

# **BAP REPORT #7: ECOSYSTEM DIVERSITY AND LANDSCAPE CONFIGURATION MODELS**

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

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**May 2000**

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## **7.1 INTRODUCTION**

In BAP, there are three levels at which biodiversity is assessed: ecosystem, landscape, and species. 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 species. The fine-filter analyses are accomplished through the use of species-based Habitat Supply Models (HSMs). Together, these models and statistics assist forest managers in determining the potential long-term effects of alternative management strategies on forest biodiversity and help to set priorities for research and monitoring to reduce the uncertainty associated with biodiversity conservation.



## 7.2 ECOSYSTEM DIVERSITY ANALYSES

Silvicultural practices will modify the distribution of ecosystems across space and in time. In order to monitor changes in the composition of the forests, BAP tracks the proportion of habitat types and diversity of the forest using the following metrics:

- ◆ Area-weighted Age;
- ◆ Tree Species Distribution; and
- ◆ Habitat Diversity.

### Area-weighted Age

The Area-weighted Age statistic reveals a single value at each time step throughout the simulation indicating the average age of the entire forest, weighted by area.

$$\text{Area-weighted age} = \frac{\sum_{i=1}^n (A_i * \text{Age}_i)}{A_{\text{total}}}$$

where:  
 $A_i$  = Area of patch  $i$ , where  $i = 1...n$  and  $n$ =total number of patches  
 $\text{Age}_i$  = Age of patch  $i$   
 $A_{\text{total}}$  = Total area (ha) within the FMA area, excluding non-forested area

### Species Distribution

There are several ways by which BAP displays the distribution of tree species within the FMA area:

- ◆ Species distribution by broad habitat type;
- ◆ Species presence; and
- ◆ Species dominance.

Species distribution by broad habitat type separates the forest into hardwood, hardwood-dominated mixedwood, softwood-dominated mixedwood, and softwood stands and provides an indication of the proportion of the entire FMA area expected to support each habitat type at each time step during the simulations. The species presence statistics give an indication of the extent of coverage

of each species over the landscape. They do not take into account the density of trees of that particular species but simply their presence. The species dominance statistics take into account both species presence and the dominance of each species (*i.e.*, comparative density). In this way, poorly represented species receive low ratings for the dominance statistics.

$$\text{Broad habitat type area}_k = \sum_{i=1}^n A_{ik}$$

where:  
 Broad habitat type area $_k$  = Total area (ha) of specific habitat type  $k$ , where  $k = 1...114$ , summarised to 4 classes for display purposes  
 $A_{ik}$  = Area (ha) of specific habitat patch  $i$  classed as specific habitat type  $k$ , where  $i = 1...n$

$$\text{Percentage by developmental stage}_j = \frac{\sum_{i=1}^n A_{ij}}{A_{\text{total}}} (100)$$

where:  
 Percentage by developmental stage $_j$  = Percentage of the FMA area covered by broad habitat type  $j$ , where  $j = 1...16$   
 $A_{ij}$  = Area (ha) of patch  $i$  classed as broad habitat type  $j$ , where  $i = 1...n$   
 $A_{\text{total}}$  = Total area (ha) within the FMA area, excluding non-forested area

$$\text{Presence}_m = \frac{\sum_{i=1}^n A_{im}}{A_{\text{total}}} (100)$$

$$\text{Dominance}_m = \frac{\sum_{i=1}^n (P_{im} * A_{im})}{A_{\text{total}}} (100)$$

where:  
 Presence $_m$  = The percentage of the FMA area on which tree species  $m$  is present, where  $m = 1...8$   
 Dominance $_m$  = The percentage of the FMA area on which tree species  $m$  is dominant, where  $m = 1...8$   
 $A_{im}$  = Area (ha) of patch  $i$  containing species  $m$ , where  $i = 1...n$   
 $P_{im}$  = Percentage of trees within patch  $i$  that are of species  $m$   
 $A_{\text{total}}$  = Total area (ha) within the FMA area, excluding non-forested area



## Habitat Diversity

Through the use of a matrix showing similarity between habitat types, habitat diversity was computed using similarity as a weighting factor. The diversity formula developed by Hendrickson and Ehrlich (1971) was used for this purpose.

