NFI — the Native Forest Inventory System

The Native Forest Inventory System comprises the Native Forest Inventory Database ($NFI) and a suite of programs to select and report inventory data.

A summary of the NFI suite of programs is given in this manual, or can be obtained by typing doc. The best way to learn about these is to try them — as long as you don't have write permission (turned on), you cannot do any harm.

Unix Basics

You need to have a basic knowledge of the Unix system, especially of files, pipes, and input and output re-direction. On a Unix system, programs obtain data from three sources:

— the command line (which you typed to invoke the program),
— standard input (your terminal, unless re-directed), and
— files.

Programs can direct output to three sinks:

— standard output (your terminal, unless re-directed),
— error output (always your terminal, cannot be redirected), and
— files.

Input and output re-direction allows standard input and output to be diverted from your terminal to files or other programs.

- Input re-direction takes standard input from the specified file rather than from your terminal:
$$program < file$$

- Output re-direction diverts the standard output from your terminal to the specified file:
$$program > file$$

- Pipes direct the standard output from one program to the standard input of another:
$$program1 \mid program2$$

These can be used simultaneously:
$$program1 < file1 \mid program2 \mid program3 > file2$$
This is an enormously powerful feature, as it allows a number of simple programs to be joined together into a pipeline which performs more complex tasks.

Unix employs a hierarchical file system, and files can be addressed using a relative name, or their full name. The delimiter / is used to indicate directories. Thus

— *file* refers to a file in the current directory,

— *directory/file* refers to a file in a sub-directory of the current directory, and

— */directory/directory/directory/directory/file* is the full name of a file (note that it commences with /).

Directories may be nested as deeply as you wish.

Unix allows the use of "wild cards" to abbreviate filenames. There are three forms:

* is a wild string, and matches any string (including null strings). Thus *e** will match any filename commencing with *e*.

? is a wild character, and matches any single character.

[*range*] allows you to specify a range of characters to be matched. For example *test.data[2–4,a–c]* is the same as

test.data2 test.data3 test.data4 test.dataa test.datab test.datac

but saves a lot of typing.

These can be used together, eg. *?[0–9] matches any filename that is at least two characters long and ends with a digit.

To see how any abbreviation is expanded, use

echo *abbreviation*

If you don't understand these details, ask one of your colleagues before you go much further.

The $NFI *Database*

Each inventory plot is stored in its own file which is named after the plot number. The standard way to refer to this number is by using the 10 character reference indicating District, Year of measure and Plot number: SS/YY/NNNN (eg. 01/78/0001). Several alternatives are possible, and the one restriction is that the plot number must have no embedded spaces:

8 digit plotnumber	01780001
10 character filename	01/78/0001
$NFI pathname	$NFI/01/78/0001
Full pathname	/usr3/nfi/data/01/78/0001
Any above with comments	01/78/0001:Some comment here
	01/78/0001!Some comment here

The plot numbers may be generated by some Unix utility such as grep or find, and these formats are acceptable. grep may print the filename followed by a colon and a line of text, and extr may print the filename followed by an exclamation (!) and text. These are suitable too, the colon or exclamation and anything following are ignored.

The following District codes are used in the NFI System.

01	Atherton	08	Maryborough
02	Beerburrum	09	Monto
03	Brisbane	10	Murgon
04	Dalby	11	Rockhampton
05	Gympie	12	Roma
06	Imbil	13	Yarraman
07	Ingham		

The NFI System

The NFI System comprises computer programs which perform several functions, including inserting, modifying and checking data; producing and modifying lists of inventory plots; generating reports and enabling interactive investigative analyses. These include programs to

Provide on-line documentation: doc.

Modify data in the database, available only to authorized users: conv, cypsi, pled, renum and vi.

Validate data in the database: valid and spock.

Create lists of inventory plots: find, get, grep, sample and search.

Add details to lists of inventory plots: dist and extr.

Modify lists of inventory plots: choose, except, exrip, sneer, sort and strat.

Produce reports from lists of inventory plots:

Tabular reports on the distribution of inventory plots: locdist, nodist, ocdist and sfdist.

Reports on the range of attributes encountered: spock.

Individual plot reports: rip and rol.

Maps showing location or other attributes of plots: map.

> **NB: map, rip, rol** and **sample** do not write to standard output, but create a file and direct the file to the printer. Thus there is no point in directing standard output from these files to **lp**.

Modify individual plot reports: **ilv** and **invis**.

Produce other reports: **spplst** and **voltab**.

Perform growth forecasts and yield calculations: **sked** and **grop**.

Interactive investigation of tree growth and silviculture: **whatif**.

Using the NFI System

To use the Native Forest System, you must be an authorized user of the Department's Unix system (you must have an account on qficus), and must ensure the following commands are inserted in your .profile:

> **PATH=/usr3/nfi/bin:$PATH**
> **NFI=/usr3/nfi/data**
> **TODAY='date '+%d/%h/%y'"**
> **export PATH NFI TODAY**

This will provide you with read-only access rights to all parts of the NFI System. Write permission will only be granted to individuals with a demonstrated need for this facility. If you want write permission, mail your case to **nfi**.

The NFI System has on-line documentation describing every aspect of the system — data and software. To obtain the introductory documentation, simply type **doc**. More detailed documentation can be obtained by doing **doc** *program-name*.

Should you discover any errors or peculiarities in the NFI System, please mail any evidence to **nfi**.

