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Software for Computing Plant Biomass—BIOPAK Users Guide

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Abstract

Means, Joseph E.; Hansen, Heather A.; Koerper, Greg J.; Alaback, Paul B; Klopsch, Mark W. 1994. Software for computing plant biomass--BIOPAK users guide. Gen. Tech. Rep. PNW-GTR-340. Portland, OR: U.S. Department of Agriculture, Forest Service, Pacific Northwest Research Station. 184 p.

BIOPAK is a menu-driven package of computer programs for IBM-compatible personal computers that calculates the biomass, area, height, length, or volume of plant components (leaves, branches, stem, crown, and roots). The routines were written in FoxPro, Fortran, and C.

BIOPAK was created to facilitate linking of a diverse array of vegetation datasets with the appropriate subset of available equations for estimating plant components, such as biomass and leaf area. BIOPAK produces reports that are formatted for people and files that are compatible with other software. Other reports document the design of a computation run and the equations used. BIOPAK includes a library of about 1,000 prediction equations and an editor for updating it. Most of the equations in the librarv were developed in the Pacific-Northwest, including southeast Alaska.

Keywords: Dimension analysis, software, plant biomass, plant leaf area, plant volume, crown mass, crown volume, manual, microcomputer, users guide.

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Detailed contents are given at the beginning of each chapter and section.

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List of Tables

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WELCOME

Thischapter introduces the BIOPAK software and users guide and its purpose and limitations. Please read the warning at the end of the chapter before proceeding.

Section


```
BIOPAK

 ─────── Main-Menu ──────────
 Design a run
 edit equation Library
 Calculate plant components
 Generate reports
 View reports or data
 goto dos Shell
 Quit

Most Recently Used File Names
  Run Design File          :  D:\BIOPAK\TESTDATA\TUTOR.RD
  Equation Library File    :  D:\BIOPAK\TESTDATA\BIOLIB.EQN
  Input Data File          :  D:\BIOPAK\TESTDATA\TUTOR.DAT
  Intermediate Binary File :  D:\BIOPAK\TESTDATA\TUTOR.IBF
```

Purpose of BIOPAK

BIOPAK is a menu-driven package of computer programs that calculates the biomass, area, height, length, or volume of plant components (leaves, branches, stem, crown, and roots). BIOPAK was created to facilitate linking a diverse array of vegetation datasets with an appropriate subset of available equations for estimating plant components.

It was developed for use on IBM-compatible personal computers (PCs). The routines are written in FoxPro, Fortran, and C.

Intended Users and Fields of Study

Plant component estimates are used by researchers and resource managers in forest and range sciences: fire management--fuels -assessment; forest management--wildlife habitat, site productivity, and ecosystem monitoring; forest ecology--nutrient cycling, plant productivity; range management--browse estimates; and wildlife ecology--foliar cover, browse and habitat.

Users should have a basic knowledge of DOS for installing and managing files used and produced by BIOPAK.

Overview of Users Guide

Reading suggestions

A general understanding of the BIOPAK software will help avoid mistakes that may-invalidate the results. We suggest you at least read Getting Started and do the first few tutorials before making any plant component calculations with your own data.

Some users will want to use the more advanced features, for example, Equation Library editing, and Customizing BIOPAK. Most of these are introduced in the tutorials. Others are covered in the appendices.

Purposes of chapters

Chapter	Contents
Welcome	Introduction to the software and users guide. Purpose of the program and its limitations.
Installation	How to install the software on a personal computer or network.
Getting Started	An overview of BIOPAK features and suggestions for its use. Logical sequences of steps for calculating plant components are discussed.
Reference	Each main menu item is covered in a separate reference section. The order of the sections corresponds to the main menu. A section on the input data file, and reports and other output, is also included.
Tutorials	Tutorials that are intended to introduce the software

	gradually.
Appendices	The appendices present more detailed information than the reference sections, such as code definitions and instructions for customizing BIOPAK. They are presented in alphabetical order.
Glossary	The glossary includes important terms and concepts covered in the software and user's guide.
Index	Detailed index covering keywords, terms, concepts, and section headings.

Notational Conventions

The following notational conventions are used in this users guide:

Bold	Used for references to BIOPAK software menu selections or commands to be typed by user.
Italics	Used for references to sections of the BIOPAK users guide.
CAPS	Used for file names.
<u>Underline</u>	Used for references to windows and section headings in the BIOPAK software.
< >	Used to indicate keyboard commands, for example, <Enter> <F3>
*	Used as a wildcard character in file names. For example, *.RD would indicate any file with the extension .RD.

Estimating Plant Components

During the past two decades, plant components, such as biomass and leaf area, have been widely viewed as increasingly important ecosystem parameters. Many different approaches have been taken to estimate them (Alemdag 1980, Pieper 1978, Standish and others 1985, Valentine and others 1984, Wharton and Cunia 1987). The most accurate techniques (clipping, separating, and weighing) are time consuming; they lend themselves to site-specific, intensive studies and destroy vegetation on the plot being sampled.

The dimension analysis approach

Over the past decade most studies of ecosystem structure and dynamics have used the allometric or dimension analysis approach to biomass sampling (Grier and Logan 1977, Whittaker and Woodwell 1968, Whittaker and others 1974). Dimension analysis involves predicting attributes that are difficult to measure from attributes that are easily measured. Prediction is made from equations developed from the destructive sampling method (Alemdag 1980, Valentine and others 1984). Dimension analysis can yield precise and realistic estimates of plant biomass in environments similar to where the original destructive data were gathered.

This approach is also useful when equations exist for individual components, such as stem, branch, and foliage biomass, but not for a component, such as total aboveground biomass, that combines several others. In this case, predicted values for the individual components can be summed to obtain the desired value. Schlaegel and Kennedy (1984) found such summations give estimates not significantly different from a single regression for the total.

Potential problems with the dimension analysis approach

The ease of obtaining estimates of plant components, especially with software like BIOPAK, makes dimension analysis one of the most. easily misused techniques, primarily from three common classes of problems.

First, problems can occur when equations are being constructed. 'Errors from inaccurate measurement, choice of model, fitting of parameters, and spatial variation within a sampled stand are discussed by Woods and others, (1991). Errors also may be caused by bias in selecting the samples used to build an equation. Marshall and Waring (1986), for example, found that equations based on tree diameter overestimated leaf area of an old-growth stand of Douglas-fir (Pseudotsuqa menziesii (Mirb.) Franco) and western hemlock (Tsuqa heterophvlla (Raf.) Sarg.) by a factor of two and suggested the problem was mainly with estimates for large trees. Apparently, the old-growth Douglas-fir trees selected to build the equations from were well formed with no large parts of crown or bole missing, yet necrosis and breakage is common in old-growth stands.

Second, problems of overextrapolation or underextrapolation can occur. In estimating tree biomass, for example, samples used to develop the relation of diameter to biomass often do not include the range of diameters that the equations ultimately will be used for. Biomass estimates for plants larger or smaller than those sampled may be inaccurate; for example, leaf biomass per Douglas-fir tree seems to increase exponentially with stem diameter initially, but increases linearly or levels off at larger diameters of 1 to 3 meters. Extrapolation to leaf areas of large trees by using an equation developed with data from smaller trees could overestimate biomass greatly. No data currently exist on this potentially serious problem.

A third type of problem is the difference in growth forms of the same species from site to site. Individuals of the same species have been shown to have different relations of plant dimensions to accumulated biomass or leaf area when found on sites with different potential productivities (Espinosa-Bancalari and others 1987, Koerper and Richardson 1980), environments (Buech and Rugg 1989, Long and Smith 1988, Madgwick 1970, Sachs 1983), or plant densities (annual herbs: Weiner and Thomas 1992; trees: Pearson and others 1984, Sachs 1983). When annual herbs are competing, the allometric relation among individuals at one point in time is not the same as the allometric growth trajectories of individuals (Weiner and Thomas 1992). Stand developmental stages (Alaback 1986, Alaback 1987, Dean and Long 1986), thinning and fertilization (Brix and Mitchell 1983), and tree canopy class (Thompson 1989) also have been related to changes in relations between biomass or leaf area and plant dimension. Thus, equations for different species of the same lifeform often are quite different (Gholz and others 1979, Standish and others 1985, Stanek and State 1978, Waring and others 1982).

