	105,14,1.0	106,43,0.8	203,32,0.2	205,21,0.2	206,44,1.0
64,32,0.3	105,21,0.2	106,44,0.8	203,33,0.8	205,22,0.3	207,11,0.2
64,33,1.0	105,22,0.4	107,11,0.2	203,34,0.7	205,23,0.8	207,12,0.4
64,34,0.8	105,23,1.0	107,12,0.5	203,41,0.3	205,24,0.8	207,13,1.0
64,41,0.1	105,24,1.0	107,13,1.0	203,42,0.3	205,31,0.2	207,14,1.0
64,42,0.3	105,31,0.2	107,14,1.0	203,43,0.8	205,32,0.2	207,21,0.2
64,43,1.0	105,32,0.4	107,21,0.2	203,44,0.7	205,33,0.7	207,22,0.4
64,44,0.8	105,33,1.0	107,22,0.5	204,11,0.3	205,34,0.7	207,23,1.0
103,11,0.2	105,34,1.0	107,23,1.0	204,12,0.1	205,41,0.2	207,24,1.0
103,12,0.5	105,41,0.2	107,24,1.0	204,13,0.7	205,42,0.2	207,31,0.2
103,13,1.0	105,42,0.4	107,31,0.2	204,14,0.8	205,43,0.7	207,32,0.4
103,14,1.0	105,43,1.0	107,32,0.5	204,21,0.3	205,44,0.7	207,33,1.0
103,21,0.2	105,44,1.0	107,33,1.0	204,22,0.1	206,11,0.2	207,34,1.0
103,22,0.5	106,11,0.1	107,34,1.0	204,23,0.7	206,12,0.4	207,41,0.2
103,23,1.0	106,12,0.4	107,41,0.2	204,24,0.8	206,13,1.0	207,42,0.4
103,24,1.0	106,13,0.9	107,42,0.5	204,31,0.3	206,14,1.0	207,43,1.0
103,31,0.2	106,14,0.8	107,43,1.0	204,32,0.2	206,21,0.2	207,44,1.0
103,32,0.5	106,21,0.1	107,44,1.0	204,33,0.8	206,22,0.4	
103,33,1.0	106,22,0.4	203,11,0.3	204,34,0.7	206,23,1.0	



File: nf-nf.codes

A single column file. A comma separates all values. A complete listing is shown in tabular form below (Table A6).

Table A6. A complete listing of contrast codes between non-forested habitat types.

207,206,0.0	205,64,0.7
207,205,0.4	204,203,0.0
207,204,0.4	204,107,0.4
207,203,0.4	204,106,0.2
207,107,0.2	204,105,0.4
207,106,0.5	204,103,0.4
207,105,0.0	204,64,0.7
207,103,0.2	203,107,0.4
207,64,0.5	203,106,0.2
206,205,0.4	203,105,0.4
206,204,0.4	203,103,0.4
206,203,0.4	203,64,0.7
206,107,0.2	107,106,0.4
206,106,0.5	107,105,0.2
206,105,0.0	107,103,0.0
206,103,0.2	107,64,0.5
206,64,0.5	106,105,0.5
205,204,0.1	106,103,0.4
205,203,0.1	106,64,0.4
205,107,0.5	105,103,0.2
205,106,0.2	105,64,0.5
205,105,0.4	103,64,0.5
205,103,0.5	

APPENDIX 2: LANDSCAPE AND ECOSYSTEM EXAMPLES



BIODIVERSITY ASSESSMENT PROJECT COARSE-FILTER EXAMPLES

This section provides example of all landscape and ecosystem biodiversity models.

The area illustrated in the following examples is a subset (approximately 150 ha in size) of Millar Western's FMA area (Figure A1).

Depending on the bioindicator, BAP statistics may be reported at three different levels: forest or landscape (entire FMA area regardless of species composition), broad species composition, and specific species composition. In addition, a bioindicator may be reported at

one of two different levels of developmental stage: broad developmental stage (consisting of opening, developing, forested, and old stands) or specific developmental stage (consisting of clearcut or burn, regenerating, young, immature, mature, and old stands). The level at which each bioindicator is reported is discussed below.



Figure A1. Subset of Millar Western's FMA area used for coarse-filter bioindicator examples.



Ecosystem Diversity Bioindicators

Area-Weighted Age

Area-weighted age calculates the weighted age for all forested stands. The age values are obtained from the timber supply or NDR database files, which are spatially linked to the FORESTG grid. An example age grid is shown below (Figure A2, Table A7).