NFI Programs:

choose plots satisfying specified criteria.

dist computes the distance of inventory plots from a specified location.

doc provides on-line documentation on running programs.

except is a filter which removes specified plots from a list of plots, and can be used to exclude unrepresentative plots from standard reports.

extr extracts information from the NFI database for further interrogation, or for reporting by **map** or **rol**.

get produces a list of inventory plots within the database or any part of it.

grop grows individual plots and writes them in NFI format to allow validation of growth models and processing of projected data by other NFI programs.

ilv interleaves output files, and is useful for customizing **rip** outputs.

invis takes tabular input data (e.g. from **rip**) and creates a visicalc file.

locdist reports the number of plots for each location.

map produces line printer maps of inventory data.

nodist summarizes the number and distribution of plots in the NFI database.

pled enables plot data to be edited and validated.

renum renumbers plots in the NFI database.

rip produces one page reports for selected plots.

rol produces one line summary reports for selected plots.

sample summarizes the values used in a specified field.

search prints plots in specified parts of the database which contain a given string.

secal calculates sampling errors.

sked enables yield forecasts to be prepared using yield scheduling or cutting cycle analysis.

sfdist reports the number of plots for each State Forest or Timber Reserve.

sneer selects inventory plots nearest to a given AMG reference.

spock shows the species occurrence by Districts.

spplst prints the Departmental species list.

strat takes a list of plots, attempts to stratify these, and generates an input file for **rip**, complete with stratum report requests.

valid is a filter which selects only those plots with invalid entries, and writes the nature of the error as a comment.

voltab prints volume tables.

whatif enables interactive use of the growth models for investigating silvicultural alternatives.

Unix Utilities:

find *directory* –type **f** –print lists all the filenames in *directory* (including any sub-directories).

grep *pattern files* searches files to find the specified *pattern*.

head –*n files* prints the first *n* lines of each of the *files*.

ls –**R** –**C** *directory* produces a compact listing of all files in the *directory*, recursively listing all sub-directories.

sort is useful for both sorting lists of files, and for sorting information produced by **extr** and reported by **rol**.

More Information?

For more information, type **doc** *name*, where *name* may be any of the NFI programs listed above, any Unix utility, **NFI** or **fields**. **NFI** contains general information about the NFI system, and **fields** gives the standard field definitions used in many of the NFI programs.

extr options

extr extracts information from the inventory plots specified on standard input, and writes the information to standard output. The *options* determine what information is extracted.

Normal usage is:

cat *list* | **extr** *options* | **sort** *s-options* | **rol** *r-options*

The *list* may be compiled using get, search, find, grep, an *editor* or may be derived from the *Area System*.

Several *options* are available:

–c is only relevant when field 8 (Comments) is being extracted, and causes extr to take the comments from the standard input rather than from the inventory data.

–e *file* will cause extr to ignore the standard equation file, and to use the alternative provided in *file*. The name *file* may comprise up to 24 characters, and the format of the file should correspond to the instructions in ham.codes.

–one indicates that one-way, rather than two-way volume equations are to be used.

–r indicates that you intend to sort into descending (sort –r), rather than ascending order.

–n and **+n** determine the inclusion or otherwise of fields in the reports produced. *n* must be a valid field number (0–17). Invalid field numbers are ignored.

  +n indicates that only the nominated fields are to be included.

  –n indicates that everything except the nominated fields are to be included. Caution: Unless used carefully, this is likely to produce output with more information than you need, and which is so wide that it is printed across two pages, making it difficult to read.

  Some field numbers may have arguments:

  +7 and **+8** (Location and Comment fields respectively) may be followed by an argument indicating the number (in the range 1 to 48) of characters to be extracted from that field. Defaults are 32 and 25 respectively, and are normally adequate.

  +9 (Species composition) may have three arguments.

      — The first indicates the number of species to be extracted, and values in the range 1 to 99 are valid (Default 4).
      — The second may be **a, b** or **v** indicating that stand composition (%) is to be calculated by numbers, basal area or volumes respectively (Default b).
      — The third argument indicates the minimum Dbh to be included in the stand composition calculation, and values in the range 0 to 99 are valid (Default 20).

  +10 or **+11** (Total stocking and basal area respectively) may have one argument indicating the minimum Dbh to be included in the calculation for that field. Values in the range 0 to 99 are valid (Default 20).

  +12 to **+17** (Merchantable stocking, basal area, volume and Visually Thinned stocking, basal area and volume respectively) may have two arguments.

      — The first is the minimum Dbh in the range 0 to 99 (Default 20).
      — The second is a product list of products included and may include up to four of **P, S, R, C, U** for Pole, Sawlog, Round, Chip and Useless respectively (Default PS). The product list should only be specified once, even if more than one argument in the range 12–17 is used. If they differ, the last list specified will be used for all arguments.

  It is assumed that a minimum dbh specified for any field also applies to all subsequent fields. Hence, if you wish to vary these dbh limits, you should specify them in order.

Examples

Suppose we wish to list only the plot number (field 0), the AMG reference (1) and only 10 characters of the Location (7) for all the plots given in the file *list*, then we should do
cat *list* | extr +0 +1 +7 10 | sort –t! *s–options* | rol

Suppose we wish to list everything except Notes (field 2) and Comments (8), but that we want to print the stand composition by volume exceeding 40 cm of the three major species, and want stockings and basal areas computed for stems 20 cm dbh or more. Then we should do
cat *list*|extr –2 –8 +9 3 v 40 +10 20|sort –t! *s-options*|rol

The –c option allows you to do some fancy reports. Suppose you wanted to compare the basal area merchantable volume exceeding 40 cm with that exceeding 60 cm. The following pipeline will present the volume 40+ in the comments column (you can ignore the warning message that you get):
cat *list* | extr +0 +14 40 S | extr +0 +8 –c +14 60 S | rol

Similarly, you can compare the volumes of cypress pine with the total volume:
get $NFI|extr +0 +14 19 S -m *cyp.only*|extr +0 +8 –c +14 19 S|rol
where *cyp.only* contains only the H&M code for cypress (CP-).