Relations of plant dimensions to biomass are not equally subject to change with different site conditions. Plant measurements most directly related to volume,

such as stem diameter (Buech **and Rugg** 1989), **height, and form factor, or related to leaf area, such as** sapwood **area and distance to live crown (Long and Smith** 1988), **may be relatively robust when applied to differing site conditions. In contrast, relations of biomass to percentage of ground cover can vary greatly with site and stand developmental characteristics** (Alaback **1987, Daubenmire 1968).**

To avoid these problems, users of BIOPAK are advised to read the section *Getting Started: Suggestions for Using BIOPAK,* **and to use the most appropriate equations.**

Be Careful

Examine results thoroughly. Though BIOPAK will select the best equation according to its logic, your logic may be different. Equations available in its library may be inadequate for some species on some sites. BIOPAK may not select the equation you wish if it is not specified completely in an Equation Reassignment. BIOPAK makes it easy to use completely inappropriate equations giving meaningless results. We strongly advise users to closely examine the equations used *(see Reference: Reports and Other Output: Diagnostic, reports)* **and output.** *Getting Started: Suggestions for Using BIOPAK* **to increase your likelihood of getting reasonable estimates.**

INSTALLATION

This chapter explains how to install the software on a personal computer or

Section

System Requirements

BIOPAK runs on IBM-compatible PCs and requires the following:

- DOS 3.3 or higher (type VER at the DOS prompt to check version).
- 550 Kbytes free RAM; 1 Mbyte total RAM will usually provide sufficient free memory if TSRs are loaded into high DOS memory. 'Available memory can be checked by typing CHKDSK.
- 6 Mbytes for installation on a hard disk.
- 8 Mbytes or more additional free memory on a hard disk, or RAM disk, to run. Eight Mbytes are required to run initially with the large equation library supplied with the package: 6 Mbytes for FoxPro temporary work files and up to 2 Mbytes for output files the user may select. More space will be required for output files from large user datasets. Less space will be needed if smaller equation libraries are used.
- A 1.2-Mbyte 5.25-inch diskette drive to read the BIOPAK disk.
- A printer, capable of printing 132 or more characters per line, to make paper copies of output.
- An EGA or VGA monitor makes it easier to understand color screens at a glance. The highlight bar cannot be seen on some monochrome systems.

Files Shipped with BIOPAK

The disk shipped with BIOPAK should contain these files:

BBAT1	BIOPAK1.EXE	INSTALL.BAT	INSTR2
BBAT2	GETDRIVE.COM	INSTR1	KEYPRESS.COM
BBAT3			

On the TSTDATA directory:

LIBRARY.EXE TUTOR.DAT TUTOR.RD

Installation on a PC

We suggest these steps for installinq BIOPAK software on a PC:

1. Make a backup copy of the BIOPAK high-density disk. Also, before proceeding to step 2, be sure to have a boot disk for the computer and external copies of the CONFIG.SYS and AUTOEXEC.BAT files from the hard drive.
2. If an earlier version of BIOPAK is on the PC, avoid problems by following these steps:
   a. Either remove all files of the earlier version, *or* put them all in a directory not labeled BIOPAK and not on the DOS path. Delete all BIOPAK.BAT files from all directories on the DOS path. Old Run Design (.RD) files will not work with the new version of BIOPAK.
   b. Remove the BIOPAK directory from the PATH statement in the AUTOEXEC.BAT file.
   c. Remove the statements SET BIODIR=... and SET BIOTMP=... from the AUTOEXEC.BAT file.
3. Increase your DOS environment space by at least 512 bytes above what currently works for the PC being used, or set it to 2,056 bytes, whichever is larger. This can be done by using a text editor or word processor to change the SHELL command in the C:\CONFIG.SYS file. Syntax of the SHELL command differs for different versions of DOS, so consult your DOS manual. Under DOS versions 3.3 and higher, this is done with a command like the following:
   SHELL=C:\DOS\COMMAND.COM /P /E:2056
   This line in the CONFIG.SYS file will set the environment space to 2,056 bytes.
4. Reboot the PC so the changes to the CONFIG.SYS file AUTOEXEC.BAT take effect. The installation program and BIOPAK require 500-800 bytes of free environment space to run.
5. Decide which hard drive (C:, D:, E:, F:, or G:) to install the BIOPAK system files on. This will require about 6 Mbytes free space. Hard drive C: is used in these instructions, but any hard drive will do. The Install program will put BIOPAK on the directory named BIOPAK on the drive selected. We refer to this as the BIOPAK directory.
6. Decide on a drive for BIOPAK to put its temporary files on when it is running. These files will go on the root directory of this drive; for example, E:\. Be sure you have permission to write here and that it can hold about 8 Mbytes in order to use the large Equation Library shipped with BIOPAK. The RAM disks are fastest.
7. Start the installation program. Put the BIOPAK disk into a diskette drive; go to that drive (for example, A:); then type at the A:> prompt:
   INSTALL
8. Answer the questions posed by the install program about the locations of files. You will be informed when installation is complete or if there are problems.
9. The file BIOPAK.BAT must be in a directory on the DOS PATH. Move it from C:\ if needed.
10. Copy the files from the TESTDATA directory on the BIOPAK disk to the directory the tutorials will be run from. We will use C:\TESTDATA to illustrate. Go to the C:\TESTDATA directory and type:
    COPY A:\TESTDATA*.*
11. If you want to modify the Library, decompress it in the TESTDATA directory (requires about 2 Mbytes) so you can make changes to this copy, saving the

copy in the BIOPAK directory. Type:
LIBRARY
This will put the Equation Library files (BIOLIB?.*) in your TESTDATA directory. Now LIBRARY.EXE can be deleted from this directory.

12. If the library in your TESTDATA directory is not decompressed, the BIOLIB.EQN (equation) file must be copied from the BIOPAK directory to your TESTDATA directory by typing:
COPY C:\BIOPAK\BIOLIB.EQN C:\TESTDATA
to run the tutorials.

13. Check whether sufficient free DOS memory is available to run BIOPAK by using MAPMEM. Type:
C:\BIOPAK\MAPMEM
Free memory is shown as, for example, "590992 free" and given in bytes.

14. If about 550,000 bytes free RAM memory is not available, uninstall some TSR pograms or load them into high or extended memory before running You may have to consult the manuals for these programs to do this. 'Often they are installed in the AUTOEXEC.BAT and CONFIG.SYS files.

To build different AUTOEXEC.BAT and CONFIG.SYS files to be used only when BIOPAK is run, save copies of the originals; for example AUTOEXEC.SAV and CONFIG.SAV. The new ones could be named AUTOEXEC.BIO and CONFIG.BIO. In this case, before running BIOPAK, the *.BIO files must be copied over AUTOEXEC.BAT and CONFIG.SYS, and then the PC must be rebooted. Use MAPMEM again to verify that enough free memory is available.

BIOPAK is now ready to run on your PC.

NOTE: You can move BIOPAK to a different drive or directory by (1) reinstalling it, starting with step 2 above; or (2) moving all BIOPAK files to a new drive and directory, and changing the SET BIODIR=tnewpath> line near the top of every BIOPAK.BAT file to point to the new BIOPAK directory.

Starting BIOPAK installed on a PC

Start BIOPAK in a directory that contains the data to be used to calculate plant components and that will contain BIOPAK report output. As you work with BIOPAK, you will need to delete files from intermediate runs. To avoid accidental deletion of files needed for running BIOPAK, do not start BIOPAK, or store input or output files, in the BIOPAK directory.

If planning to log on to a network, do so before starting BIOPAK. To start BIOPAK that is installed on the hard drive of a PC, type:
BIOPAK
Instructions for,starting BIOPAK that is installed on a network are given in the section, *Installation on a Network.*

Verifying BIOPA K installation on a PC

Verify that BIOPAK has been installed correctly by following these steps:

Go to your TESTDATA directory and

- Type BIOPAK to start. BIOPAK.
- Type D to select Design a Run.
- Type F to select File.
- Type R to select Read existing run design file. The Foxpro <u>File Selection</u>

Window, commonly used in BIOPAK, will appear.

- Select the file TUTOR.RD by highlighting it, and type <Enter>
- Press <Esc> to remove the File Menu
- Type D to select Default Settings

If the screen looks similar to the one shown below, especially the values in the highlighted fields, BIOPAK can find its files and is apparently installed correctly. If the screen does not look like this, BIOPAK has not been installed correctly.

```
BIOPAK    Design a Run    Default Settings

 ---------------Modify or Add Default Settings------------------

   Area1 Defaults (use when not present in data)
      Fixed Plot Area                              Units
      Prism Basal Area Factor                      Units
      Plot Slope Correction                        Units


   Equation Key Defaults (use when not present in data)
      Geographic  Area  Code  W
      Seral Stage Code        0


  Equation Selection Penalty Defaults
      Maximum ESP level     79999
      Threshold ESP level       0
      Summation ESP level       0


   Select Only Reassigned Species?    N

   <Ctrl-S> Save/Exit                <Ctrl-Q> Cancel/Exit
D:\BIOPAK\TESTDATA\TUTOR.RD    <F10> Units & Codes    <F1> Help
```

Press <Ctrl-Q> and continue to back out to the Main Menu without saving this file. Quit BIOPAK.