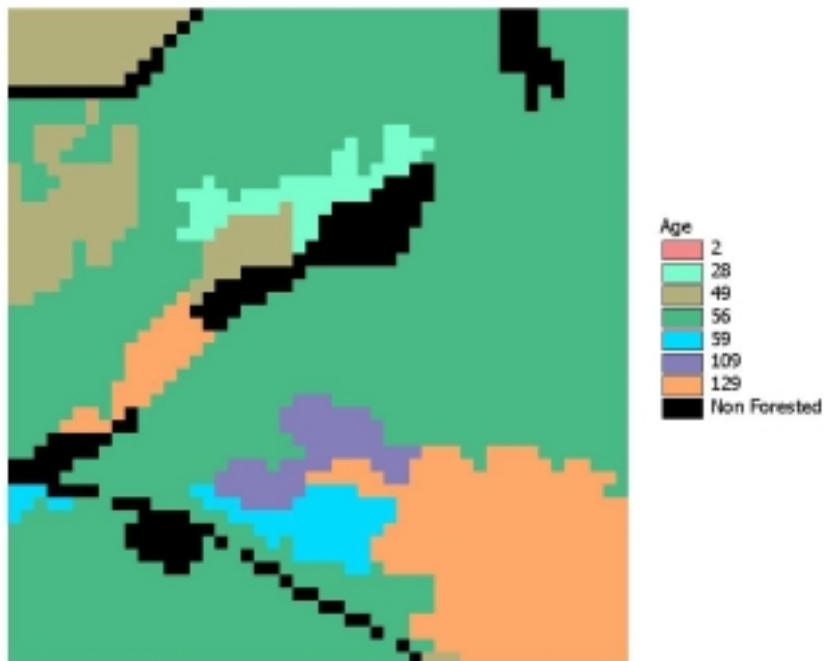


Figure A2. Example age grid.

Table A7. Example area-weighted age calculation.

Weighted Age
211
5446
287
106
98
338
436
2289
29
202
9



Developmental Stage Proportion

Determines the proportion of the landscape that supports each broad habitat type. Statistics are reported at the forest (all patches regardless of habitat type) and broad species composition levels. The following grid and tables illustrate the results of the proportion of developmental stages bioindicator at the forest level (Figure A3, Table A8).

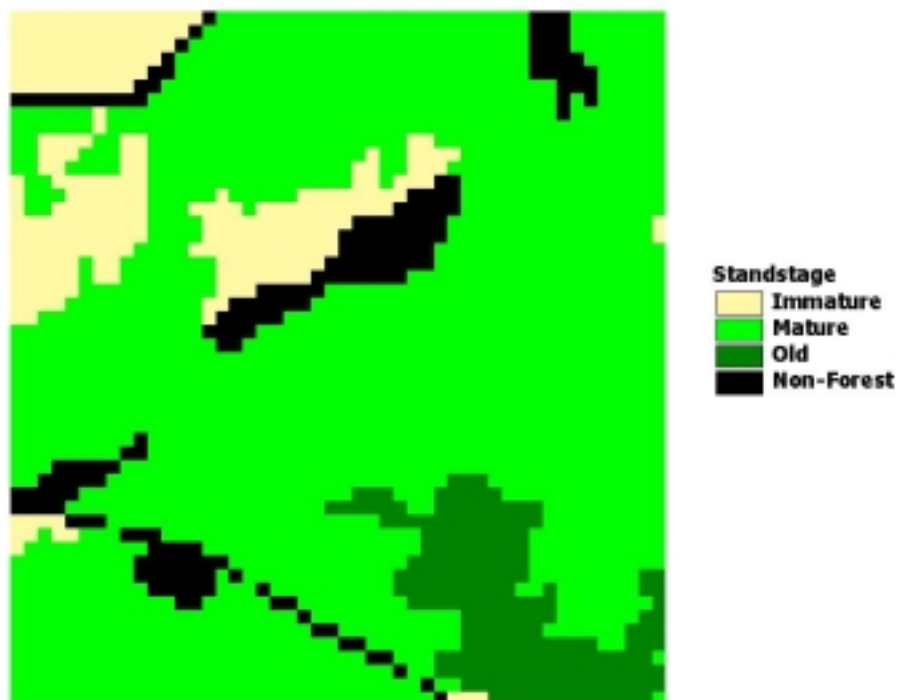


Figure A3. Example developmental stage proportion grid.

Table A8. Proportion of the forest supporting each broad developmental stage at the forest level.

Forest Level		
Developmental Stage	Area (ha)	Proportion of Landscape
1	0.0	0%
2	0.0	0%
3	0.0	0%
4	16.9	12%
5	113.2	80%
6	11.8	8%

Habitat Distribution

Habitat distribution reports the total area (ha) by specific habitat type. The following grid and table illustrates the habitat distribution (Figure A4, Table A9).