Note that the +0 option on the first extr is essential to enable the second extr to get the same plots.

The format of *list* is quite flexible. *list* will frequently be generated by get, search, grep or find, and these formats are acceptable. Sometimes grep will print the filename followed by a colon and a line of text. This is suitable too, and anything following the colon is treated as a comment.

You should also know about find, get, grep, rol, search and sort.

Standard field definitions for extr|sort|rol and other programs.

0. Plot number

1. AMG Reference (Zone, Easting, Northing)
2. Notes: Access (C/U/I), Evidence of Logging(y/n), Representative of SU (y/n), Typical of Forest Type (y/n)
3. Forest Type
4. Site Quality
5. Soil or Geological Description
6. Plot Specification (Origin, Type, Area/BAF, Dbh limits)
7. Location
8. Comments
9. Species Composition
10. Total Stocking (stems/ha)
11. Total basal area (sq m/ha)
12. Stocking of Merchantable stems (defined by species, size and product)
13. Basal area of Merchantable stems (sq m/ha)
14. Volume of Merchantable stems (cu m/ha)
15. Stocking of Visually Thinned stems (stems/ha)
16. Basal area of Visually Thinned stems (sq m/ha)
17. Volume of Visually Thinned stems (cu m/ha)
18. List of species recorded on plot

<center>**grop** *—options*</center>

grop grows a file for a requested time, and stores the resultant stand in the standard NFI format. The plot can be logged in particular years if required. The output plots are stored in the same directory structure as the NFI database. The plot is stored in the YY directory corresponding to the year it has been grown to. For example, the plot 04/88/0001 would be stored as /usr/tmp/04/99/0001g if grown to 1999. The suffix 'g' after the plot number identifies it as a "grown" plot.

Plot numbers are assumed to commence with a digit (or ., / or $). The plot numbers on standard input may be followed by a number which will be assumed to be the year when the plot is to be logged, and the logging method to be used. The logging methods available are:

> *V* - remove all visually thinned stems
>
> *L* - use the harvesting model
>
> *n* - remove all stems greater than or equal to *n* cm dbh

For example 04/88/0001 1988 25 grows the plot 04/88/0001 to 1988, removes all stems greater than or equal to 25cm dbh, and continues growing the plot.

All the arguments except -m are optional, and the options can be specified in any order.

Several *options* are recognised:

—d specifies the directory that the plots are to be stored in. The default directory is /usr/tmp.

—e *file* will cause grop to ignore the standard equation file, and to use the one given in *file*. The name *file* may comprise up to 24 characters, and the file should be formatted according to instructions given in ham.codes.

—g*n* where *n* is a year (eg. 1989) will use a growth model to "grow" inventory plot data to that year. The default is to grow the plot to the current year. A plot is ignored if there are no increment or mortality equations for a species, or there is no site form, soil type, or forest type recorded on the plot, and the -u option isn't used.

—m *n* specifies the model type to be used. THIS OPTION IS COMPULSORY. The valid model types are :

> *1* Rainforest
> *2* Fraser Island
> *3* Cypress Pine
> *4* Western Hardwood

—u *num* specifies the default site index to be used if there is none recorded on the plot. The field *num* specifies the site index. This option is only available if the option —m 3 option is used (i.e. cypress pine model).

get $NFI | map *options*

map produces line printer maps showing the approximate location of plots at one of the following scales, the largest scale which will enable all plots to fit within one page width:

> 1:50,000
> 1:100,000
> 1:250,000
> 1:500,000
> 1:1,000,000
> 1:2,000,000

map will where possible, print the corresponding plot numbers on the margins of the map. Note that only two plot numbers per output line is given. If that line contains more than two plots, the numbers given will be the leftmost (most western) and rightmost (most eastern) plots respectively.

There are several options available:

−a *addfile* causes map to add the reference marks defined in *addfile* to the maps produced. See below under "Customizing your maps" for more details.

−c *lowerleft topright* specifies corners for the map, where *lowerleft* and *topright* are the 12-digit AMG references for the bottom left and top right corners of the map respectively.

−k keeps a copy of the output file.

−max prints the maximum value encountered at that print position, rather than the average or * for numerical and text fields respectively.

−s*scale* specifies a scale to use (eg. −s50000 for 1:50000 scale and so on).

> If you specify a scale, it is possible that map may not be able to fit all the plots on a single page, and will produce as many maps as necessary.

−t*title* provides a title of up to 40 characters. If *title* contains embedded blanks, it must be enclosed in quotes.

+*n* *m* where *n* is a valid field number (in the range 0 to 17, do doc fields for more details), will cause map to prepare a "type" map, rather than just indicating plot locations.

> If *n* is a text field (ie. 0–3 or 5–9), map will indicate the *m*th character of that field; unless dissimilar characters occur in the same print position, when * is printed (unless the −max option has been specified). The default value for *m* is 1. For example, map +7 will produce a map showing S for State Forests, T for Timber Reserves, H for Holdings, etc. Similarly, +2 will indicate accessibility, +3 Soil types, and +7 6 the units digit of State Forest Numbers.

> If *n* is a numeric field (ie. 4 and 10–17), map will produce a map showing deciles of that field. For example, map +10 would print digits indicating the observed stocking expressed as deciles of the maximum observed. If more than one plot co-incide on the same print position, their mean value will be used (unless the −max option has been specified). You may specify *m* to specify the ranges to be used, but must use Map (see below) to use this feature for fields 10–17.