The installation can be checked further by comparing the files on the BIOPAK directory with those shown below.

Installation on a Network

The installation described here runs on the Novell network-at our development site, the Forestry Sciences Laboratory in Corvallis, Oregon. It may have to be modified to fit your network brand and configuration. Several of these steps must be done with a text editor or word processor that can edit flat ASCII files.

1. Make a backup copy of the BIOPAK disk.
2. Decide which network server, drive, and directory you want to install the BIOPAK system files and the Equation Library on. There must be about 6 Mbytes free space. We refer to this as the BIOPAK directory and call it

K:\BIOPAK in these instructions, but any drive and path will do. Users should not be able to change these files. This directory need not be on the search paths of potential users.

3. Use the DOS Copy or Xcopy command to copy files on the BIOPAK disk to that directory. For example, if reading the disk on the A drive, type:
   COPY A:*.* K:\BIOPAK
   COPY A:\TESTDATA*.* K:\BIOPAK
4. Go to the BIOPAK directory, then unpack BIOPAK system files and the library using these commands at the DOS prompt:
   BIOPAK1
   LIBRARY
5. The files that match these names can now be deleted: BBAT? INSTR? INSTALL.BAT LIBRARY.EXE BIOPAKl.EXE.
6. If BIOPAK will be installed on a drive other than K:, then all occurrences of K:\ in the file BIOPAKN.BAT shipped with BIOPAK must be changed to point to the drive it will be installed on.
7. Copy BIOPAKN.BAT from the BIOPAK directory to a network directory that will be on the search path of every potential BIOPAK user.
8. Instruct users to copy the tutorial files (TUTOR.*) in K:\BIOPAK to a personal directory on which they can write. The library files (BIOLIB?.*) -also should be copied if they anticipate changing them.
9. Make two changes to each PC that will be used to run BIOPAK.
   a. Increase the DOS. environment space by at least 512 bytes above what currently works for each PC. This can be done by using a text editor or word processor to change the SHELL command in the C:\CONFIG.SYS file. Syntax of the SHELL command differs for different versions of DOS, so consult your DOS manual. Under DOS versions 3.3 and higher, this is done with a command like:
      SHELL=C:\DOS\COMMAND.COM /P /E:2048
      This line in the CONFIG.SYS file will set the environment space to 2,048 bytes.
   b. Be certain there is enough free DOS memory to run BIOPAK and, if not, free some up, as described above in the section, *Installation on a PC.*

BIOPAK is now ready to run over your network.

Starting BIOPAK on a network

Start BIOPAK in a directory containing data that you want to calculate plant components from and that will contain BIOPAK output. While working with BIOPAK, delete files from intermediate runs. To avoid accidental deletion of files needed for running BIOPAK, do not start BIOPAK, or store input or output files, in the BIOPAK directory.

To start BIOPAK over a network, type:
 BIOPAKN E:\temp
where E:\temp is any full path, including <drive>:\<path> on which BIOPAK can write its temporary files. You must have permission to write there. It should have a minimum of 3 Mbytes of free space, or more, depending on the size of files to be processed with BIOPAK. About 8 Mbytes will be required to use the large equation library shipped with BIOPAK. RAM drives are faster; network drives are slower.

Verifying BIOPAK installation on a network

Verify that BIOPAK has been installed correctly by performing the steps described above under *Verifying BIOPAK Installation on a PC,* **except start BIOPAK as just described.**

Files on the BIOPAK directory

These files will be in the BIOPAK directory after successful installation:

BATCHMAN.COM
BATCHMAN.DOC
BIOCMP .EXE
BIOCODES
BIOLIB .DBF
BIOLIB .EQN
BIOLIB .FPT
BIOMSGS
BIOPAK .BAT*
BIOPAKN .BAT
BIOPROJ .EXE
BIORPTS .EXE
BIOSUMM
CHECK .COM
FOXSWAP .COM
INSTALLC.BAT**
KEYPRESS.COM
LHA .EXE
LHA .HLP
LHA213 .DOC
LISTR .COM
MAPMEM .COM
SD .COM
WAIT .EXE

*** not in network installation.**
**** optional, can be deleted.**

The utilities BATCHMAN.COM (.BAT file enhancement), CHECK.COM, LHA.EXE (file compression), LISTR.COM (file viewing), MAPMEM.COM (map of memory usage), SD.COM (directory listing) and WAIT.EXE (pause execution for n seconds) are used by BIOPAK and can be used independently.

Performance Enhancement

Use of RAM disk as temporary directory

Specifying that BIOPAK put its temporary files on a RAM disk considerably speeds operations. This can be done when using the installation program to put BIOPAK on a hard disk or when starting BIOPAK over a network. There must be a minimum of 4 Mbytes free on this directory for BIOPAK to run.

Use of smaller equation library and

The Equation Library shipped with BIOPAK has about 1,000 equations, including documentation. Each time the Equation Library is retrieved, a copy is made in the designated temporary directory. If you are working with a complete Equation Library and planning to access the Library on a regular basis, it may be desirable to create a subset of the Library. For example, if concerned only with tree species, you could save a subset of the Library with just tree species.

Many of the runs made to determine which equations to use are best made with subsets of large datasets.

GETTING STARTED

This chapter includes an outline of the major BIOPAK features and suggestions for using BIOPAK.

Section

Overview of Features

BIOPAK has been designed for calculating and summarizing species-specific plant components for large datasets. Several plant components, such as biomass, leaf area, and stem volume, can'be calculated, though we often refer only to plant component(s) or biomass to improve readability. The package is menu-driven to facilitate use. BIOPAK was designed with several major functions. These are accessed through the Main Menu and are described briefly in this chapter.

The relations among BIOPAK procedures and important files are shown in figure 1. You must become familiar with these relations to use BIOPAK.

