

Spec2Harv

Converting Spectrum output to HARVEST input

Version 1.0a

Spectrum/HARVEST Linker
File Help

Global Parameters for HARVEST Script

Script Header Parameters

- Save Age Map Each Time Step
- Base Map Name:
- Allow Manual Harvests After Script Completes
- Create results table file (spreadsheet format)
- Random Number Seed (0 for computer generated):

Harvest Parameters

- Even age spatial dispersion:
 - Dispersed
 - Clustered
 - Oldest First
- Uneven age treatments simulated as:
 - Group Selection
- Time Step Length (yrs):
- Number of Time Steps (<= 20):

OK Cancel

User's Guide

Written by:

Eric J. Gustafson
Luke V. Rasmussen

North Central Research Station
USDA Forest Service



Larry A. Leefers
Department of Forestry
Michigan State University

MICHIGAN STATE
UNIVERSITY

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Version 1.0b

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Description

Spec2Harv was developed to automate the conversion of harvest schedules generated by the Spectrum model into script files that can be used by the HARVEST simulation model to simulate the implementation of the Spectrum schedules in a spatially explicit way.

Spectrum produces output files that include the acres to be treated with various timber harvest methods by Analysis Unit over the time period of the planning horizon. If the Analysis Units are designed to coincide with Management Areas (MA) and forest types (FT), the output can be converted into the parameters that HARVEST requires for spatial simulation. This conversion is not trivial because Spectrum produces treatment prescriptions for each Analysis Unit over all time periods in a single record, while HARVEST sequentially implements all treatments for all Analysis Units (MA and FT combinations) within each time period.

Spec2Harv was designed to automate the conversion process. Algorithms were developed to interpret the Spectrum output and to automatically create a HARVEST script file. Script files eliminate the need to manually specify the harvest parameters for each Analysis Unit, saving time and reducing the risk of typographical errors. Because Spec2Harv is designed to produce input files for the HARVEST model, the user should be familiar with the HARVEST v6.0 User's Guide (Gustafson and Rasmussen 2002), which can be found at http://www.ncrs.fs.fed.us/4153/Harvest/v60/v6_0.asp.

Spec2Harv was written by Luke Rasmussen in Fortran 95 using the Winteracter Windows libraries. Larry Leefer, Eric Gustafson, Phil Freeman and Luke Rasmussen developed the conceptual design.

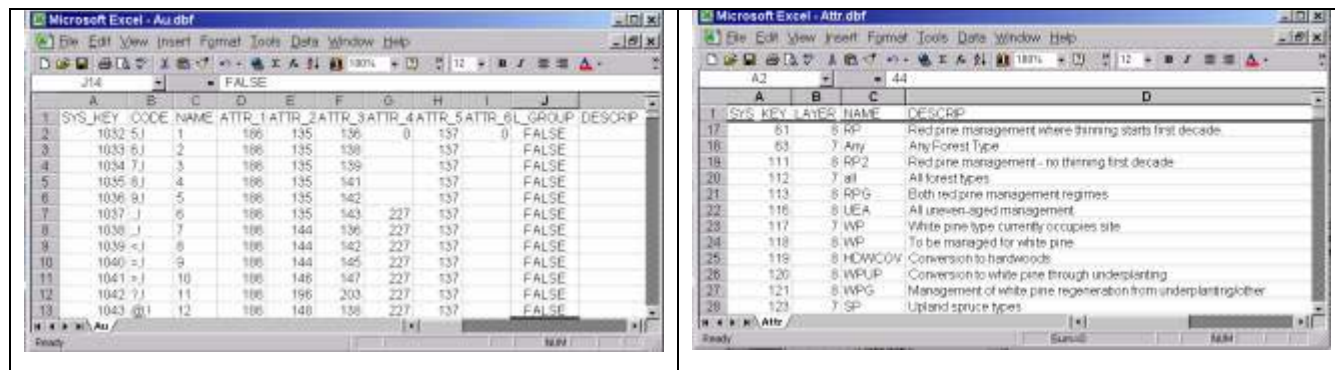
Address comments and questions to:

Eric Gustafson
USDA Forest Service
North Central Research Station
5985 Highway K
Rhinelander, WI 54501-9128
egustafson@fs.fed.us

The most recent version of Spec2Harv and its documentation may be obtained from the North Central Research Station Web site: <http://www.ncrs.fs.fed.us/4153/software.asp>. Spectrum can be downloaded at the USDA Forest Service Inventory and Monitoring Institute (IMI) Web site: http://www.fs.fed.us/institute/planning_center/download_center.html.