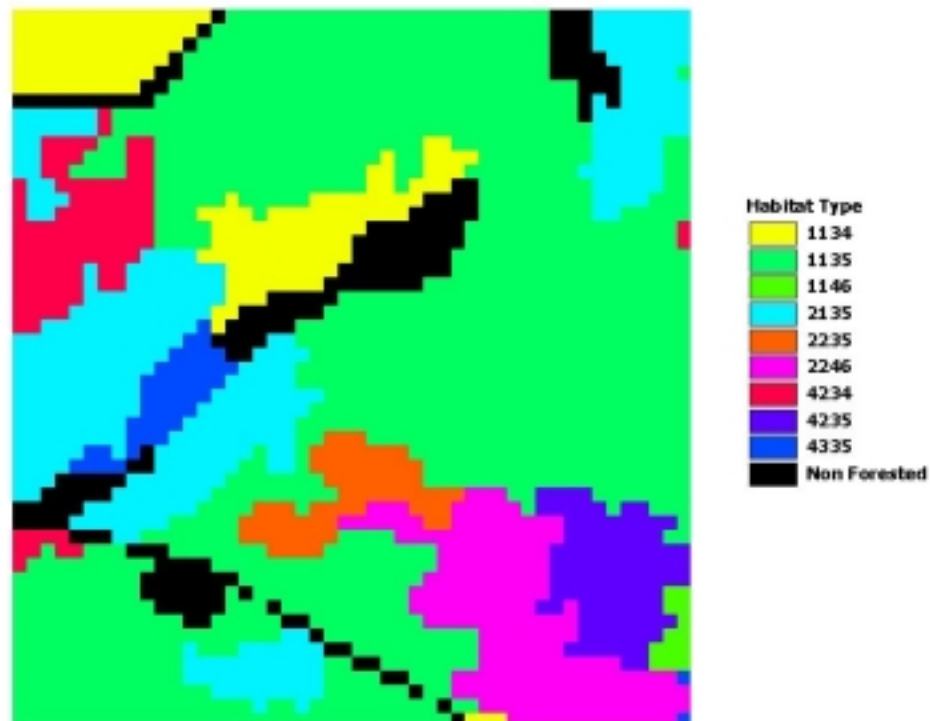


Figure A4. Example habitat distribution grid.

Table A9. Total area by specific habitat type.

Habitat Type	Area (ha)
1134	70.9
1135	70.9
1146	71.6
2135	133.4
2235	139.7
2246	140.4
4234	264.6
4235	264.7
4335	270.9



Habitat Diversity

Habitat diversity calculations are done at the broad habitat type level. The example below illustrates sample diversity index calculations (Figure A5, Table A10).

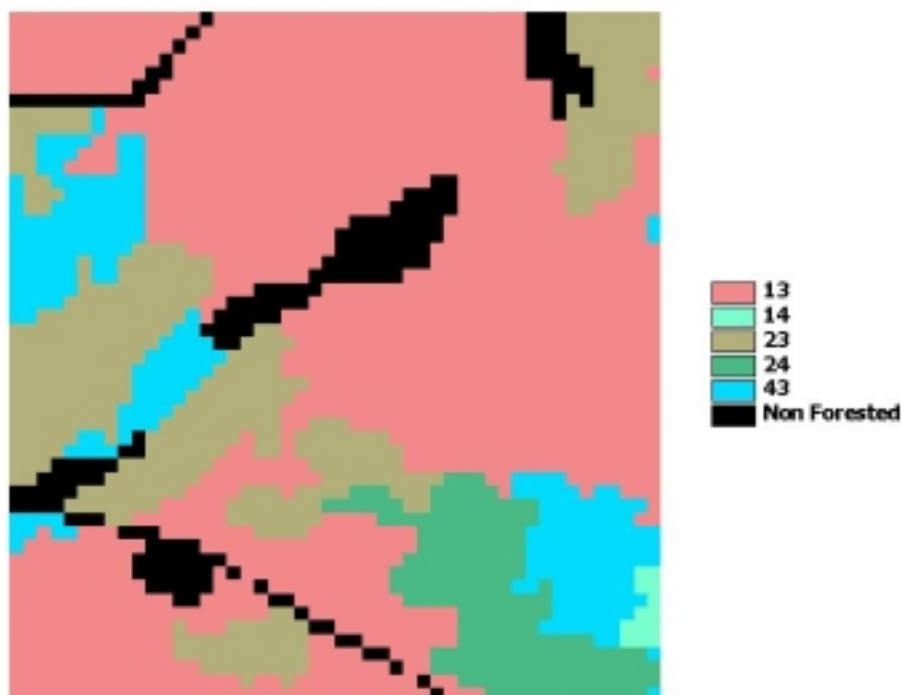


Figure A5. Example habitat diversity grid.



Table A10. Example of habitat diversity calculations.

Habitat 1	Habitat 2	Area (ha)	Contrast Weight	Weighted Area	Area of Habitat 1	Weighted Area * Habitat Area
13	13	86.9	0.0	0.00		
13	14	0.8	0.4	0.33		
13	23	28.1	0.2	5.61		
13	24	11.0	0.5	5.50		
13	43	15.1	0.6	9.08		
Total				20.51	86.9	1782.02
14	13	86.9	0.4	34.75		
14	14	0.8	0.0	0.00		
14	23	28.1	0.4	11.23		
14	24	11.0	0.2	2.20		
14	43	15.1	0.8	12.10		
Total				60.28	0.8	48.97
23	13	86.9	0.2	17.38		
23	14	0.8	0.4	0.33		
23	23	28.1	0.0	0.00		
23	24	11.0	0.4	4.40		
23	43	15.1	0.8	12.10		
Total				34.20	28.1	959.74
24	13	86.9	0.5	43.44		
24	14	0.8	0.2	0.16		
24	23	28.1	0.4	11.23		
24	24	11.0	0.0	0.00		
24	43	15.1	0.8	12.10		
Total				66.93	11.0	736.18
43	13	86.9	0.6	52.13		
43	14	0.8	0.8	0.65		
43	23	28.1	0.8	22.45		
43	24	11.0	0.8	8.80		
43	43	15.1	0.0	0.00		
Total				84.03	15.1	1270.88
Total					141.88	4797.79
Diversity Index						0.23835774



