LANDIS-II Output Leaf Biomass Reclass v1.0
Extension User Guide

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1 Introduction

This document describes the **Output Leaf Biomass** Reclass extension for the LANDIS-II model. Readers should read the *LANDIS-II Model User Guide* prior to reading this document. Other output extensions produce biomass output data (see *LANDIS-II Biomass Output User Guide*).

The output extension described herein uses cohort information at each site to classify every active site into a forest type defined by the User (see below). A dominance value is calculated for each species. The dominance value will be equal to the total biomass (B) ($g\ m^{-2}$) for the species or [B * -1], as determined by the User.

Each forest type has an associated group of species. The species dominance values are summed for each forest type to which they are assigned. Some species may have a negative dominance for a given forest type, as determined by the User. A site is assigned to (given the value of) the forest type with the highest total dominance value.

1.1 Acknowledgements

2 Input File

The input parameters for this extension are specified in one input file. This text file must comply with the general format requirements described in section 3.1 Text Input Files in the *LANDIS-II Model User Guide*.

2.1 LandisData

The first parameter is the title of the input file:

```
LandisData  "Output Leaf Biomass Reclass"
```

2.2 Timestep

The second parameter is the time step in years. For example:

```
Timestep   15
```

2.3 Reclass Map Descriptions

The next suite of parameters defines the desired reclassification(s) and must be preceded by the keyword ReclassMaps. The input is a table or tables describing the name of the reclassification, the forest types for the reclassification, and the species within (or excluded from) each forest type (Table 1).

Table 1.

Parameter	Data type	Example
Reclassification Name	string	Reclass1
Forest Type	string	MapleHardwood
Species	string	acersacc - pinubank

First, the Reclassification name must be given, followed by the symbol '->'. Do not use spaces in the reclassification name. Immediately following is the first forest type, such as NorthernPine or "Southern Oak" (quotes required if spaces used). Each subsequent forest type is listed on a separate line. Following the name of each forest type is a list of species to be included or excluded. If a species should contribute to the dominance value of a forest type, list the species name. If a species should be subtracted from a forest type, list the species name preceded by a '-' (negative) sign. **Not all species need be included and a species may be listed in more than one forest type.** An example reclassification:

```
       ReclassMaps
       >> Map Name     Forest Type     Species
       >> --------     -------------   -------
          reclass1 -> MapleHardwood  acersacc betualle -pinubank
                      NorthernPines  pinubank pinuresi pinustro
                      Oaks           querelli querrubr
```

If a site cannot be classified, or is not forested, the default value is zero (0). Otherwise, the map numbering will follow the order of the forest types (e.g., MapleHardwood = 1, NorthernPines = 2, Other = 3).

Note: If the reclassification calculates equal values for more than one forest type (a tie), then the forest type listed first among equals will be assigned to that cell.

Multiple reclassifications can be defined. Simply create a new reclassification name with forest types and species below the first reclassification defined.

2.4 Map Names

The next parameter, `MapFileNames`, describes where output maps are placed and their format. The first portion lists the directory where the maps should be places, relative the location of the scenario text file (e.g., `reclass/`). The second portion includes two variables for creating file names. `{reclass-map-name}` will be replaced with the reclass map name. `{timestep}` will be replaced with the output time step. Other characters can be inserted as desired. A meaningful file extension (e.g., `.gis`) should also be included. For example:

```
    MapFileNames  output/bio-{reclass-map-name}-{timestep}.img
```