This guide has been formatted for double-sided printing and insertion into a loose leaf binder.

Attr.dbf: This file, along with Au.dbf, translates the arbitrary values for Analysis Units from the comma-delimited file (above) into strings that the user and HARVEST can readily interpret. This file is most often named ATTR.DBF and is produced by Spectrum.



Forest Type Lookup Table: This file is a user-defined lookup table. For each forest type, the user must enter into the first column (labeled FTMAPVAL) the integer value used in the Forest Type Map to represent each forest type. The second column (labeled FTDESC) holds a character string (up to 30 characters) describing the forest type. This string is not used by either HARVEST or Spectrum, but Spec2Harv displays it so that you will not have to interpret the cryptic codes used by Spectrum. The third column (labeled SPECVAL) holds the value that is used to represent the forest type in the Attribute Database File (Attr.dbf). For example, a Spectrum user may create a harvest schedule for red pine, which is represented in the Attribute Database File as RP. Let's say that the user arbitrarily coded red pine as the integer 1 in the Forest Type Map. The Forest Type Lookup file would have the following entry for the red pine type:

1	Red Pine	RP
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Some hints for generating this file:

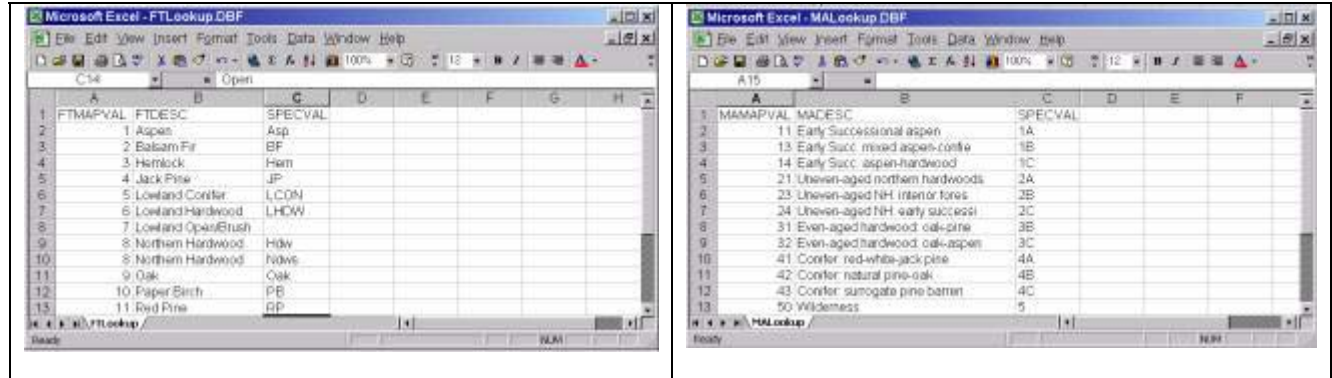
1) If you use a forest type more than once and give it more than one name (i.e., Red Pine as RP, rp, and RdPn), you must create a separate entry for each definition. The example given would have the following entries:

1	Red Pine	RP
1	Red Pine	rp
1	Red Pine	RdPn

2) Use the template (FTLookup.dbf) provided with the Spec2Harv distribution, or be sure to use the following file structure. Otherwise your lookup table will generate an error.

The file format is as follows:

Column Title: FTMAPVAL	Column Title: FTDESC	Column Title: SPECVAL
Field Type: Integer	Field Type: Character	Field Type: Character
Field Length = 3	Field Length = 30	Field Length = 6



Management Area Lookup Table: This file is a user-defined lookup table and has a structure similar to the Forest Type Lookup File. The user must enter in the first column (labeled MAMAPVAL) the integer value that will be used to represent the Management Area in the Management Area map used by HARVEST. The second column (labeled MADESC) holds a string describing the Management Area. The third column (labeled SPECVAL) holds the value representing the Management Area that appears in the Attribute Database File. For example, a Spectrum user may create harvests in a certain Management Area represented in the Attribute Database File as 1A. Let's say that this particular Management Area has been given an integer code of 11. The Management Area Lookup file would have the following entry for this Management Area:

11	Early succ. aspen	1A
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Some hints for generating this file:

1) If you use a Management Area more than once and give it more than one name (i.e., Calling a Management Area both 1A and 1a), you must create a separate entry for each definition. The example given would have the following entries if Management Area 1A was coded as 11:

11	Early succ. aspen	1A
11	Early succ. aspen	1a

2) Use the template (MALLookup.dbf) provided with the Spec2Harv distribution, or be sure to use the following file structure. Otherwise your lookup table will generate an error.

The file format is as follows:

Column Title: MAMAPVAL	Column Title: MADESC	Column Title: SPECVAL
Field Type: Integer	Field Type: Character	Field Type: Character
Field Length = 3	Field Length = 30	Field Length = 6

Forest Type Map file: This map contains cells whose values are an integer code value (between 0 and 255) denoting a specific forest type. This map should also contain at least one non-forest type to be used in the delineation of forest interior. Any features that will require non-harvest buffers to be maintained next to them (e.g., streams or roads) must also be included in this map. This map is in Erdas *.gis format and is used by HARVEST to apply harvest rules to the correct forest type. See the HARVEST documentation for details on the preparation and use of this map. HARVEST does not allow you to attach labels to the integer values in this map, so you must keep their meanings clear as you reference

these values when using Spec2Harv and HARVEST. Because Spectrum uses areal units of acres, the Forest Type Map must also reference area in units of acres. (Areal unit information is stored in the header of Erdas *.gis files and is specified when the file is created).

Table 1. Summary of input files needed by Spec2Harv. See above for more details.

File Type	Example File Name	Description
Spectrum comma-delimited file	Comadel_alt4.txt	Harvesting information produced by Spectrum
Spectrum Attribute file	Attr.dbf	Translates arbitrary values for Analysis Units
Spectrum Analysis Unit file	Au.dbf	Database to hold data for each Analysis Unit
Forest Type Lookup Table	FTLookup_alt4.dbf	User-defined Forest Type lookup table
Management Area Lookup Table	MALookup_alt4.dbf	User-defined Management Area lookup table
Forest Type Map file	P-Ftype.gis	Map of forest type and other land cover

Generating HARVEST Scripts using Spec2Harv

FILE

This menu item contains the Spec2Harv commands.

New

This command initiates the process of converting Spectrum output to a HARVEST input script.

You will be asked to specify the **Comma-delimited text file** output from Spectrum. This file is specified using a common Windows File selection dialog. You will then be asked to select the **Analysis Unit file** (.dbf extension), followed by the **Attribute file**.

Two File selection dialog windows will ask you to specify the FT Lookup and MA Lookup files. These files are prepared using a spreadsheet or database management program as described under the *Preparing Data* section.

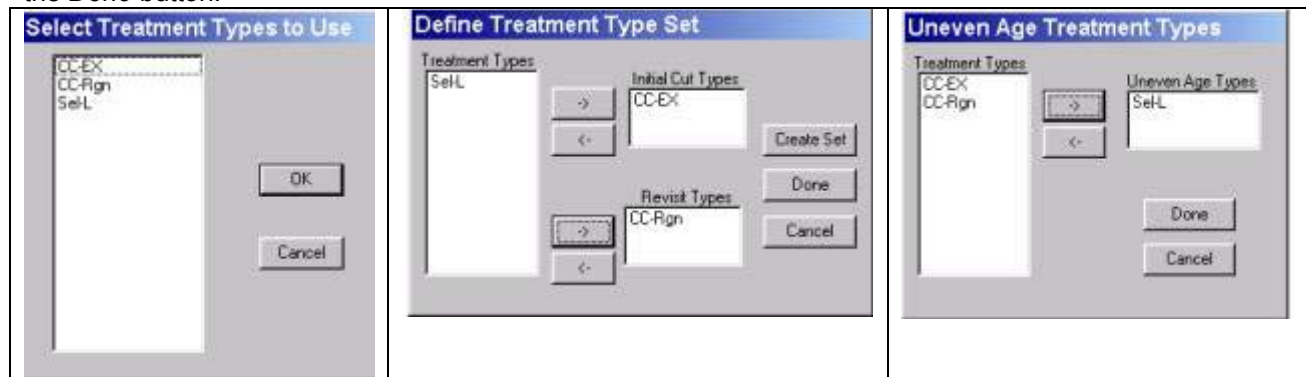
Before Spec2Harv can scan these files to see what Spectrum Treatment Types are contained in the Spectrum output, you must tell Spec2Harv what fields to use to find the Analysis Unit names, Treatment Types, and the Area Type (areal units used, such as ACRES). Highlight the correct fields in the list presented for each field (use the Ctrl key for multiple selections), then click *OK*.