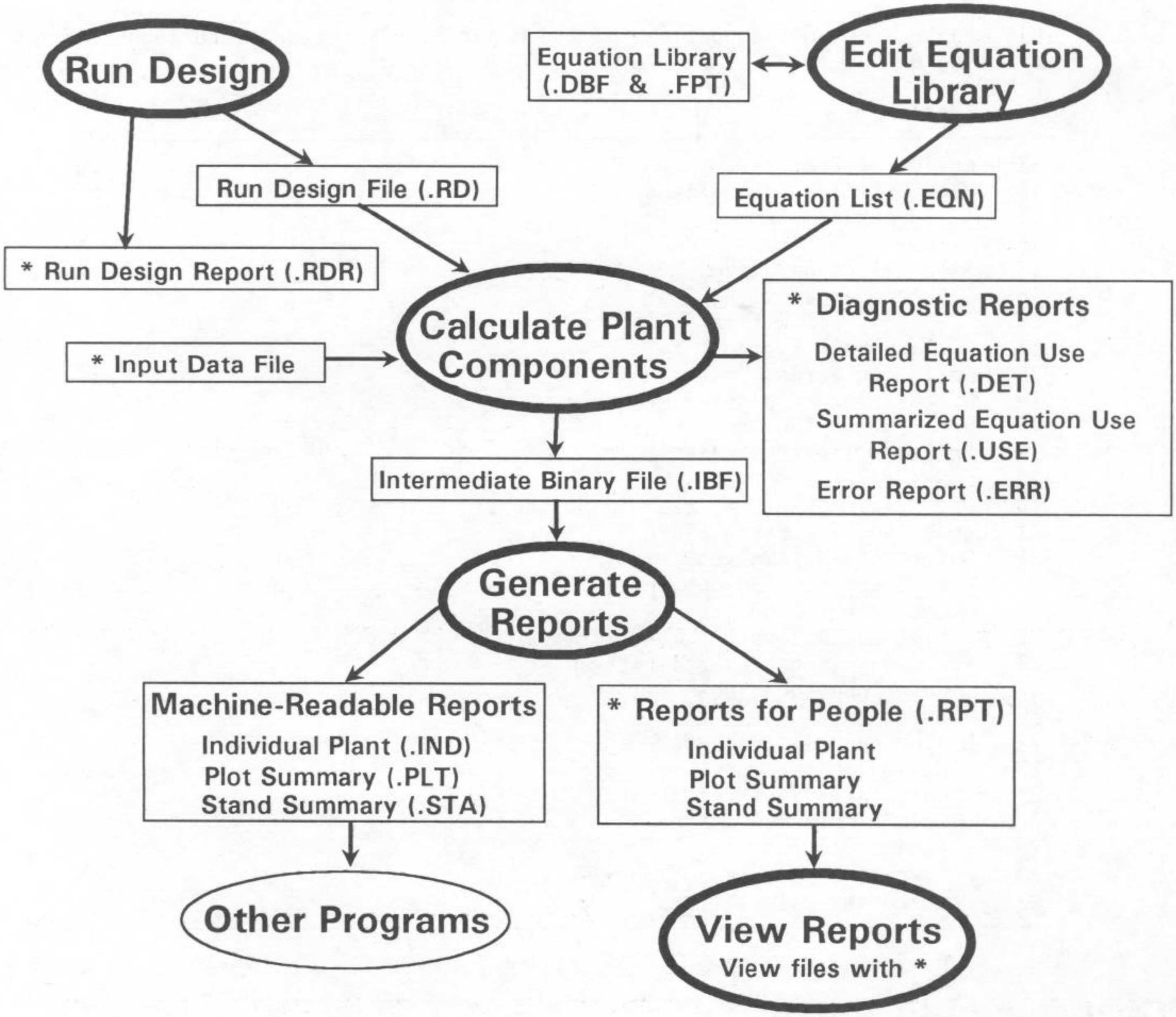


Figure 1--Relations between BIOPAK procedures and important files. Procedures are in ellipses; files are in boxes.

User interface operations

Keyboard--

The following keys operate as consistently as possible throughout BIOPAK. Most exceptions are noted in the documentation for that section.

When in a menu:

Key	Function
Hot Keys:	The capitalized key in a menu selection is a hot key that selects that item.
<Esc>:	In most submenus, exits to next highest menu without doing any work. You will have a chance to save, work that might be lost.
<Enter>:	Selects line or action from menu.

When in an edit or modify window:

Key	Function
<Ctrl-S>:	Saves all changes and exits to next highest menu or window.
cCtrl-Q>:	Cancels all changes to current record or window and exits to next highest menu or window.
<F1>:	Brings up the on-line help system.
<F10>:	When in the relevant data-entry cell, displays a list of valid codes for selection.
<Arrows>:	Moves to adjacent character or line.
<Tab>:	Moves cursor to next data-entry cell.
<Shift-Tab>:	Moves cursor to previous data-entry cell.
<Del>:	Deletes a character, or entry.
<Ctrl-Del>:	Deletes a line of data.
<Enter>:	Selects code from list, or moves cursor to next data-entry cell.

Mouse--

In many cases the mouse can be used to position the cursor and select menu items; when a mouse driver is loaded before starting BIOPAK. We suggest working the tutorials to learn to use the mouse. Mouse usage is not consistent, unfortunately, due to insufficient development resources. In particular, use only single clicks to select menu items.

File selection windows

There are two FoxPro File Selection Windows; one for selecting an existing file, the other for naming a file that will be produced. They allow easy selection of a file, or specification of a new file name, on any drive and path available to DOS. Instructions for their use with cursor keys are given here.

The following keys will help you move around in the windows:

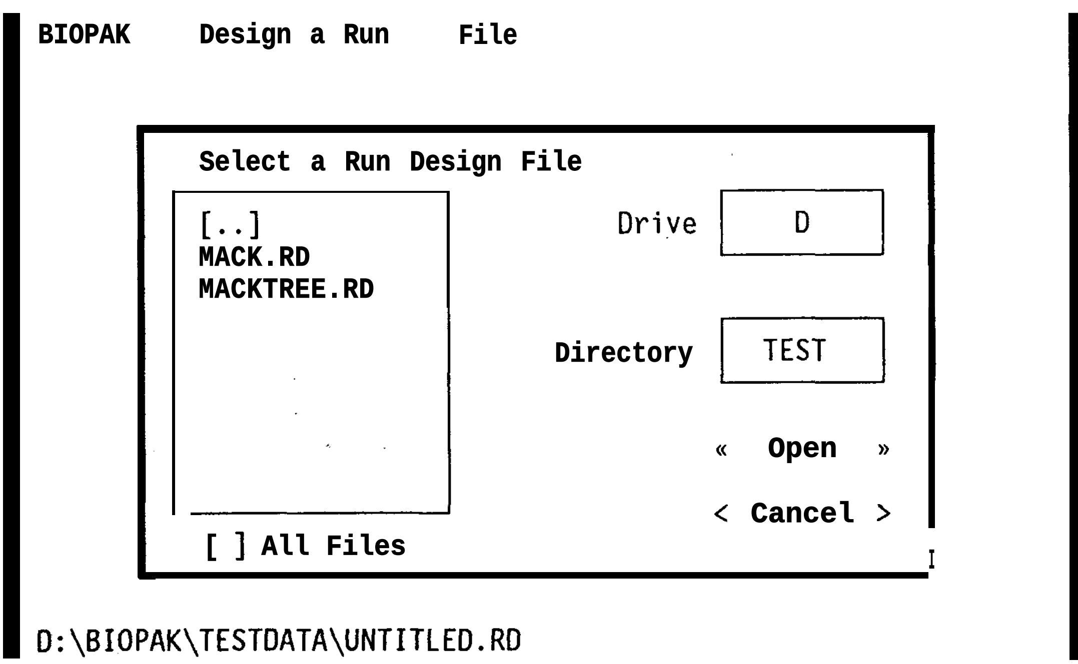
Key	Function
<Tab>:	Moves cursor to next box or field, clockwise
<Shift-Tab>:	Moves cursor to previous box or field, counterclockwise
<Esc>:	Cancels all changes and exits

Select an existing file--

Follow these steps to select a file (or use a mouse and double-click the options):

1. If the wrong drive is shown, move the cursor to the Drive letter box, press <Enter> (a list of all available drives will be shown), highlight the drive to be used, and select it by pressing <Enter>.
2. If the wrong directory is shown, <Tab> to the Directory box, press <Enter> (a list of all the available directories will be shown), highlight the directory to be used, and select it by pressing <Enter>. Or, <Tab> to the File display box on the left side, highlight the desired directory and press <Enter>. The symbol [..] indicates the parent directory to the one shown. This step can be repeated to move up and down directory trees until the desired directory is reached.
3. When the desired drive and directory are shown, highlight the desired file name and press <Enter> (or select <Open>) to select it.

The window used for selection of files looks similar to this:



Specify a new file--

To specify a new file name, follow steps 1 and 2, above, as needed. Then <Tab> to the bottom line of the <u>File Selection Window</u>, enter a new file name, <Tab> to the « Save » box, and press <Enter>. The file that will be saved is the one shown in the box at the bottom of the window.

The window used to name a file, will look similar to this:

```
BIOPAK     Calculate Plant Components

┌────── Main Menu ──────
│ Design a run
│ edit equati ┌──────────────────────────────────────────────────────┐
│ Calculate p │ Enter New Intermediate Binary File:                  │
│ Generate re │ ┌────────────┐                                       │
│ View report │ │ [..]       │        Drive      │ D     │          │
│ g┌──────────│ │ AVERYF.IBF │                                       │
│ Q│ Title: T │ │ AVERYPK.IBF│                                       │
└──│ Run desi │ │ MACK.IBF   │                                       │
   │ Equation │ │ MACKTREE.IBF│   Directory    │ TEST2 │            │
   │ input Da │ │ NOSLOPE.IBF│                                       │
   │ Intermed │ │            │                                       │
   │──────────│ │            │              «  Save  »               │
   │ summariz │ └────────────┘                                       │
   │ detAiled │   [ ] All Files              < Cancel >              │
   │ errOr re │                                                      │
───│──────────│  TEST2.IBF                                           │
Mos│>>>>>>>>> │                                                      │
  R└──────────└──────────────────────────────────────────────────────┘
  Equation Library File       :  D:\BIOPAK\TESTDATA\BIOLIB.EQN
  Input Data File             : D:\BIOPAK\TESTDATA\MACK.DAT
  Intermediate Binary File    : D:\BIOPAK\TESTDATA\MACK.IBF
```

On-line help system

A major feature of BIOPAK is its on-line help system. In most windows and menus, <Fl> will display a help window that is sensitive to the context. There is also a reference section where users can find definitions of terms and descriptions of files.