Species Dominance

Species dominance reports species percentage weighted by area. Table A11 presents each stand's area, the percentage composition of each species within the stand (e.g. SB (%)), and the area-weighted species percentage (e.g. W-SB (%), Table A11).

Species Presence

Species presence reports the percentage a tree species is present within the entire landscape. It does not consider species dominance, only presence (Table A12).

Table A11. Example of species dominance calculations.

Patch-ID	Patch-ID	Area (ha)	SB (%)	W-SB area	SW (%)	W-SW area	PL (%)	W-PL area	FB (%)	W-FB area	AW (%)	W-AW area	PB (%)	W-PB area
11623	1	2.9					1.0	0.3			7.0	2.1	1.0	0.3
11628	2	11.0					1.0	1.1			7.0	7.7	1.0	1.1
11695	3	5.2					3.0	1.5			5.0	2.6		
11697	4	0.2					1.0	0.0			7.0	0.2	1.0	0.0
11697	5	0.5					1.0	0.1			7.0	0.4	1.0	0.1
11697	6	0.6					1.0	0.1			7.0	0.4	1.0	0.1
12134	7	0.1					1.0	0.0			7.0	0.1	1.0	0.0
12134	8	10.7					1.0	1.1			7.0	7.5	1.0	1.1
12164	9	12.3					1.0	1.2			7.0	8.6	1.0	1.2
12330	10	1.5	1.0	0.1	1.0	0.1	3.0	0.4			5.0	0.7		
12330	11	4.2	1.0	0.4	1.0	0.4	3.0	1.3			5.0	2.1		
12331	12	5.8	1.0	0.6	3.0	1.7	3.0	1.7			3.0	1.7		
12365	13	6.1					1.0	0.6			7.0	4.3	1.0	0.6
12383	14	2.4					1.0	0.2			7.0	1.7	1.0	0.2
12393	15	0.4					1.0	0.0			7.0	0.2	1.0	0.0
12433	16	0.2					1.0	0.0			7.0	0.1	1.0	0.0
12463	17	0.1	1.0	0.0	3.0	0.0	3.0	0.0			3.0	0.0		
12467	18	1.3					1.0	0.1			7.0	0.9	1.0	0.1
12504	19	1.0					1.0	0.1			7.0	0.7	1.0	0.1
12519	20	1.1					1.0	0.1			7.0	0.8	1.0	0.1
12575	21	4.6	1.0	0.5	1.0	0.5	3.0	1.4			5.0	2.3		
12680	22	2.7	8.0	2.2	1.0	0.3	1.0	0.3						
12681	23	17.8					1.0	1.8			7.0	12.4	1.0	1.8
12694	24	6.0	1.0	0.6	1.0	0.6	3.0	1.8			5.0	3.0		
12721	25	1.9					1.0	0.2			7.0	1.3	1.0	0.2
12858	26	4.1	1.0	0.4	2.0	0.8	1.0	0.4			4.0	1.6	1.0	0.4
12942	27	0.5	1.0	0.1	3.0	0.2	3.0	0.2			3.0	0.2		
12946	28	10.7	1.0	1.1	3.0	3.2	1.0	1.1			4.0	4.3	1.0	1.1
12947	29	5.8	1.0	0.6	7.0	4.1	1.0	0.6	1.0	0.6				
13016	30	3.6					1.0	0.4			7.0	2.5	1.0	0.4
13036	31	0.7			1.0	0.1					7.0	0.5	1.0	0.1
13049	32	12.8					1.0	1.3			7.0	9.0	1.0	1.3
13156	33	2.5	1.0	0.2	1.0	0.2	3.0	0.7			5.0	1.2		
13210	34	0.1	8.0	0.1	1.0	0.0	1.0	0.0						
13271	35	0.2					1.0	0.0			7.0	0.2	1.0	0.0
Total		141.7		6.8		12.3		20.1		0.6		81.4		10.3
Dominance				5%		9%		14%		0%		57%		7%



Table A12. Example of species presence calculations.