In default mode, with no arguments, single plots are shown as +, where two to nine plots occur within the same vicinity the corresponding digit is shown, and ten or more plots are represented as *.

map *options* invokes the following commands

> extr +0 +1 *options* | sort −t! +1 | Map *options* >*overflow*

and then, until overflow is empty, repeatedly does

> Map *options* <*overflow* >*overflow*

Map allows you more flexibility than map, but you must manage the *overflow* yourself. Map must be used to draw stocking, etc maps with user defined ranges, or with minimum diameters other than 20. For example,

extr +10 40 PS | Map +10 10

would print 0 for 0–9.9 stems (poles and sawlogs exceeding 40 cm dbh) per hectare, 1 for 10–19.9 stems/ha, etc, and * for 100 or more stems per hectare.

You may wish to use Map rather than map to achieve special results. For instance, you may wish to omit the plot numbers from the map margins, or wish to use grep between extr and sort to select specific plots. You may find sed useful to ensure that the extracted strings have unique characters when mapped.

extr is used to compile the basic information. If the +0 argument is omitted, map will omit the plot numbers from the margins of the map.

sort is required only if more than one zone will be involved. If there is more than one zone, the sort must be given.

Customizing your maps

You can also add extra features to your maps. The −a option allows you to nominate a file contianing reference marks to be included on your map. This file should locational information as follows

Columns 1–12: AMG code

Column 13: blank

Column 14: map scale code (blank means draw on all maps, 1 means only for maps of 1:250,000 or larger, 2 for maps of 1:50,000 or larger.

Column 15: character to be drawn.

Column 16: blank

Columns 17–26: A name (up to 10 characters in length) to be printed on map margins, if space permits.

You can use any character (in column 15), but should choose carefully so that your features are distinct from information derived from the inventory plots. Don't try to include too much data representing lines — concentrate on the corners, adding points which you can later join manually.

These files must be sorted into the correct order. Use the following command, every time after you edit these files:

sort -r +0.6 map.eg −omap.eg

rip −*options* +*rows* +*cols* −*select*

rip produces *individual plot* reports for each of the plot numbers (use any standard format in NFI) read from standard input. Plot numbers are assumed to commence with a digit (or ., / or $). One or more minus signs (−) followed by some text will cause a *stratum report* (ie. management subunit totals) to be produced, and the text will be printed as a header at the top of the page. One or more equals signs (=) followed by text will initiate a subtotal report (ie. management unit totals), and an end-of-file will produce the grand total (ie. District total).

The plot numbers on standard input may be followed by a number which will be assumed to be the area represented by the plot, and used as a weight in computing the stratum report. If this number is omitted, and area of 1.0 hectares is assumed, so if it is desired to exclude any plots from the stratum report, an area of 0.0 hectares must be explicitly specified. The area can be followed by the year when the plot is to be logged. The logging year is only significant if the plot is to be "grown" (see -g below). If a logging year is given, then the area must precede it. The logging year can be followed by the method of logging to be used. This can be *L* (use the logging rule), *V* (remove all stems which are visually thinned), or *n* (where n is the minimum merch. dbh, and all stems greater are logged).

rip can produce a bewildering variety of reports, depending upon how you invoke it. All the arguments except −m are optional, and rip will usually do something sensible even if incomplete arguments are given. The −m option must be specified first if the −u option is to be used. All the other options can be specified anywhere (eg. you may put the title last), but the order of the *rows* and *cols* arguments is significant.

Several *options* are recognised:

−a prints the values corresponding to the total area, rather than the per hectare values.

−b*n* prints brief reports; no individual plot reports will be printed. If *n* is omitted or is 1, a brief report comprising the stratum, subtotal and total reports will be printed. If *n* is 2 a very brief report comprising only the subtotal and total reports will be printed.

−c provides a complete list of all species given in *ind* (see +S below), even if that species does not occur on a plot (in this case a line of zeroes will be printed). This option is only effective if you specify +S and supply a list of species. Default is to omit any species which do not occur on a plot.

−d*chars* where *chars* may be one or more of N, B, V, L which indicate that the stand table should include number of stems, basal area, volume, and lineal metres of logs per hectare respectively. The order of these characters is significant, and indicates the order in which they will be displayed in the output (Default is NV).

−e *file* will cause rip to ignore the standard equation file, and to use the one given in *file*. The name *file* may comprise up to 24 characters, and the file should be formatted according to instructions given in ham.codes.

−g*n* where *n* is a year (eg. 1989) will use a growth model to "grow" inventory plot data to that year prior to reporting. It will also search the standard input for a year, which if found causes "logging" (removal of visually thinned stems only) in that year. A plot is ignored if there are no increment or mortality equations for a species, or there is no site form, soil type, or forest type recorded on the plot, and the -u option isn't used.

−i*n* ignores stems smaller than *n* cm dbhob.

−k keeps a copy of the output file (it is normally deleted after printing). rip generates a unique filename, always prefixed by rip.out.

−l*n* specifies the page length (in inches) for the printed output. Default is 11, but 8 or 13 may be useful for foolscap. rip will alter the lines per inch to fit. If it cannot fit on one page, two pages will be used. Two physical pages will be used only where necessary — most reports will use only one physical page.

−m *n* specifies the type of growth model which is to be used. THIS OPTION IS COMPULSORY. The valid model types are :

> *1* Rainforest
> *2* Fraser Island
> *3* Cypress Pine
> *4* Western Hardwood

−n*bc* will include the botanical and/or common species names on the output. For this option to be meaningful, you must specify +S as the *rows* argument.

−one or −1 uses one-way rather than two way volume equations.

−p*n* specifies that *n* extra digits after the decimal place are to be shown. Valid values of *n* are restricted to 1, 2 or 3. Default is 0.

−q ensures that the output is directed to a toshiba printer in letter quality.

−s will direct output to the screen using less, provided that the output does not exceed 80 characters in width. If it is too wide, rip will simply write the filename in which the output is saved.