The Help Topics List is organized as follows:

1. BIOPAK Main Menu: List of Main Menu items. Displayed when <Fl> is used from the Main Menu, or Calculate Plant Components, Generate Reports, and View Reports Windows. Selection of an item from the list will display contents for that' item.
2. Before You Begin: List of topics covering information about BIOPAK. A detailed explanation about how to use the FoxPro Help System is included.
3. Run Design Menu Items: List of Design a Run Menu items. Text includes description of each menu item.
4. Library editor Menu Items: List of Library Editor Menu items.' Text includes description of each menu item.
5. Run Design Interfaces: List of Design a Run windows and menus. Pressing <Fl> exhibits help text when in the relevant window or menu.
6. Library Editor Interfaces: List of Library Editor windows and menus. Pressing <Fl> displays help text when in the relevant window or menu.
7. Reference: List of topics that covers terms, concepts, and files referred to in other BIOPAK Help windows. All topics are included in at least one "See Also" of another Help window.

In BIOPAK windows and menus, the Help Window that appears looks similar to this:

```
I BIOPAK    Design a Run    Default Settings
┌─────────────────────────────Help────────────────────────┐
│                 │ ┌──────────────────────────┐           │
│ «  Topics  »    │ │  Default Settings Window │           │
│                 │ └──────────────────────────┘           │
│ <   Next   >    │                                        │
│                 │ INTRO TO DEFAULT SETTINGS >            │
│ < Previous >    │    This window displays the current    │
│                 │    BIOPAK default settings in          │
│ < Look Up >     │    reversed-video fields. They may be  │
│                 │    changed by tabbing to the desired   │
│ ┌──────────┐    │    field and typing over the           │
│ │ See Also │    │    information.  While in the relevant │
│ └──────────┘    │    field, pressing <F10> will produce a│
└─────────────────┴────────────────────────────────────────┘
    Equation Selection Penalty Defaults
         Maximum ESP level     79999
         Threshold ESP level     0
         Summation ESP level     0


       Select Only Reassigned Species?    N

 <Ctrl-S>  Save/Exit                        <Ctrl-Q> Cancel/Exit
D:\BIOPAK\TESTDATA\UNTITLED.RD <F10> Units & Codes <F1> Help  I
```

Selections in the Help Window:

Selection	Function
<< Topics >>	Displays a complete list of topics. User can scroll through Help Topics List, and select from it.
< Next >	Shows contents of next help topic in list.
< Previous >	Shows contents of previous help topic in list.
< Look Up >	Allows specification of word or subject to find in Help Topics List.
| See Also |	Displays a list of related topics. User can choose from the list and view the contents.

Designing a run

You can Design a Run (see fig. 1) by specifying the default settings, the format of input data, the plant components to be calculated, and how BIOPAK is to select equations from a library.

Two methods of selecting equations are available: (1) BIOPAK can select the most appropriate equations for individual plants based on certain criteria, or (2) BIOPAK allows you to specify the equation(s) to be used. The latter method, called Equation Reassignment, most reliably selects the most appropriate equations and takes the least computer time. This can be done directly from the Reassignments Add/Modify Window of Design a Run.

Most often, a combination of both methods will best facilitate the users objectives. If uncertain about the most appropriate equation, compare results for various reassignment specifications with a small subset of the data.

The design specifications for a run are put in a Run Design File (*.RD), used to direct the calculation of components (see fig. 1). You can request a Run Design Report (*.RDR) of these specifications.

Calculation of plant components

Plant components are calculated in a separate step from the Run Design (see fig. 1). You specify the Input Data File (*.DAT) the Run Design File (*.RD), and the Equation List File (*.EQN) to be used. An Intermediate Binary File (*.IBF) is produced. To help diagnose problems with a run, select reports that summarize the equations used (*.USE), list all equations used (*.DET), and show errors detected for each plant component requested (*.ERR).

Reports of plant components

Reports may be generated as needed from the Intermediate Binary File (see fig. 1). Component data for individual plants, and plot and stand totals, are available in reports formatted for people (*.RPT) and as machine-readable reports (*.IND, *.PLT, and *.STA) for analysis by other software. BIOPAK does not support printing so files must be printed outside the program.

Output can be requested in either English or metric units. The specific units are listed in *Appendix: Units.*

Equation library and editor

BIOPAK comes with an Equation Library of about 1,000 equations. The equations are primarily from the Pacific Northwest region of North America. A Library Editor (see fig. 1) allows you to add and delete equations from this Library, or to make an entirely new Equation Library. Users from outside of this region should make libraries for their own region or subregions. You must make an Equation List File (*.EQN) from a Library by using the Library Editor. This file is used in calculations (see fig. 1).

BIOPAK matches species in the data with equations in the Library by using a six-character (maximum) Species code. We used the species codes for the Pacific Northwest standardized by Garrison and others (1976) for the equation in the Library distributed with BIOPAK. Most codes are only four letters long; the first two letters represent the first two letters of the genus, and the last two letters represent the first two letters of the species.

Many plant component equations have been compiled on paper (for example, Gholz and others 1979, Standish and others 1985, Stanek and State 1978, Tritton and Hornbeck 1982), but this Equation Library apparently is the first published incorporation of such equations into a computer database.

DOS shell

To execute some DOS commands without exiting BIOPAK, go to the DOS Shell. Return to the directory BIOPAK was executed from before returning to the program. To return to BIOPAK, type EXIT, and press <Enter>.

Use outside the Northwest

BIOPAK can be used in other regions. Equations for plants in a new region must be entered into a new or existing library by using the Library Editor in BIOPAK. New Geographic Area and Seral Stage codes must be entered when needed as described in *Appendix: Customizing BIOPAK.*

Suggestions for Using BIOPAK

In this section we recommend procedures that increase the efficiency and accuracy of component estimates. They may have to be adapted to your own circumstances.

Before field sampling

List species and components--

First, make a list of the plant species and their components that BIOPAK is to estimate. This may take preliminary field work.

Locate equations to use--

Second, decide which equations will be used. Use the Library Editor to see what equations are already available in the Equation Library (shipped with BIOPAK). An Equation Library can be searched by Species and Plant Component codes as described in *Reference:* **Library** *Editor.* **You may decide on a given equation because it requires easier measurements (for example, DBH) than an alternative equation (for example, height and form factor). Choose equations carefully. Comparisons of estimates by different equations may help in selecting the appropriate one.**

If no available equations fit your needs, several options exist:

1. **You can search the literature and contact local botanists, foresters, -and ecologists to see if other suitable equations exist; this could start with references in this paper.**
2. **You can sum the results of several equations for several other components to estimate a desired component. For example, stem biomass and foliage biomass could be summed to estimate total aboveground biomass for a shrub. First, however, see if BIOPAK will choose an acceptable summation automatically as described in** *Appendix: Selecting Equations and Summations:* ***BIOPAK Selects.*** **Alternatively, BIOPAK can be instructed to use specific equations as described in** *Appendix: Selecting Equations* **and Summations:** *User Selects.*
3. **BIOPAK can use an equation for a different geographic area, seral stage, or species as described in** *Appendix: Selecting Equations: User Selects.* **For example, an equation for <u>Vaccinium alaskaense</u> could be used for <u>Vaccinium ovalifolium</u>, or an equation for <u>Libocedrus decurrens</u> Torr. in California could be used for this species along the west side of the Cascade Range in Oregon.**
4. **You can build equations by measuring (and usually harvesting) plants of a wide range of sizes in a specific area. Alemdag (1980), Pieper (1978), Standish and others (1985); Valentine and others (1984), and Wharton and Cunia (1987) describe methods for doing this.**

List parameters and make forms--

With the equations to be used, make a list of the field measurements required to obtain the parameters for each species and plant component. Potential measurement parameters and units are listed in *Reference: Input Data File: Parameters.* **Then design field forms (on paper or a field data recorder) to facilitate recording these measurements, given the sampling system chosen. The**

forms should be designed so a dataset can be created easily as described in *Reference: Input Data File.*

Field sampling and data entry

Field sampling can now be done. If feasible, record all parameters in separate columns on your field sheets. For example, keep DBA and DBH in separate columns.

Enter new equations--

Enter any equations found in other sources, or that you made yourself, into the Equation Library to be used, as described in *Reference: Library Editor.* **Then make an Equation List File for use in computations. This can be done before field sampling.**

Enter data--

Enter field data, observing the instructions in *Reference: Input Data File.* **In general, each input record (1) may not exceed 255 characters, (2) must occupy only one line in the Input Data File, and (3) must have fixed-length data fields (for example, DBH is always in columns 23-28).**

calculation runs

It is helpful to give each run a name, for example FALLCRK1 and use this as the root for all associated output (for example, FALLCRK1.RD FALLCRKl.USE, FALLCRKl.IBF, and FALLCRKl.RPT).

Plan to use your whole dataset in the initial run. If it is so large that execution times or file sizes prohibit this, use a subset that includes each species and the full range of sizes within each species.