Spec2Harv will scan these files to determine the Spectrum Treatment Types contained in them. A list box will appear, allowing you to **select the Treatment Types** that you wish to simulate with HARVEST. Do not select Treatment Types that you do not wish Harvest to simulate (i.e., that should be ignored).

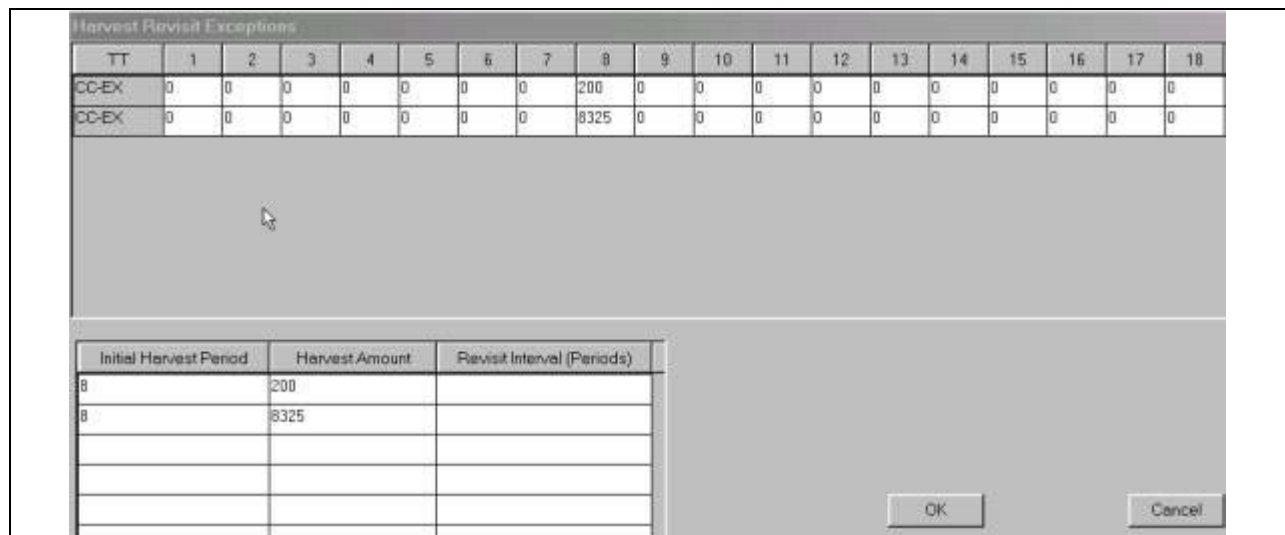
Sometimes these Treatment Types appear in pairs, where one type refers to initial harvest cuts and another refers to subsequent cuts (revisits) in the same stands. For example, "CC-EX" may refer to initiation clearcuts and "CC-Rgn" may refer to the subsequent re-entry cuts in those stands. The "Define

Treatment Types” dialog is used to identify these paired Treatment Types. Highlight the initial cut Treatment Type and click on the arrow button pointing to the right. This will copy that Treatment Type in the *Initial Cut Type* field. If you inadvertently copy the wrong field, highlight the errant field in the right-hand box and use the arrow button pointing to the left to remove the incorrect field. Similarly, highlight the Treatment Type for subsequent revisit harvests and move it into the *Revisit Type* field. When the correct fields are in the *Initial Cut Type* and *Revisit Type* fields, press the *Create Set* button. If there are other paired Treatment Types to specify, repeat this process. When all pairs are specified, press the *Done* button.