−t*title* allows you to provide a *title* up to 40 characters long, enclosed in quotes: eg. −t"*** Demo Title ***"

−u *num* specifies the default site index to be used. −u *num* indicates that a default site index is be used, with a value of *num*. This option can only be specified after the −m option.

−w*n* specifies the maximum width of the printed output in inches (Maximum and Default is 13). rip will determine the number of characters per inch required to attain output not exceeding this width. If the resulting number of characters per inch is greater than 20, the default width is used.

The *rows* and *cols* arguments define the layout of the report. The *rows* argument indicates what each row will contain, and *cols* indicates the content of the columns. The default for *rows* is +S v 9 and for *cols* is +D 20 10 5. Valid entries for both *rows* and *cols* are:

+D *min siz num* indicates diameters, commencing with *min* cm dbh, and presenting *num* classes each of *siz* cm dbh. Thus +D 20 10 5 would generate five dbhob classes (20−29.9, 30−39.9, 40−40.9, 50−59.9 and 60−69.9). Two additional entries for stems smaller than, and greater than these classes will also be generated.

+DL is the same as +D but generates D-Line classes rather than dbhob classes.

+DU is the same as +D but generates DbhUb classes rather than dbhob classes.

+L *min siz num* indicates log length, with classes defined as above, but representing decimetres length. For example, +L 18 3 4 would generate four log length classes (1.8−2.09, 2.1−2.39, 2.4−2.69, 2.7−2.99), in addition to the smaller than, greater than, and total classes.

+S *seq ind* indicates species or species groups.

> *seq* indicates the collating sequence to be used — a for alphabetic; n, b, v, l for stocking, basal area, volume and log length respectively of *select* fraction (see below); N, B, V, L for stocking, basal area, volume and log length respectively of total stand; and o for order of occurrence (this is only useful when *ind* is a file).

> *ind* may be a number in the range 1−199 (or 1−49 if species are columns rather than rows) which indicates the maximum number of species to be displayed (any additional species will be grouped under the heading "Others"), or may be a filename identifying how species are to be displayed. Care should be taken in choosing a file name not ambiguous with other arguments (the filename should not be a number or a single letter). The file should contain species which are to be grouped not more than 27 to a single line (at the end of which may be a label up to 12 characters long commencing with a single quote) and as many lines as species to be displayed. For example, in western areas we could use:

> CP-'Cypress Pine
> SPG'Spotted Gum
> NRIGRIBRI'Ironbarks

select causes two stand tables to be produced for each plot, one with the selected stand fraction, the other for the total stand. Valid arguments include:

–D *mindbh maxdbh* selects the given range of stem diameters (cm dbhob).

–L *minlen maxlen* selects the indicated range of log lengths (lengths in decimetres).

–P *list* selects only those products given in *list*, where *list* may contain one or more of **P, S, R, C, U** for pole, sawlog, round (including sleeper), chip and useless respectively. Eg. **–P PS**

–S *list* where *list* may be a list of up to 10 H&M species codes (eg. **–S SPGNRIBRIGRI**), or may be the name of a file containing a species list of up to 10 H&M species codes in any format (anything following any punctuation or space will be ignored). For example:

> CP– Cypress
> BRIGRINRI'Ironbarks
> SPG:Spotted gum & Lemon scented gum

–V *list* selects the visually thinned component of the stand, where *list* is a product list (as for the –P option) containing one or more of **P, S, R, C, U.**

Note: If you want to customize rip reports with specific layouts, you may find ilv useful.

BUGS:

The maximum number of species accomodated depends on whether species are shown as rows (is +S is first argument) or columns (ie. +S is second argument). When species are rows, 199 species can be accomodated, and this is adequate even for rainforests. If species are columns, only 49 are accomodated,, and this is insufficient for rainforests. The resulting output may not necessarily show the most common species for any particular plot, depending upon the order in which species were encountered. When additional species are grouped as others, a warning message is given. This problem can be avoided by showing species as rows, or by providing a species list.

All the numbers specified as arguments must be integers (whole numbers without decimal points) and must be space delimited. It should be possible to specify real numbers, but this will have to wait till a later version.

The sampling errors are calculated assuming that inventory used stratified random sampling. Other sampling schemes will lead to incorrect estimates of sampling error. The sampling error will be slightly underestimated for random and two-stage sampling, and slightly overestimated for systematic sampling.

If you request species groups for both rows and columns, the result will be unpredictable and unintelligable.

sked *target* +*start-year* -*end-year* *options* < *input-file*

sked does yield scheduling (and cutting cycle analysis), and produces a report on standard output.

sked will simulate the effects of removing *target* cubic metres of compulsory log volume per annum from the area simulated, during the period *start-year* to *end-year*. Inventory data read is updated to *start-year* before yield scheduling commences. *target* may optionally take the form *target1:year:target2* in which case *target1* will be harvested from *start-year* until *year* and then *target2* will be harvested until *end-year*.

The following options are available:

-**a** followed by up to three real numbers indicates the minimum acceptable average stem volume from subunits, management units and the running average respectively. If less than three numbers are given, the subunit and running average may be set equal to the management unit minimum. Default is zero. See also -y.

-**b***n* produces brief output. If *n* is 1 or omitted, only subunit and management unit yields will be printed; and if *n* is 2 only management unit yields will be printed. Default is to print yields for each plot.

-**c***n* uses cutting cycle analysis with an *n* year cycle, instead of yield scheduling. With this option, *target* is ignored and access groups will not be recognised. Management units are ignored and all subunits are treated as if part of a huge management unit.

-**d** *d1* *d2* displays the running average percentage of volume in three size (dbh) classes: less than *d1*, between *d1* and *d2*, and exceeding *d2*. Defaults are 60 and 100.

-**e** *file* will cause sked to ignore the standard equation file, and to use the alternative provided in *file*. The name *file* may comprise up to 24 characters, and the format of the file should correspond to the instructions in ham.codes.