Designing the run--

Create a Run Design File including the Default Settings, Data Input Format, Components to Output, and any Equation Reassignments needed (to use summations and to use an equation for one species in place of another species). This process is described in *Reference: Design a Run.*

At this point you should know all the species in the Input Data File to be used, the components to be calculated for each, and the equations likely to be used. You will probably make several runs.

Calculate plant- components--

After selecting the files to be used in the run, request the Summarized Equation Use Report (*.USE) on the Calculate Plant Components Window, then select Go.

Choose Generate Reports from the Main Menu and make all three of the Reports for People (*.RPT): Individual Plant Report, Plot Summary Report, and Stand Summary Report, then select Go.

Initial run evaluation--

Examine the Summarized Equation Use Report (*.USE). Were the appropriate equations used? Did the Equation Reassignments you created function as

intended? Review the Individual Plant Report in Reports for People (*.RPT). Do the estimates seem reasonable? Are the detected errors acceptable? Lastly, check the estimates on the Plot Summary and Stand Summary Reports in Reports for People to see if they are reasonable. Information in these reports is described in *Reference: Reports and Other Output.*

If results seem acceptable, use this as the final run and generate the reports to be used for further analyses.

Additional runs--

If results are unacceptable, determine what caused the problems and design a new run to correct them. Problems often can be corrected by modifying and adding equation reassignments and adding more appropriate equations to the Library. For example, you may choose to avoid an overextrapolation or underextrapolation by reassigning large or small plants to an equation based on large or small plants, respectively.

Diagnosing problems--

If you need to determine the specific equation (or summation) used for a given calculation, make another run and request a Detailed Equation Use Report (*.DET). This report is the largest and may require using a subset of the data. The Error Report (*.ERR) also may be helpful because it shows error codes, Original Equation Request, and Equation Selection Penalty (ESP) for each value calculated. Error messages, other difficulties and suggested fixes are in *Appendix--Troubleshooting.*

Now make another trial run and evaluate the results.

Documenting calculations

Keep copies of the Run Design File (*.RD), Summarized Equation Use Report (*.USE), Equation Library (*.DBF), as well as the Input Data File, used for important computations (for example, as FALLCRK1.RD FALLCRK1.USE and FALLCRKl.DBF). These will serve as documentation of the equations used to generate your results. If results ever need to be repeated, compared, or defended, this information will be valuable. Also keep a copy of the Intermediate Binary File (*.IBF) for a short period to make other reports.

REFERENCE

This chapter covers the requirements for the input file, the features and basics in each BIOPAK module, and a description of reports.

Section

Input Data File

Section

BIOPAK reads input data (for example, variables such as species codes, plant identifier, and values for DBH) from a data file during execution. Specify the input data variables available to BIOPAK by defining the Data Input Format when using Design a Run. The variables, and valid units, that may be used by BIOPAK from the Input Data File are shown in *Appendix: Codes* and *Appendix: Units.* The Parameter codes listed with the units are the codes used in the Data Input Format Window of Design a Run and in the Equation Library; these codes are not necessary in the Input Data File.

Required organization of the data

The order of input records is important in obtaining correct totals and averages in reports. Specifically, in a given Input Data File, all plot identifiers in each stand must be contiguous, and all stand identifiers must be contiguous. That is, all data from a plot must be clustered together', and all data from a stand must be clustered together. Otherwise, Plot Summary and Stand Summary Reports will give erroneous results.

To be read directly by BIOPAK, the Input Data File must be organized as specified below:

1. Each input record must occupy only one line of the file and be no more than 255 characters long.
2. Fixed field-length records. Each data point, or variable, must always occupy the same columns. In other words, if the species code is in columns l-6 of record 1, then species must be in columns 1-6 for all other records.
3. Spaces, commas, or other data delimiters are not necessary. If they are used, do not include them when counting the field length for the variables.
4. No two variables should occupy the same field. BIOPAK will still process the data, but problems may occur as described in *Parameters.*

A few lines from a sample dataset which meets BIOPAK requirements, are shown below. The column headings are included for interpretation and are not part of the data file.

Dataset ID	Stand #	Plot	Date	Spp	Tree #	DBH (cm)	HT (m)
TP9801	MACK	riparl	830623	TSHE	5478	18.3	5.9
TP9801	MACK	riparl	830623	TSHE	5477	44.9	21.1
TP9801	MACK	riparl	830623	THPL	5479	8.5	3.2
TP9801	MACK	riparl	830623	TABR	469	5.7	3.0
TP9801	MACK	ripar2	830623	CONU	463	5.8	7.1
TP9801	MACK	ripar2	830623	TABR	5480	7.2	4.3
TP9801	MACK	ripar2	830623	ACMA	468	9.4	14.8
TP9801	MACK	ripar2	830623	TSHE	5476	42.6	24.8

Data input format

The Data Input Format Window of Design a Run is where the Input Data File specifications are made. A detailed description of this can be found in *Reference: Design a Run.*

Site and Plant Identification codes

To request Plot or Stand Summary reports, Plot or Stand must be included in the Input Data File for each plant so BIOPAK will function correctly as described below.

Date, Locale, and Plant identifiers provide additional ways to identify input records. They are not used in the execution of BIOPAK but do appear in reports if included in the Data Input Format.

The Site and Plant Identification codes are included in the output reports and may be used for purposes other than what their names imply. This can be facilitated by renaming them when using Design a Run. For example, Date, Locale, Stand, Plot and Plant id may be relabeled, respectively: Year, County, Tract, Plot, Tree #; or Month, Basin, Plot, Subplot, Plant; or Date, Stand, Plot, Microplt, Treatment.

Species code--

This code may be up to six characters long. It must match the Species code of the desired equation(s) in the Library if BIOPAK is to find the equation(s) without a reassignment *(see Appendix: Design a Run).* Most Species codes appearing in the supplied Equation Library conform to Garrison and others (1976). Exceptions include codes for bryophyte species and for equations based on data from several species. See Appendix: Codes for a list of the Species codes included in the BIOPAK Equation Library.

Seral Stage and Geographic Area codes--

These codes can be in the Input Data File, or they can be set constant when using Design a Run. BIOPAK uses them when it tries to choose equations that most closely match the environmental characteristics of the input data. The Geographic Area and the Seral Stage codes crudely classify the growth environment(s) of plants harvested to build equations and of plants in the Input Data File.

When a Geographic Area or Seral Stage code is not included in the Input Data File, or when the input value is a blank, the default value provided by you in the Default Settings of Design a Run will be associated with input records.

For the currently recognized Geographic Area and Seral Stage codes, see the *Appendix: Codes.*

Lifeform code--

BIOPAK must associate a lifeform code with each input record processed. Lifeform codes affect equation selection, the matching of equation reassignments to input records, the components calculated for the current input record, and the community stratum within which output is listed in reports. *See Appendix: Codes* for a list of valid *Lifeform* codes.

A plant lifeform variable should be included in the Data Input Format when you Design a Run if these data are in the Input Data File. BIOPAK will try to read a lifeform code from the input record if this variable is included in the format. If not included in the format, or if the lifeform code value of the input record is a blank, lifeform substitution procedures described in *Appendix: Lifeform* are used to assign a *lifeform* to the plant. If the species occurs in an Equation Reassignment, or in the Library used in the run, BIOPAK will try to find the taxonomic lifeform from these sources; In general, you need not be concerned if lifeform does not come in from the Input Data File.

The coppice lifeform is recognized for trees and shrubs because stump sprouts often have a different growth form than plants grown from seed.

Parameters

Parameters in the Input Data File are used as predictor variables in plant component prediction equations. The following information on individual plants, called parameters in this manual, can be used by BIOPAK.

Code	Standard metric units	Description
BIO	g	Biomass
CIR		Circumference
COV	%	Canopy cover
CR	%	Crown ratio
DBA	cm	Diameter at or near base
DBH	cm	Diameter at breast height
FC	%	Form class
HT	cm	Height
LEN	cm	Length (for example, along stem, projected crown length)
NP	NA	Number of plants
NUM	NA	Number (for example, of fronds, stems, or flowers)
*PLOTAREA	m2	Fixed-plot area
*PRISMFAC	m2/ha	Prism basal area factor
*PLTSLOPE	%	Plot slope correction
SAP	cm	Sapwood radial thickness
SPA	cm2	Sapwood cross-sectional area
VOL	dm3	Volume (for example, of bole, or crown)
WID		Width (for example, projected crown width)

In the Equation Library, Parameter codes represent the independent variables used to calculate the plant components, with the exeception that codes marked

by asterisks cannot be used in equations and are only relevent for plots. Other metric and English Units can be input as listed in *Appendix: Units.* **These are converted to standard metric units for calculations.**

The types of measurements can be different for different species. Input data, for example, may contain basal diameters for some shrubs, cover for some herbs, number of fronds and mean frond length for a fern, and diameter, height and crown ratio for a tree.