The habitat diversity index considers the relative position of broad habitat types throughout the landscape using a rating of similarity between the habitat types as a weighting factor. The diversity equation outputs one single value at each time-step. It is a unitless value between 0 and 1 with a rating of 0 representing a very uniform landscape and a rating of 1 indicating the most diverse landscape possible. Incorporated into the index are both considerations of the number of habitat types present within the FMA area and the proportion of the landscape covered by each habitat type. Landscapes containing many habitat types distributed evenly across the area are considered more diverse than those dominated by one habitat type, yet containing small portions of others.

$$\text{Habitat diversity} = \frac{\sum_{i=1}^n A_{ij} * (\sum_{i=1}^n A_{ij'} * C_{jj'})}{(\sum_{i=1}^n A_{ij})^{1/2}}$$

where:

$A_{ij}$  = Area (ha) of patch  $i$  classed as broad habitat type  $j$ , where  $i = 1...n$ ;

$j = 1...16$

$A_{ij'}$  = Area (ha) of patch  $i$  classed as broad habitat type  $j'$ ,  $j' = 1...16$

$C_{jj'}$  = Contrast weight value between broad habitat type  $j$  and broad habitat type  $j'$



### 7.3 LANDSCAPE CONFIGURATION ANALYSES

In choosing bioindicators for use in the landscape configuration analysis, the BAP team wanted to ensure that the output would predict the impact of forest management on forest connectivity. It was decided that it would be best to use habitat types as the class attributes for the landscape analysis since they can be weighted by contrast. As well, different levels of distinction among the habitats can be used following the classification hierarchy. BAP's landscape configuration analysis was comprised of several types of biostatistical analyses (Riitters et al. 1995):

- ◆ Patch;
- ◆ Edge;
- ◆ Core area;
- ◆ Adjacency; and
- ◆ Nearest neighbour.

#### Patch

A patch can be defined as a certain area of land that has similar characteristics throughout. As described in BAP Report 3: Habitat Classification (Doyon 2000), the classification of patches includes the broad developmental (*i.e.*, opening, developing, forest, and old) and composition classes (*i.e.*, hardwoods, mixedwoods, and conifers). The combination of these factors yielded 16 patch types. The metrics were computed for each patch type and for all types combined. Only patches that change over time either by succession or disturbance were used in the patch analysis. Marsh and water bodies, for example, form "static" patches and were thus excluded from the analysis. The following patch metrics were computed:

- ◆ Patch area; and
- ◆ Patch shape (*i.e.*, perimeter/area ratio expression).

Patch shape is described by the index, Mean Patch Fractal Dimension (MPFD). MPFD is expressed as a single unitless value between 1 and 2. MPFD approaches 1 for shapes with very simple perimeters (e.g. squares and circles) and approaches 2 for shapes with highly convoluted perimeters.

$$\text{Mean patch area}_j = \frac{\sum_{i=1}^n A_{ij}}{n_{ij}}$$

$$\text{Mean patch fractal dimension}_j = \frac{\sum_{i=1}^n \left( \frac{2 \ln(0.25P_{ij})}{\ln A_{ij}} \right)}{n_{ij}}$$

where:  
 Mean patch area<sub>j</sub> = Mean patch area (ha) of broad habitat type j, where j = 1...16  
 Mean patch fractal dimension<sub>j</sub> = Mean patch fractal dimension index of broad habitat type j, where j = 1...16  
 A<sub>i</sub> = Area of patch i classed as broad habitat type j, where i = 1...n  
 P<sub>ij</sub> = Perimeter of patch i classed as broad habitat type j  
 n<sub>ij</sub> = Total number of patches i classed as broad habitat type j

#### Edge

Edge metrics are particularly meaningful since they can account for the level of contrast between two adjacent patches. This analysis uses information on both the developmental stage and tree species composition attributes from the AVI data to evaluate the contrast between two neighbouring polygons. For example, the edge between a patch that has been recently clearcut and a patch supporting mature forest would receive a high contrast rating. The metrics used were:

- ◆ Mean edge contrast index; and
- ◆ Contrast-weighted edge length.