-**f***n* indicates that sked is to operate in *fast* mode, choosing sufficient MUs in each cycle to sustain an *n*-year harvest (for yield scheduling only). Default is zero, and chooses exactly one MU per cycle. Execution time decreases as *n* increases.

-**g** *filename* indicates that access groups are to be recognised during the scheduling, and provides a *filename* containing relevant data (See below).

-**i***n* ignores stems smaller than *n* cm dbhob in the inventory data. Default is 10 cm.

-**m***n* indicates the model number of the growth and harvesting models to be used. This influence the parameters retrieved from the ham.codes control file. Model 1 is north Qld rainforest, 2 is Fraser Island, 3 is cypress pine, and 4 is cypress growth model with wetern hardwoods harvesting model.

-**n***n* *f* indicates the number of management units over which running averages for the options -a, -p, -d, -w and -y are to be computed, and the frequency of reporting. Defaults are 10 and 5, maximum is 20.

-**one** uses one-way volume equations for all volumes reported. Default is to use two-way equations for original data, and one-way equations for projected data.

-**p***n* *list* indicates the maximum acceptible percentage of the yield in the species given in *list*, a string of up to 10 H&M codes.

+**p***n* *list* indicates the minimum acceptible percentage of the yield in the species given in *list*, a string of up to 10 H&M codes. NB. If both -p and +p are specified, *list* should be specified only once. If it is given twice, the last occurrence will be used for both options.

-**q***list* allows you to specify stem quality and visual thinning codes recognised by sked. Efficiency demands as few codes as possible, so the default (UUUSST) recognises only sawlogs and useless trees (ie. codes UCRSP are translated into UUUSS respectively), and visual thinning only if recorded as T. The first five characters in *list* indicate the mapping for stem quality codes, the

remaining characters (max 5) indicate valid visual thinning codes.

–r*n* indicates that the minimum return period is *n* years (ie. successive loggings may not be less than *n* years apart). Default is zero.

–s*Pa* indicates the criterion to be used in selecting the next management unit to be logged, subject to the constraints defined by the –a, –p, –r, –w and –y options. *P* indicates the parameter to be used, and valid values include B for Basal area, T for Time since last logging, V for loggable Volume per management unit, and Y for Yield per hectare. *a* indicates the area over which this parameter is to be computed, and valid values include s for subunits and m for management units. Default is Ym. Note that *sequence numbers (see input-file below)* always over-ride this criterion.

–u*n* allows users to specify a default site quality *n* for plots on which site quality is omitted.

–v*n* indicates the minimum volume which must be assured before harvesting of any Management Unit will be commenced.

–w*n* indicates the percentage of volume which is to be derived from management units able to be logged in wet weather. Default is zero.

–y followed by up to three real numbers indicates the minimum acceptable yields per hectare from subunits, management units and the running average respectively. If less than three numbers are given, the subunit and running average yields may be set equal to the management unit minimum. Default is zero. See also –a.

–z *p m n s* specifies a number of run control variables which influence the speed of execution and the precision of the result. If you choose not to use the default, carefully check the impact of your choice with sensitivity analyses (i.e. compare your choice with the default). *p* indicates the maximum number of plots simulated for any subunit (Default 5, valid range from 1 to 50). If a subunit has more than *p* plots, some will be amalgamated before simulation commences. Execution time increases as *p* increases. *m* indicates the inverse of size of the simulated plot (e.g. 1=one ha plot, 2=half ha plot, etc.) (default 1, any positive number is valid). As *m* increases, execution time and precision decrease. Parameters *n* and *s* are used only for stochastic simulations when *n* indicates number of random number draws per cohort before determinism is used (default=0=deterministic, suggest 5 for stochastic) and *s* is a seed to initialize the random number generator (any integer, default=1).

The *input-file* should contain a title up to 80 characters long on line 1, and details of management units and subunits on subsequent lines. Any number of management units may be given, and there may be any number of subunits within each management unit.

· The first record for each management unit should contain the access group name in columns 1–10, the management unit name in columns 12–20, the number of subunits in columns 23–26, the date of last logging (if any) in columns 28–31, the percentage of the management unit able to be logged in wet weather (or other special conditions) in columns 33–34, and an optional *sequence number* in columns 36–37, in format (a10,1x,a9,1x,2i5,2i3). The remainder of the record may be used for comments.

· For each subunit, the first 11 columns are ignored (may contain access group, comments, or be left blank), columns 12–20 may be blank, or may contain the management unit name exactly as on the first record for the management unit, and column 21 should contain the subunit identifier. Columns 23–26 should contain the area (hectares, a decimal point may, but need not be given). If the subunit was logged since it was measured, columns 28–31 should contain the year of logging and columns 32–33 should indicate the logging rule (V indicates visual thinning, L indicates logging rule, *nn* indicates the diameter for diameter limit cutting). Columns 35–42, 44–51, ... may contain up to fifty plot numbers. Note that if you give more than 5 (or as varied by –x *p* option) plot numbers, some will be amalgamated before simulation starts (amalgamation on adjacent plots, so arrange plots in some sensible order). Format is (11x,a9,a1,f5.0,i5,1x,a1,50(1x,a8)).

If the –g option was specified, the Access group file may contain up to 30 access groups, containing one line per access group, with the access group name in columns 1–10, the minimum volume to enter in columns 12–20, the year before which the group cannot be operated in columns 22–25, and the year after which the group will be removed from the productive estate in columns 27–30. Format is (a10,1x,f9.0,1x,i4,1x,i4).

NOTE: Specifying minimum average stem volumes (–a) and yields per hectare (–y) will affect the inclusion of subunits in the simulated logging of a management unit, wheras the options –p, –r and –w will only affect the entire management unit.