Spec2Harv next asks you to identify any Treatment Types that will be simulated using the Group Selection dispersion method (in HARVEST), to produced uneven aged stands. Use the arrow buttons to move Treatment Types into and out of the box on the right. When the list in the right box is correct, press the *Done* button.



Spec2Harv infers the revisit intervals (length of time between harvest events in a given Analysis Unit) for any Treatment Type pairs. HARVEST assumes that the revisit interval for a particular Analysis Unit (if there is one specified) does not change throughout all time steps. If Spec2Harv is unable to infer a revisit interval, a **Harvest Revisit Exception** dialog box will appear and display the record from the comma-delimited file that it is having trouble interpreting. You will be given the **time step when the initial harvest is to occur** and **harvest amount**. From these you should manually enter the **revisit period (in years)**. You may also split up the harvest amounts and put them in the blank fields below, but the total harvest amount from these fields cannot be larger than the original harvest amount.



Spec2Harv will ask you to select a disaggregation option.

Results spatially disaggregated: Select this option if the comma-delimited file contains only harvest prescriptions for the mapped area that will be simulated with HARVEST. That is, any spatial subsetting has already been done before the comma-delimited file was generated by Spectrum.

Spatially disaggregate results with level: Select this option if you want Spec2Harv to use only a subset of the records in the comma-delimited file. For example, if you only want to simulate harvesting on one of several Ranger Districts. The comma-delimited file must have a field that identifies the spatial area (e.g., District) you wish to simulate with HARVEST.

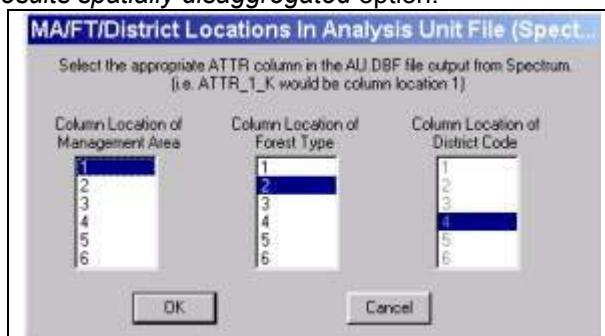
Spatially disaggregate with crosswalk table: This option is currently not functional.

You will then be presented with a dialog containing three list boxes. You may need to examine the file Au.dbf to determine the correct column numbers to enter. Select one item from each list, as described below. **Note: Spec2Harv is interested only in ATTR columns; ATTR_1_K is column 1, even though other columns may precede it in the .dbf file.**

Column location of Management Area: This specifies the data field column in the Analysis Unit file that contains the Management Area code. The LAYER number in the Attr.dbf file identifies the column number for Management Area.

Column location of forest type: This specifies the data field column in the Analysis Unit file that contains the forest type code. The LAYER number in the Attr.dbf file identifies the column number for forest type.

Column location of District Code: This specifies the data field column in the Analysis Unit file that contains the code that allows Spec2Harv to select a subset of the records in the comma-delimited file to be simulated by HARVEST. This typically is used to select a subset made up of specific spatial portions of the land base, such as a Ranger District or other ownership block. This list box will be disabled if you previously selected the *Results spatially disaggregated* option.



If you selected the *Spatially disaggregate results with level* option, Spec2Harv will then ask you to specify the values in the District Code field that you want to include in the HARVEST simulation. The LAYER number in the Attr.dbf file identifies the column number for District.

Spec2Harv will then ask for the **Forest Type Map file**. This should be the same file you will use for the simulations with HARVEST. Spec2Harv will scan the map for the forest type values present in the map. **Note: it is critical that the units for cell width (meters or feet) and area (hectares or acres) in the Forest Type Map are the same as the units coming out of the Spectrum model.**

You will then be asked for a **Defaults file**. This file will likely have meaningful numbers only after you have completed entering all the Spec2Harv parameters during a prior run. The file contains values for harvest parameters by treatment and forest type that have been saved from a previous Spec2Harv run. These values will appear as default values in dialog boxes during your Spec2Harv session, potentially

saving you a lot of time entering parameters. Use of this file is optional (if you choose not to use this file, press *Cancel* when prompted).