The mean edge contrast index metric takes the average of the contrast ratings of all adjacent habitat patches within the FMA area and outputs a single unitless value between 0 and 1 which indicates the abruptness between edges. The sum of the lengths between all adjacent habitat patches, weighted by contrast, gives the contrast-weighted edge length.



## Adjacency

With the implementation of a forest management strategy, it is expected that the spatial distribution of habitat types will differ from that resulting solely from the NDR. Consequently, the proportion of adjacencies (adjacency being defined as an edge having a particular combination of one habitat type on one side with another on the other side) might be different. Many species use a combination of different habitats to fulfil their needs. Therefore, the adjacency of these required habitats is important. The adjacency metric investigated whether specific adjacency lengths would be different under particular forest management practices versus those expected under a NDR. Broad habitat types were used as the mapping units.

These statistics generate output that can be displayed in charts which indicate the total length of the adjacencies between two particular habitat types. There are a total of 325 codes that represent possible habitat type adjacencies.

$$\text{Adjacency}_f = \sum_{h=1}^n L_{hf}$$

where:  
 Adjacency<sub>f</sub> = Total edge length (km) f between two habitat types (includes forested and non-forested adjacency combinations), where f = 1...325  
 L<sub>hf</sub> = Length of patch edge h between two adjacent broad habitat types, where h = 1...n

$$\text{CWEL} = \sum_{h=1}^n (L_h * C_h)$$

$$\text{MECI} = \frac{\sum_{h=1}^n (L_h * C_h)}{L_{\text{total}}}$$

where:  
 CWEL = Contrast weighted edge length (km)  
 MECI = Mean edge contrast index  
 L<sub>h</sub> = Length of edge h between two different adjacent broad habitat types, where h = 1...n  
 C<sub>h</sub> = Edge contrast weight value of two adjacent broad habitat types  
 L<sub>total</sub> = Total edge length (km)

## Core area

Many species are negatively affected by edge and tend to prefer interior forest habitats (Robinson *et al.* 1995). Therefore, it is expected that the composition of the animal community of edge habitat will differ from that of an interior forest area (Harris 1988; Yahner 1988). Thus, it is important to track the availability of core habitat over time.

It is thought that the impact of edge on wildlife is linearly related to the abruptness of the habitat structure change at the edge. Therefore, the edge buffer width varies with contrast between adjacent habitat patches. Buffer widths are described in detail in BAP Report #8: Program Documentation (Rudy 2000). Core area was computed for each broad habitat type.

$$\text{Mean core area}_j = \frac{\sum_{i=1}^n CA_{ij}}{n_{ij}}$$

where:  
 Mean core area<sub>j</sub> = Mean core area (ha) of broad habitat type j, where j = 1...16  
 CA<sub>ij</sub> = Core area of patch i classed as broad habitat type j (refer to BAP report # 7: BAP Program Documentation for user specified buffer distances), where i = 1...n  
 n<sub>ij</sub> = Total number of patches i classed as broad habitat j



## **Mean Nearest Neighbour**

Following the theories of island biogeography (MacArthur and Wilson 1967) and of metapopulation (Kereiva 1990), a population using an isolated habitat is highly prone to local extinction. In addition, an organism using dispersed habitat patches may not be able to defend a sufficiently large territory from which to extract its needed resources (Keller and Anderson 1992). The nearest neighbour metric gives an indication of the dispersion of similar habitat types.

$$\text{Mean nearest neighbour}_j = \frac{\sum_{i=1}^n D_{ij}}{n_{ij}}$$

where

Mean nearest neighbour<sub>j</sub> = Mean nearest distance (km) j between patches classed as broad habitat type j, where j = 1...16  
D<sub>ij</sub> = Nearest distance between patch i classed as broad habitat type j and all other patches classed as broad habitat type j  
n<sub>ij</sub> = Total number of patches i classed as broad habitat type





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