BAPKEY	Patch-Id	AREA	SB	SB_AREA	SW	SW_AREA	PL	PL_AREA	FB	FB_AREA	AW	AW_AREA	PB	PB_AREA	BW	BW_AREA
11623.0	1	2.9					1	2.9			7	2.9	1	2.9	1	2.9
11628.0	2	11.0					1	11.0			7	11.0	1	11.0	1	11.0
11695.0	3	5.2	1	5.2			3	5.2			5	5.2			1	5.2
11697.0	4	0.2					1	0.2			7	0.2	1	0.2	1	0.2
11697.0	5	0.5					1	0.5			7	0.5	1	0.5	1	0.5
11697.0	6	0.6					1	0.6			7	0.6	1	0.6	1	0.6
12134.0	7	0.1					1	0.1			7	0.1	1	0.1	1	0.1
12134.0	8	10.7					1	10.7			7	10.7	1	10.7	1	10.7
12164.0	9	12.3					1	12.3			7	12.3	1	12.3	1	12.3
12330.0	10	1.5	1	1.5	1	1.5	3	1.5			5	1.5				
12330.0	11	4.2	1	4.2	1	4.2	3	4.2			5	4.2				
12331.0	12	5.8	1	5.8	3	5.8	3	5.8			3	5.8				
12365.0	13	6.1					1	6.1			7	6.1	1	6.1	1	6.1
12383.0	14	2.4					1	2.4			7	2.4	1	2.4	1	2.4
12393.0	15	0.4					1	0.4			7	0.4	1	0.4	1	0.4
12433.0	16	0.2					1	0.2			7	0.2	1	0.2	1	0.2
12463.0	17	0.1	1	0.1	3	0.1	3	0.1			3	0.1				
12467.0	18	1.3					1	1.3			7	1.3	1	1.3	1	1.3
12504.0	19	1.0					1	1.0			7	1.0	1	1.0	1	1.0
12519.0	20	1.1					1	1.1			7	1.1	1	1.1	1	1.1
12575.0	21	4.6	1	4.6	1	4.6	3	4.6			5	4.6				
12680.0	22	2.7	8	2.7	1	2.7	1	2.7								
12681.0	23	17.8					1	17.8			7	17.8	1	17.8	1	17.8
12694.0	24	6.0	1	6.0	1	6.0	3	6.0			5	6.0				
12721.0	25	1.9					1	1.9			7	1.9	1	1.9	1	1.9
12858.0	26	4.1	1	4.1	2	4.1	1	4.1			4	4.1	1	4.1		
12942.0	27	0.5	1	0.5	3	0.5	3	0.5			3	0.5				
12946.0	28	10.7	1	10.7	3	10.7	1	10.7			4	10.7	1	10.7	0	0.0
12947.0	29	5.8	1	5.8	7	5.8	1	5.8	1.0	5.8						
13016.0	30	3.6					1	3.6			7	3.6	1	3.6	1	3.6
13036.0	31	0.7			1	0.7					7	0.7	1	0.7	1	0.7
13049.0	32	12.8					1	12.8			7	12.8	1	12.8	1	12.8
13156.0	33	2.5	1	2.5	1	2.5	3	2.5			5	2.5				
13210.0	34	0.1	8	0.1	1	0.1	1	0.1								
13271.0	35	0.2					1	0.2			7	0.2	1	0.2	1	0.2
Total		141.7		53.7		49.3		141.0		5.8		133.1		102.9		93.2
Prsence				38%		35%		99%		4%		94%		73%		66%



Landscape Bioindicators

Patch Area and Patch Shape

Patch area reports mean patch size and shape at three levels: forest, broad composition class, and broad habitat type. The example shown below illustrates mean patch area and shape at the forest level (patches without consideration to habitat type, Figure A6, Table A13).

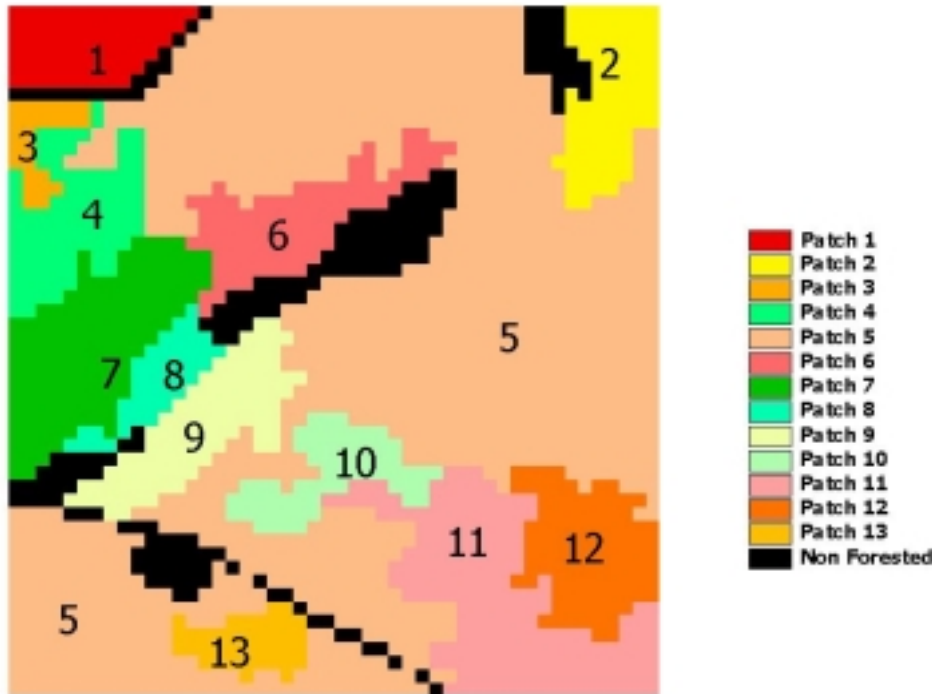


Figure A6. Example patch grid.