The answers to the next several questions asked by Spec2Harv will be used by HARVEST when it begins to run the script file generated by Spec2Harv:

Institutional Memory file: This file (.mem extension) is used by HARVEST to keep track of which stands are harvested, when they were harvested, and when they should be harvested again. You should generally not specify the name of an existing file, because it will be overwritten. Give attention to the directory to be specified. The file will be created by HARVEST at run-time in the directory you specify here.

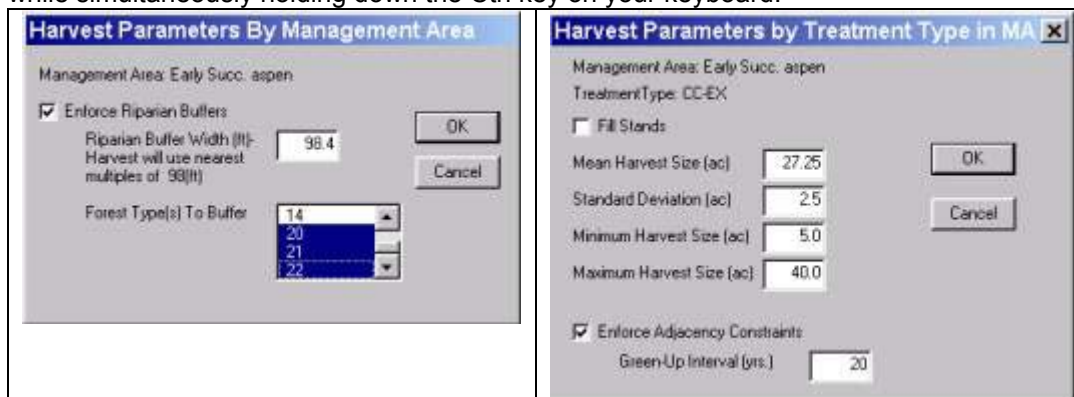
Global parameters: These are parameters and file names needed by HARVEST. See the HARVEST User's Guide for more detail on HARVEST parameters and their use.

- *Save age map at each time step:* Check this box if you want the entire time series of age maps saved at each time step of the HARVEST simulation. These files will be created by HARVEST at run-time using the base name you have provided, with the time step number appended to it (i.e., LabRun00.gis, LabRun01.gis).
- *Allow manual harvests after script completes:* Check this box if you will want to simulate additional time steps beyond those that will be simulated by the script generated from the Spectrum output.
- *Create results table file (spreadsheet format):* Check this box if you want a table of the parameters and results of the HARVEST simulation saved in a file that can be imported into a spreadsheet. This is useful for viewing and summarizing the HARVEST results.
- *Random number seed:* This integer value may range from -2^{16} to $+2^{16}$. It is used to initialize the random number sequence. If you wish to exercise control over this sequence for replication purposes, specify a value. If you enter a zero, HARVEST will generate a seed value using the system clock each time the script is run.
- *Even age spatial dispersion:* This is an option within HARVEST that controls the spatial dispersion of even aged treatments. See the HARVEST documentation for details.
- *Uneven age treatments simulated as:* This is simply an informative label. The uneven age Treatment Type(s) you specified earlier are interpreted as 'Group Selection' by Spec2Harv and HARVEST.
- *Time step length:* Specify the length of time that each Spectrum time period represents. This is typically 10 years (1 decade).
- *Number of time steps:* Enter the number of time periods represented in the Spectrum output (e.g., 15 decades).

You will now be presented with a series of dialog boxes requesting harvest parameter information for each Management Area and Treatment Type found in the comma-delimited file. Spec2Harv loops through each Management Area and Treatment Type sequentially.

For each Management Area you will be asked to consider the following option:

- **Enforce riparian buffers:** This option requires that cells cannot be cut if they are within the specified riparian buffer width. Note that HARVEST will round the value you enter here to the nearest multiple of the cell width. The units of width (m or ft) are those found in the Forest Type Map. You must also specify the cell value(s) in the Forest Type Map that represent(s) riparian areas. To select multiple values, click on the first value, and then select the additional value(s) while simultaneously holding down the Ctrl key on your keyboard.