No two parameters should occupy the same location in the Input Data File used with BIOPAK. If, for example, the measurements for DBH and DBA were recorded in the same columns in the input data records, a serious problem may occur. For example, there are species in the Library having some equations using DBA and others using DBH; Acer macrophvlum (ACMA) is one. If the collected data are for the DBH of ACMA, and if both DBA and DBH are specified as being in the same data field, when BIOPAK encounters equations that use DBA, it may use these thinking that DBA was a measured parameter. BIOPAK will then use the DBH values in your Input Data File as DBA values in its calculations. This can be handled best by modifying the Input Data File with a text editor so that no two parameters occupy the same data field.

It is possible, though usually not recommended, to specify DBA as being in the same location as DBH in the Data Input Format of Design a Run. This can be done in either of two ways:

1. **Use the Reassisnments Add/Modify Window of Design a Run to select equations from the Library which use the specific parameter you measured, or,**
2. **Create a new Equation Library for the Input Data File, in which you delete all equations using parameters not measured. In other words, if you measured the DBH of THPL, delete all equations for THPL having DBA as a parameter. If you measured the DBA of ACMA, delete all equations with DBH as a parameter. Then, save the Equation Library as a different file name.**

If you will measure cover or measure one plant to represent others of the same size *see Reference: library Editor: Requirements, assumptions and possibilities for BIOPAK equations* **for the special way BIOPAK handles plant cover and number of plants.**

Design a Run

```
 Main Menu
Design a run
edit equation Library
Calculate plant components
Generate reports
View reports or data
goto dos Shell
Quit
```

Section

In this section of BIOPAK you specify much of the information used in a component calculation run. You produce a Run Design File (*.RD) that contains modifications of default settings, the format of the Input Data File, the plant components to be calculated, and any Equation Reassignments. The Run Design File is used when calculating plant components. This 'file may be saved for use in further runs.

To start this process, select:

Design a run at the Main Menu.

A Run Design Menu will be displayed. After using any procedure listed, the program will automatically return to this menu after exiting from that procedure.

```
BIOPAK    Design a Run

              — Run Design Menu
               File              1
              ----------------------
               Default  settings
               data Input format
               Components to output
               Reassignments
              ----------------------
              'Exit run design

D:\BIOPAK\TESTDATA\UNTITLED.RD
```

Run Design Menu

This section of the manual provides brief descriptions of the choices on the Run Design Menu. The following sections cover these menu choices in more depth.

Fife--

This selection will display a File Menu. Use this to create, read in, or save a Run Design File (with extension .RD). Selecting run Design report will create an easily read report, with labeled columns, from the current Run Design File (with extension .RDR).

Default settings--

This selection will display a Default Settings Window. From this window, you can edit or view Area1 defaults (plot size and slope); Equation Selection Penalty (ESP) defaults (Maximum, Threshold, and Summation ESP); Equation Key defaults (Geographic Area and Seral Stage codes); and "select only reassigned species?" option.

Data input format--

This selection will display a Data Input Format Window. From this window, you can edit or view specifications for input record variables and their format, variable labels, and associated missing data indicators.

Components to output--

The Components to Output Window allows you to edit or view the selection of plant components to be calculated for each vegetation stratum (trees, shrubs, herbs, and mosses).

Reassignments--

This selection will display the Reassignments Summary Window. This window allows you to view current equation reassignments. From here the Reassignments Add/Modify Window can be accessed, thereby allowing you to add or edit reassignments.

Exit run design--

· **Exits to the Main Menu. If changes have been-made to the current Run Design File, you will be asked** *Do you want to quit without saving? Y/N?* **To save the changes to the Run Design File, go back and select File. When the File Menu appears, select Save run design file. Now, the file name can be either changed, or overwritten.**

File Menu

Select File and a new menu will appear with the following choices:

- **Read existing run design file**
- **Create new run design file**
- **Save run design file**
- **run Design report**

Each time the Design a Run module is entered, you are starting with a new Run Design File (UNTITLED.RD); empty, except for a few default settings. It therefore is not necessary to create a new file at this time. When additions and changes have been made to the Run Design File, Save the file and name it. All BIOPAK Run Design Files must have an .RD extension.

```
BIOPAK    Design a Run    File

          — Run Design Menu 1
          File
          ─────────────── File Menu ────────────
          Default│ Read existing run design file
          data In│ Create new run design file
          Compone│ Save run design file
          Reassig│──────────────────────────────
          ───────│ run Design report
          Exit ru│──────────────────────────────

D:\BIOPAK\TESTDATA\UNTITLED.RD
```

Read existing run design file--

To modify an existing Run Design File, select Read existing run design file. A <u>File Selection Window</u> will appear. With tabs or arrows, move the cursor to the target file name and press <Enter>. The program will return to the File Menu, and the Run Design File you selected will appear as the current file in the bottom left corner of the screen. Press <Esc> to get out of the File Menu.

Create new run design file--

To create another .RD File, make this selection, and another new file, UNTITLED.RD will be available for editing. If changes had been made previously to the UNTITLED.RD file, which was created when opening the Design a Run module, but those changes were not saved, you will be warned that the file has not been saved. Press <Esc> to get out of the File Menu.

Save run design file--

To save the changes previously made to the Run Design File, select Save run design file. A File Selection Window will appear to prompt you to name the file. It will be given the extension .RD. Press <Esc> to remove the File Menu.

NOTE: Be sure the file is being saved where it should to be saved. If you want to change the location where the file will be saved, see Getting Started: Overview of Features: File Selection Windows.

Run design report--

To save the Run Design File in a report format, with titles and column headings, select run Design report. A File Selection Window will appear to prompt you to name the file. It will be given the extension .RDR. Press <Esc> to get out of the File Menu. (To view the Run Design Report, go to View reports in the Main Menu.)

Often, you will want to modify an existing .RD File to make a new one and save it before exiting.

Default Settings

When Default settings is selected, the current BIOPAK settings are 'displayed in reversed-video fields in the Default settinqs window. They may be changed by tabbing to the desired field and typing over the information. While in the relevant field, pressing <F10> will produce a list of codes and units from which you can make a selection. See Appendix: Codes for a list of valid codes.

```
BIOPAK    Design a Run    Default Settings

 ---------------Modify or Add Default Settings---------------

  Area1 Defaults (use when not present in data).
     Fixed Plot Area                         Units
     Prism Basal Area Factor                 Units
     Plot Slope Correction                   Units

  Equation Key Defaults (use when not present in data)
     Geographic Area Code
     Seral Stage Code

  Equation Selection Penalty Defaults
     Maximum ESP level        79999
     Threshold ESP level          0
     Summation ESP level          0

  Select Only Reassigned Species?    N

   <Ctrl-S> Save/Exit                  <Ctrl-Q> Cancel/Exit
D:\BIOPAK\TESTDATA\UNTITLED.RD <F10> Units & Codes   <F1> Help
```

The window sections are defined below:

Areal defaults--

These defaults are used if plot area and slope are not present in the Input Data File. Plot area and slope are required for BIOPAK to execute areal calculations. If plot area and slope were not recorded in the Input Data File, and you intend to request areal calculations or areal-based reports, include them here. User may specify either Fixed Plot Area or Prism Basal Area Factor, but not both.

Fixed Plot Area: Should be specified if the sample plots were of a fixed area (that is, if plants were sampled from within a given area), and either there are some missing data, or the plot area is not present in the Input Data File. May be up to eight characters long, including the decimal.

Prism Basal Area Factor: Should be specified if data in Input Data File are from variable radius plots (that is, if the plants were sampled by using a prism basal area factor). May be up to six characters long, including the decimal.

Plot Slope Correction: Even if the slope of the test plots were zero, plot slope is still required for BIOPAK to do areal calculations. May be up to six characters long, including the decimal.

Equation Key defaults--

These defaults are used if the codes are not in the Input Data File. For a record to be considered complete, codes for Geographic Area and Seral Stage are required. If these codes are not included in the Input Data File, they must be specified here.

Geographic Area default: Code assigned when Geographic Area is not given in the input record. The acceptable codes are shown when pressing <F10>. If an invalid code is entered, an error message will appear.

Seral Stage default: Code assigned when Seral Stage is not given in the input record. The acceptable codes are shown when pressing <F10>. If an invalid code is entered, an error message will appear.