The scheduling of any management unit for logging is influenced firstly by sequence numbers — these override all other conditions, even those which would otherwise inhibit that management unit from being logged. The next most influential criteria relate to access groups: no logging will be simulated within an access group unless it satisfies the specified minimum volume, and commencement and completion dates.

BUGS: If you kill sked, its work files will not be deleted, and you should do this yourself by doing:

         rm /usr/tmp/sked.?.*USERID*

where *USERID* is your userid (eg. jerry, rob, mack, wayne). Caution: If you have more than one sked run active and you type the command above, you will remove the workfiles of all your runs, and crash them. So if you have more than one sked run, you will have to name the files individually. Eg.

         rm /usr/tmp/sked.A.jerry
         rm /usr/tmp/sked.B.jerry

whatif: User Interface for Growth Model

whatif enables interactive use of the growth model. Studies of the growth of real or hypothetical stands can be simulated under different silvicultural regimes.

Getting Started

Simply type **whatif**. The program will then seek some information from you before simulation can begin. It will ask:

Standard ham.codes (y/n) ? This determines whether you wish to use the standard H&M codes. This determines whether a species is compulsory, non-compulsory, or useless, indicates the minimum merchantable dbh, and specifies the volume and growth equations to be used for that species. If you want to use the standard codes, answer y, otherwise answer n. If you answered n to standard codes, then you will be asked for the file name. whatif assumes that the file you wish to use has the same format as the standard file 'ham.codes'. If the file you specified doesn't exist the standard H&M codes are used.

Model Type

whatif needs to know what type of model is to be used. This is needed for the growth model.

Model type (1=NQ, 2=Fraser Island, 3=Cypress pine, 4=W. H'wood) ? This determines the type of model to be used. The model types are North Queensland (rainforest), Fraser Island, cypress pine, and Western Hardwood. The model type is used to determine default values for soil type and growth index / forest type / site form in the growth models.

If you answer 1 then the soil type and growth index will be requested.

Soil type : XXX

CZL	Alluvial and Colluvial
CZA	Basic Volcanic
CL	Acid Volcanic
CGA	Coarse Granite
AD	Sedimentary Metamorphic
PGB	Tully Granite

Soil type ? The soil type affects the growth rate for rainforest species. Invalid soil types will be rejected. Soil type should consist of three characters.

Growth Index ? The growth index for rainforest plots should lie between 0 and 10. This affects the growth model for the stand.

If you answered 2 to the above question, for Fraser Island, then the forest type is required.

Forest Type : XXXYYYHTT

XXX Primary species on plot
YYY Secondary species on plot
 H Forest height (Extremely tall, Very tall, Tall)
 TT Forest type (Open Forest, Closed Forest)
                    E.g. bbtstyecf

Forest type ? The forest type is used in the growth model.

If you answered 3 to the above question, then the site form is required. The site form must lie between 10 and 20.

Site Form ? Site form is required for the growth models. When site form isn't used in the growth model for a particular area, it can be set to zero.

Inventory Files

List of files (y/n) ? This allows a list of inventory files to be entered, and considered as a single data set. whatif will ask for the name of a file containing a list of inventory file names. If required, the inventory file list can be entered from the keyboard, by entering a blank line. The inventory file names are of the form dd/yy/nnnn, where dd is the district code, yy is the year of measurement, and nnnn is the plot identification number. Each plot is grown to the current year, and the plots are then combined. For example, the file 08/89/7052 would be grown for one year, and the file 08/88/7001 would be grown for two years (to bring them to the year 1990). The data for both files would then be combined. If the information required to use a particular form of model (e.g. soil type and growth index for N.Q.) is not recorded on the inventory file, then the values entered when the model type was requested are used.

Inventory File (y/n) ? You may specify whether or not the data is to be read from an inventory file. If you answer y, then you are asked for the filename. The file name is assumed to be of the form given above. If the plot file has no soil type, forest type, or site quality recorded on it, then the default values entered when the model type is requested are used. If a species which has no diameter increment or mortality functions occurs whatif responds as follows :

No equation codes for SPP. Continue (y/n) ? If you answer n, then you will quit whatif. If you answer y then whatif will continue, until you attempt to 'grow' the stand. When an attempt is made to grow the stand, an error message is given, and whatif quits.

Non-inventory Files

The following details are required if the tree list was not from an inventory file. The soil type and growth index / forest type / site form are taken as the values entered when the model type is specified.

Years since last logged? Time since logging affects both the growth model and the volume equations.

Years since last treated? Time since treatment affects the growth model.

Tree list from file (y/n)? This causes whatif to read the tree list from a computer file, when the data isn't stored as an inventory file.

Now give tree list:

Species Dbhob (cm), Stems/ha, Stem Class:
This can be a stand table (use class mean diameters), or a list of trees as measured. whatif isn't case sensitive, so entering "BBT 20 12.5 S" is equivalent to entering "bbt 20 12.5 s". This is true for all whatif options.

Tree List File

This section is only required if you answered y to the question "Tree list from file" above. whatif asks two more questions:

Filename? Here it expects a valid filename which exists on the computer system.

FORTRAN Format: If the file contains data in free format, a blank line or the keyword free may be used, otherwise a standard FORTRAN format statement is expected, and must be enclosed in parentheses. The format should contain descriptors for 2 real and two character variables.

The file should contain a list of species, size, stocking and stem class (in that order), one per line, in an appropriate format.