Table A13. Example of patch area and shape calculations.

Patch	Area (ha)	Area (m2)	Perimeter (m)	Shape Index
1	4.31	43125	1000	1.035
2	5.25	52500	1300	1.064
3	1.56	15625	800	1.097
4	5.88	58750	1950	1.127
5	77.19	771875	12300	1.185
6	5.81	58125	2050	1.137
7	8.88	88750	1800	1.072
8	2.63	26250	1200	1.121
9	6.00	60000	1800	1.111
10	4.00	40000	1500	1.119
11	11.81	118125	2800	1.122
12	6.13	61250	1500	1.075
13	2.44	24375	900	1.072
Mean Patch Area	10.91			
Mean Shape Index	1.103			



Mean Core Area

Mean core area statistics report at three levels: forest, broad composition class, and broad habitat type. The example shown below illustrates mean core area at the forest level (patches without consideration to habitat type, Table A14 and Figure A7).

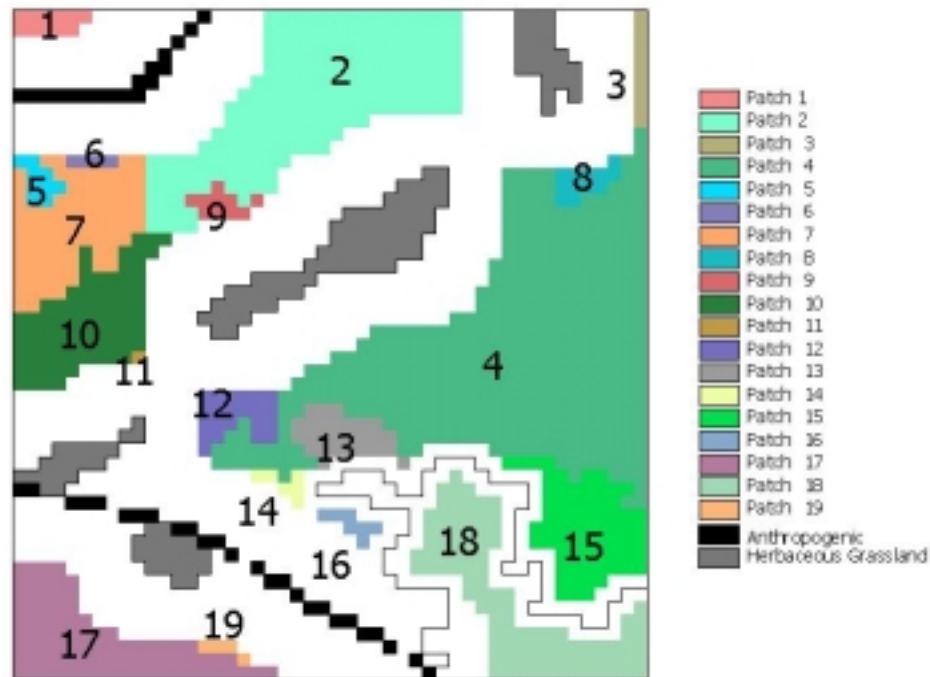


Figure A7. Example mean core area grid.



Table A14. Example mean core area calculations.

Patch	Area (ha)
1	0.7
2	12.4
3	0.6
4	24.8
5	0.6
6	0.3
7	5.1
8	0.8
9	0.6
10	4.8
11	0.1
12	1.4
13	1.7
14	0.4
15	4.3
16	0.4
17	5.3
18	6.1
19	0.3
Mean Patch Core Area	3.7

Contrast-Weighted Edge Length and Mean Edge Contrast Index

Contrast weighted edge length (CWEL) and mean edge contrast index (MECI) report the total edge weighted by a user-specified contrast value based on the adjacency of an edge between two habitat types. Contrast values are based on broad habitat and non-forested habitat types. The example below illustrates the CWEL and MECI calculations (Figure A8 and Table A15).