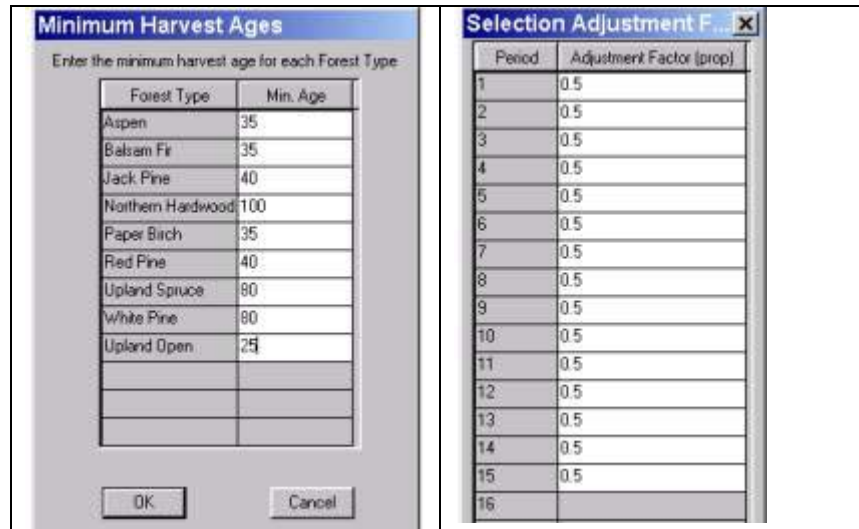


For each Treatment Type (within a Management Area), you will be asked:

- **Fill stands:** This will disable the rest of the size fields on the dialog. This option will cause HARVEST to sequentially harvest entire stands until the total harvest amount from the Spectrum input is reached.
- **Mean harvest size:** This specifies the mean of the harvest size distribution. The units of area (ha or ac) are those found in the Forest Type Map.
- **Standard deviation:** This specifies the width of the harvest size distribution.
- **Minimum and maximum harvest size:** These values can be used to truncate either (or both) tails of the harvest size distribution.
- **Enforce adjacency constraints:** This option will require that stands selected for even age treatment may not be adjacent to any stand that is less than the age you specify in the *Green-up interval* field.

When you have completed the loops through all the Management Areas and Treatment Types, you will be asked to specify the **minimum harvest ages** for each forest type. HARVEST will not cut stands younger than the ages you specify here. These ages should correspond with the minimum ages used in Spectrum. **Note: HARVEST will simulate the Spectrum harvest schedule, but will not perfectly mimic it.**

Selection harvests can be approached in two ways. First, Spectrum model results may generate actual selection harvest acres treated (i.e., openings created). If this approach is used, **Selection harvest adjustment factors** are simply "1.0". That is, for every Spectrum acre, there will be one HARVEST acre. A second approach is to model a broader area that receives selection harvests in Spectrum, but that has only a portion of the area actually harvested. For example, a value of 0.5 will cause 50% of the Spectrum harvest area to actually be cut in each time period (see example in adjoining figure).



The next step is to provide a directory and **name for the script file** that Spec2Harv will now create. After you provide a name, Spec2Harv will generate a script file. This will not take much time, because Spec2Harv has been generating and saving information throughout the process of interacting with you.

Spec2Harv will finally ask you for a directory and file name to **save defaults**. This will enable you to use the parameter information you have just entered for use in future Spec2Harv runs, potentially saving you a great deal of time. If you do not wish to save defaults, press *Cancel*.

Exit

This option will close the Spec2Harv program.

HELP

The help menu provides access to an online version of the document you are now reading. You may also determine the version of Spec2Harv you are using by selecting *About*.

Common Problems and How to Fix Them

Problem: The script will not run in HARVEST.

Fix: Check to make sure that the Management Area Map and the Forest Type Maps that you used to create the Spectrum output have the same values as the maps used in HARVEST.

Problem: After you select the columns in the Au.dbf file where the data for Management Area, forest type, and District code are located, Spec2Harv freezes.

Fix: Verify that you have selected the correct fields and that the commadel.txt and *.dbf files are from the same Spectrum model run.

References

Gustafson, E.J. and L.V. Rasmussen. 2002. HARVEST for Windows: User's guide. Published on INTERNET server, [http://www.ncrs.fs.fed.us/4153/Harvest/v60/Harv60 User.pdf](http://www.ncrs.fs.fed.us/4153/Harvest/v60/Harv60%20User.pdf).