Simulation Options

g *n*   whatif will grow the stand for *n* years (unless n is more than 100, in which case it will ask for your next option after 100 years).

ga *x*   Grow until the standing asv (of the merchantable component) exceeds *x* cu m/stem (or for 100 years, whichever is lesser).

gb *x*   Grow until the stand basal area exceeds *x* sq m/ha (or 100 years).

gv *x*   Grow until the standing volume (of the merchantable component) exceeds *x* cu m/ha (or 100 years).

l *n d*   Log stand, and solicit user's intention for each *n* cm dbh class starting at a minimum diameter of *d*. When more than one inventory plot is being considered, the intentions for each *n* cm dbh class from the "average" stand is requested. This strategy is then applied to each plot separately.

lp *n d*   Log stand, and solicit user's intention for each *n* cm dbh class starting at a minimum diameter of *d*. The percentage to be removed from each dbh class is requested, instead of the residual stocking. When more than one inventory plot is being considered, the intentions for each *n* cm dbh class from the "average" stand is requested. This strategy is then applied to each plot separately.

ld *x a b*   Log stand, removing all merchantable stems exceeding *d* cm dbh, within stem classes a, b, etc. If no stem classes are given, all merchantable stems exceeding *d* cm dbh will be logged, regardless of stem class. Any number of stem classes may be given.

t *n*   Treat stand, soliciting user's intention for each *n* cm dbh class. When more than one inventory plot is being considered, the intentions for each *n* cm dbh class from the "average" stand is requested. Each plot is then treated using the strategy given for the "average" stand.

ta *s b c*   Treat all stems of species *s*, stem classes *b*, *c* etc. An * can be used as wild card. For example:

                                                ta * U S
          will treat stem classes S and U for all species.
                                                ta CP- *
          will treat all CP- stem classes.

tr *s a l u r*   Treat stems of species *s*, stem class *a* whose dbh is between *l* (lower) and *u* (upper) cm dbh, so as to leave a residual stocking of *r* stems/ha. An * acts as a wild card in the same way as for the above option. When more than one inventory file is being considered, each file is treated separately as requested. If no appropriate stems exist on a plot, a relevant message is displayed.

u   Undo the last command.

s   Save the present situation for future reference. This is useful for examining different logging or treatment options for one stand. The stand can be entered and saved. It can then be treated and grown several times. Then to get back to the original untreated stand, do restore (r), and a different strategy can be examined.

r   Restore stand as at last save (s).

n   Next stand. whatif asks you for details of the next stand, but uses the H&M codes and model type specified at the start.

d *s x y z l*   Display current stand as a stand table, using *x* cm dbh classes, and starting at y cm dbh. The numbers z and l are optional, and may be used to control the size and scale of the display. *l* indicates the size of the display in lines (default is 10, maximum permissible is 30), and z indicates the full scale (eg. if you wish to fix 100 stems/ha as the full scale on the display, and thus use 10 stems/ha for each line of output, then z should be 100). *s* indicates the species to be displayed. This is optional. If ommitted, all species are displayed. If a list of species is given, then a stand table is displayed for each species individually, and then for a combined stand containing only the species in the list. Nine species is the maximum number that can be displayed at once. The information is displayed one stand table at a time.

dl   Display the stand using the general report form, one page at a time.

f   Read commands from a specified file (See below).

p   Enables or disables the printed copy option. This is normally disabled, but if you want a printed copy, simply type p, and a copy of relevant output will be made. The name of an output file is requested.

c *text*   Copy *text* to the printed output. Text may be up to 78 characters long. This may be used to record comments or background on the printed version.

q   Quit. You will be asked to confirm this by answering y.

Command Files

A command file can be set up and invoked by the f option. This option requests the name of the file that the commands are stored in. The commands are then read from this file. All options work normally except the commands l, lp, t, and the p.

To use the l or the lp commands the number of groups to be considered, and the ways in which the groups are to be logged. The method of logging should be given by:

Species, Class, min dbh, max dbh, res stk/% removals

If the class is omitted, all merchantable stems of the species are considered. For example :

```
lp
4
cp- s 39.0 100.0 100.0
cp- 30.0 38.9 20.0
cp- s 20.0 29.9 30.0
cp- s 19.0 19.9 40.0
```

The above logs all sawlog cypress pine stems between 39 cm dbh and 100 cm dbh, and removes 100%. Similarly 20% of all merchantable cypress pine stems between 30 cm dbh and 38.9 cm dbh are logged, and so on. An additional option lt has been added. This logs all of the visually thinned stems.

The option t works in a similar manner to the l and lp options. To indicate that loggable stems are to be removed, the command becomes t y (N.B. The options t and t n indicate that no loggable stems are to be removed).

A command, lt is available only for use in a command file. This option logs all the visually thinned stems in the stand.

The file name to be used for printing when the p option is used can be given by : p *<filename>*. If no *<filename>* is given, the output will be sent to the file "Whatif.Out".

Comments can be included in the file by commencing line with a '#'. For example,

this is a comment

If an incorrect command is given in the file, then processing of the file ceases.

Note :

(1) visually thinned stems will be ignored when a stand is treated.

(2) the first time the stand is logged, an option is given to log
        Consider visually thinned stems from data only (y/n) ? If you answer y to this, then all visually thinned stems will be logged, and no other stems touched. This occurs for all

logging options. If you answer n to the question, then the visually thinned stems will be treated as normal stems from then on, and processing will continue as requested.

(3) If a species which has no volume equation codes occurs on an inventory file then processing can continue. However, an error message will be displayed, and the volume set to zero when an attempt is made to calculate the volume.

(4) If a group of inventory files are being used, then each file is grown, treated, and logged separately. The results for each plot are averaged for reporting purposes.

Output Produced

The output is fairly self-explanatory. Note that whatif produces output on your terminal, and optionally on a printer as well.

NOTE: If you kill **whatif**, the work files used by **whatif** won't be removed. These can be removed by typing   'rm /usr/tmp/gro.?.userid'. For example,   'rm /usr/tmp/gro.?.jane'.