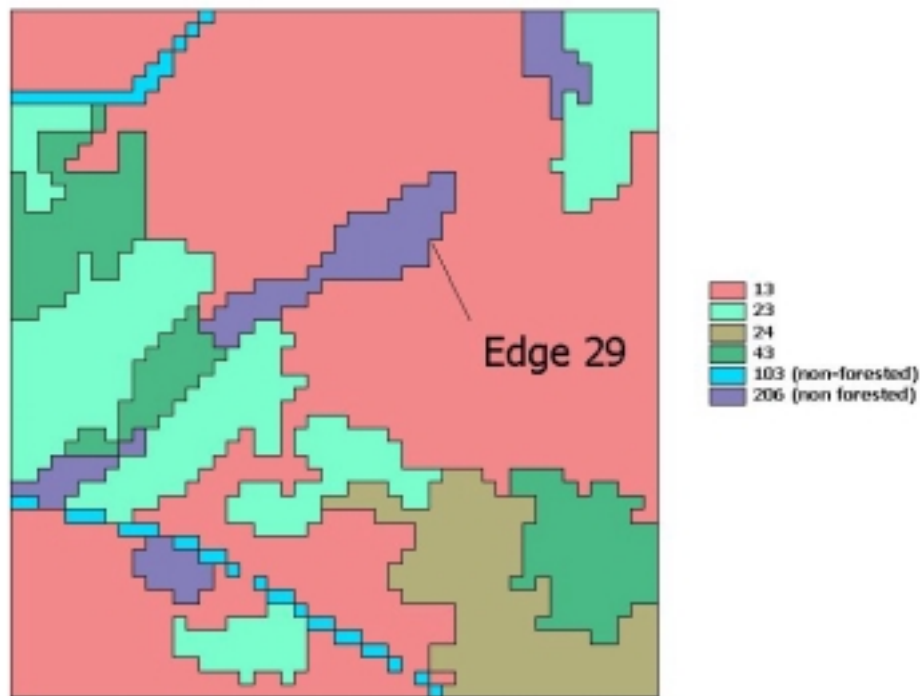


Figure A8. Example contrast grid.

**Table A15. Example contrast-weighted edge length and mean edge contrast index calculations.**

Patch Habitat	Patch Habitat	Edge-Id	Adjacency Code	Edge Length (km)	Contrast Weighted Edge Length
13	23	85	2	0.78	1.55
13	23	60	2	1.10	2.20
13	23	52	2	0.90	1.80
13	23	25	2	0.28	0.55
13	23	23	2	0.55	1.10
13	24	42	5	0.18	0.88
13	43	55	6	0.53	3.15
13	43	28	6	0.03	0.15
13	43	24	6	0.55	3.30
13	43	19	6	0.08	0.45
103	13	5	10	0.05	0.50
103	13	7	10	0.05	0.50
103	13	83	10	0.10	1.00
103	13	81	10	0.08	0.75
103	13	78	10	0.08	0.75
103	13	76	10	0.08	0.75
103	13	73	10	0.05	0.50
103	13	70	10	0.08	0.75
103	13	66	10	0.10	1.00
103	13	64	10	0.08	0.75
103	13	61	10	0.08	0.75
103	13	57	10	0.08	0.75
103	13	15	10	0.23	2.25
103	13	9	10	0.05	0.50
103	13	86	10	0.03	0.25
103	13	88	10	0.03	0.25
206	13	68	10	0.38	3.75
206	13	59	10	0.03	0.25
206	13	29	10	1.35	13.50
13	23	51	2	0.03	0.05
23	43	27	8	0.50	4.00
23	43	32	8	0.30	2.40
103	23	53	10	0.03	0.25
103	23	49	10	0.10	1.00
206	23	16	10	0.35	3.50
206	23	31	10	0.15	1.50
206	23	46	10	0.20	2.00
206	23	38	10	0.10	1.00
13	24	89	5	0.10	0.50
13	24	84	5	0.70	3.50
23	24	48	4	0.40	1.60
24	43	80	8	0.83	6.60
103	24	92	10	0.03	0.25
23	43	18	8	0.05	0.40
23	43	22	8	0.48	3.80
23	43	33	8	0.40	3.20
23	43	35	8	0.18	1.40
206	43	37	10	0.10	1.00
103	13	4	10	0.03	0.25
103	13	6	10	0.05	0.50
103	13	8	10	0.05	0.50
103	13	11	10	0.38	3.75
103	13	45	10	0.05	0.50
103	13	50	10	0.10	1.00
103	13	56	10	0.08	0.75
103	13	65	10	0.03	0.25
103	13	67	10	0.10	1.00
103	13	69	10	0.03	0.25
103	13	77	10	0.05	0.50
103	13	79	10	0.08	0.75
103	13	82	10	0.08	0.75
103	13	87	10	0.08	0.75
103	13	90	10	0.03	0.25
103	23	13	10	0.15	1.50
103	23	71	10	0.05	0.50
103	23	74	10	0.05	0.50



Adjacency Length

Adjacency length reports the edge length (km) for all broad habitat adjacency combinations. The example below illustrates the adjacency lengths for all habitat combinations (Figure A9, Table A16).

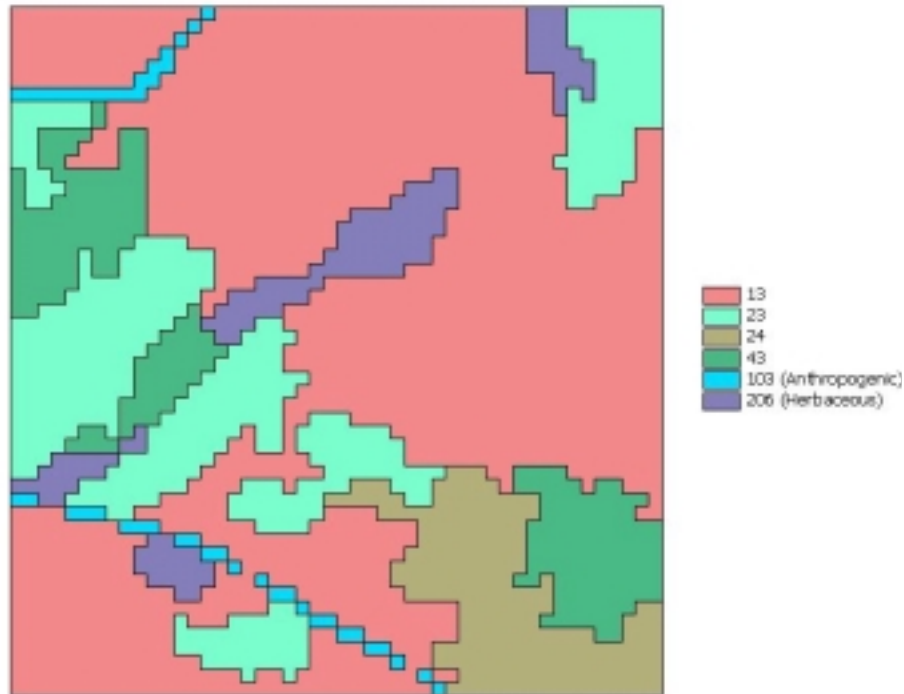


Figure A9. Example adjacency grid.

Table A16. Example adjacency length calculations.

Adjacency Code	Habitat	Habitat	Edge Length (km)
53	13	23	3.63
54	13	24	0.98
61	13	43	1.18
64	13	103	2.38
71	13	206	2.08
136	23	24	0.40
143	23	43	1.90
146	23	103	0.40
153	23	206	0.95
161	24	43	0.83
164	24	103	0.03
262	43	103	0.03
269	43	206	0.30
296	103	206	0.23

Mean Nearest Neighbour Distance

Mean nearest neighbour distance reports the average distance between patches of the same broad habitat type. Single patches of a particular habitat type or a patch with distances greater than 5,000 meters are assigned a nearest neighbour value of 5,000 m. The example shown below illustrates the nearest neighbour calculations for a pure conifer patch within the forest developmental stage (Figure A10, Table A17).

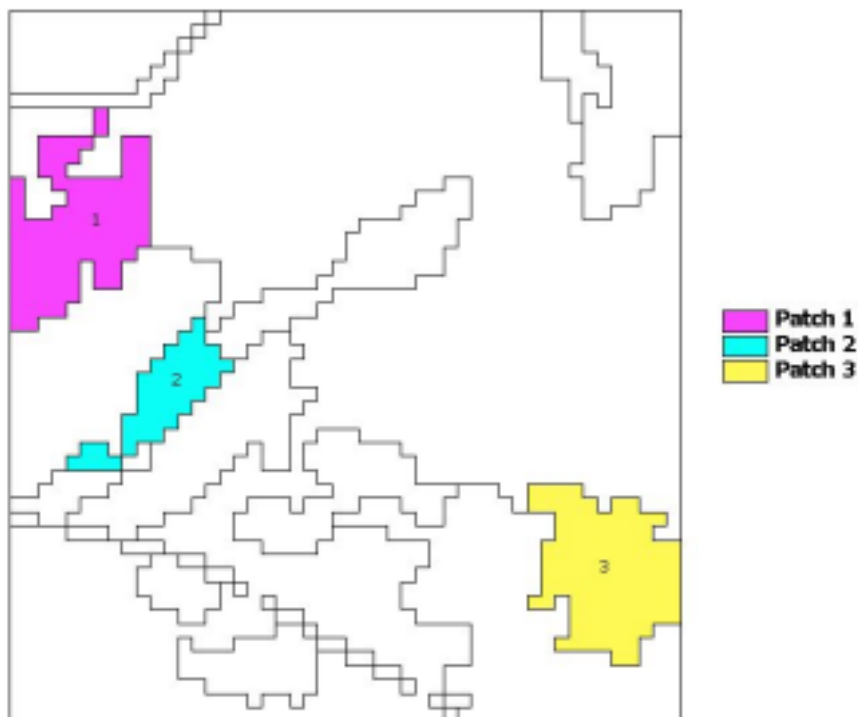


Figure A10. Example mean nearest neighbour grid.

Table A17. Example mean nearest neighbour calculations.

Patch	Nearest Patch	Distance to Nearest Patch
1	2	55
2	1	55
3	2	269
Mean Nearest Neighbour (m)		126