Equation Selection Penalty defaults--

These settings are required. Without them, BIOPAK cannot select equations from the Library or perform calculations. User must specify a value for each of the three Equation Selection Penalties (ESPs). The upper range of the ESP may be modified by you as described in *Appendix: Customizing BIOPAK* **(the allowable upper range will always be the "NO VALUE CALCULATED" value specified by you in BIOCODES, minus one). The upper range for ESPs in BIOPAK, as shipped, is 79999. ESPs are discussed under** *Appendix: Equation Selection Penalties.*

Maximum Equation Selection Penalty: Maximum ESP value that a selected equation may have (range:l-79999). Default = "79999"

Threshold Equation Selection Penalty: ESP value at or below which the program search for a better equation is terminated (range: O-79999). Default = "0"

Summation Equation Selection Penalty: ESP value above which a summation will be attempted (range: O-79999). Default = "0"

Select only reassigned species--

Setting the select species option instructs BIOPAK whether to process only those species in the data file that occur in an equation reassignment. This is especially useful if there are many input records-and this is a second run after reassignments were done.

Select Only Reassigned Species?: Press <Enter> to toggle the Yes/No selection (Y/N). Default = "N".

Keys to use when editing:

Key	Function
<F1>:	Help
<F10>:	Displays list of valid codes and units
<Tab>:	Moves cursor to next cell in row
<Shft-Tab>:	Moves cursor to previous cell in row
<RightArrow>:	Moves cursor to next character
<LeftArrow>:	Moves cursor to previous character
<Delete>:	Deletes a character or entry
<Ctrl-Q>:	Quits without saving and exits to the Run Design Menu
<Ctrl-S>:	Saves changes and exits to Run Design Menu

Data Input Format

In this section of Design a Run, you specify the format of the input data. No calculations can be executed if this step is omitted. All data for an individual record must occur in a single line of the input file. The maximum length for each record is 255 characters. Position and field width must be set for each variable to be read. The number of decimal digits is ignored when set for integer data types. *See Reference: Input Data File* for more details about input data requirements.

When selected from the Main Menu, a table of variables currently specified for input is displayed in the <u>Data Input Format window</u>. Press <PgDn>, <PgUp> or arrow keys to see the rest of the variables.

```
BIOPAK    Design a Run    Data Input Format

 ------------------FORMAT OF DATA INPUT FILE------------------
  Var  Name  Label/Description      Units Type Pos Len Dec Mis
 --------------------------------------------------------------
  DATE      Date                           A
  LOCALE    Locale                         A
  STAND     Stand                          A
  PLOT      Plot                           A
  PLANT ID  Plant ID                       A
  SPECIES   Species                        A
  LIFEFORM  Lifeform
  GEO AREA  Geographic Area                A
  SERSTAGE  Seral Stage                    A
  BIO       Biomass                        F
  CIR       Circumference                  F
 ---------------------Scroll for more...-----------------------

 Var Name = Variable Name         Pos = Beginning field position
 Label/Description = of variable  Len = Field length of variable
 Units = Units of measurement     Dec = Number of decimal places
 Type = Data Type (A, E, F, or I) Mis = Missing data indicator

 <Ctrl-S> Save/Exit <Ctrl-Del> Delete Line <Ctrl-Q> Cancel/Exit
 D:\BIOPAK\TESTDATA\UNTITLED.RD   <F10> Display Units <F1> Help
```

For each variable in your dataset (Input Data File), most of the following entries are required:
Variable Name: The first five names can be changed. These are used in headings of some reports.
Variable Label/Description: These cannot be changed.
Units: Only the variables from BIOMASS to PLOT SLOPE have units associated with them (except NP and NUM). When in the units column, <F10> displays a list of valid units to select from.
Data Type: Required for variables 10-27 only (BIOMASS-PLOTSLOPE). I = integer, F = floating point (real) and E = exponential format. Other variables are alphanumeric (A).
Position (required): The first column position of this field in an input record.
Field Length (required): Number of character positions. The maximum field width is 6 characters for Species, Prism Basal Area Factor, and Plot Slope Correction; 8 characters for Date, Locale, Stand, Plot ID, Plant ID, and Fixed Plot Area; and 10 characters for all others.
Decimal Places: Number of decimal digits in an I, F, or E datatype.
Missing Data Indicator: A string which, when it occurs in an input record, signifies a missing datum for this variable (usually a blank or ".").

Keys to use when editing:

Key	Function
<F1>:	Help
<F10>:	Displays list of valid units and codes
<Tab>:	Moves cursor to next cell in row
<Shft-Tab>:	Moves cursor to previous cell in row
<RightArrow>:	Moves cursor to next character
<LeftArrow>:	Moves cursor to previous character
<UpArrow>:	Moves cursor up rows
<DnArrow>:	Moves cursor down rows
<Delete>:	Deletes a character
<Ctrl-Del>:	Deletes a line of entries
<Ctrl-Q>:	Quits without saving and exits to the Run Design Menu
<Ctrl-S>:	Saves changes and exits to Run Design Menu

Components to Output

You can specify the components to be calculated, up to eight. Though only eight Component codes can be output for any particular BIOPAK run, more components can be calculated in additional runs. Note that the strata codes used by this procedure are not equivalent to lifeform codes, but instead represent groups of lifeforms, or community strata.

The currently defined Component codes are listed with definitions in Appendix: *Codes.* Users may expand this list as described in *Appendix: Customizing BIOPAK.* Some of these codes are included to facilitate future addition of equations to the Library, but there are no equations in the Library shipped with BIOPAK that calculate them.

If Components to output is chosen from the Run Design Menu, a table of the current component selections (if any) is displayed. You can modify this table

by doing the following:
1. Move the cursor to the relevant cell and delete or add components and strata.
2. Press <Ctrl-S> to save and exit, or <Ctrl-Q> to cancel changes and exit.

There are two ways to add components:
1. Type the Component codes directly on the screen. To do this:
   a. Move cursor to a blank line.
   b. Type appropriate code.
   c. Press <Tab> to tab over to the right to specify the strata, OR
2. Select them from the list of components as follows:
   a. Move cursor to a blank line.
   b. Press <F10> for a list of Component codes. Move up and down by using arrow keys or mouse.
   c. Move highlight bar to the appropriate component. Select by pressing <Enter>. The program will then return to the <u>Components to Output Window</u>. The selected component will have been entered under the heading <u>Code</u>.

```
BIOPAK    Design a Run    Components to Output

  Components to be Calculated for Selected Vegetation Strata
 Code Definition of Plant Component Code               |T|S|H|M|

  1  BAT Biomass, aboveground, total                    Y N N N
  2
  3
  4
  5
  6
  7
  8

                                     Strata Codes
                               T - Trees
                               S - Shrubs, Coppice
                               H - Herbs, Grasses, Sedges
                               M - Mosses, Lichens, Bryophytes

<Ctrl-S> Save/Exit <Ctrl-Del> Delete Line <Ctrl-Q> Cancel/Exit
 D:\BIOPAK\TESTDATA\UNTITLED.RD <F10> Component Codes <F1> Help
```

For each component selected, specify that it be computed either for species of all plant community strata, or only for species of a particular stratum. To specify that a stratum be selected, enter "Y," for yes.. To indicate that a stratum not be selected, enter "N" ("N" is the default).

Keys to use when editing:

	Function
<F1>:	Help
<F10>:	Displays list of valid codes
<Enter>:	Selects from pop-up list of Component codes
<Tab>:	Moves cursor to next cell in row
<Shft-Tab>:	Moves cursor to previous cell in row
<RightArrow>:	Moves cursor to next character
<LeftArrow>:	Moves cursor to previous character
<UpArrow>:	Moves cursor up rows
<DnArrow>:	Moves cursor down rows
<Delete>:	Deletes a character
<Ctrl-Del>:	Deletes a line
<Ctrl-Q>:	Quits without saving and exits to the Run Design Menu.
<Ctrl-S>:	Saves changes and exits to Run Design Menu.

Equation Reassignments

This section of the Design a Run module allows you to specify Equation Reassignments (described in detail under *Appendix: Selecting Equations and Summations:* **User** *Selects)* **including specific summations and Primary** *Lifeform* **Default codes. A Reassignment is executed when the Criteria matches the Original Equation Request, as described in** *Appendix: Selecting Equations and Summations.*

Through use of the Local Equation Number for an individual equation in the Library, you can precisely identify a substitute equation. To use this technique, obtain the correct Local Equation Number from the Equation Library. This is described under *Appendix: Selecting Equations and Summations: User Selects Equations and Summations: Reassigning Equations.*

It is possible to select equations directly from the Equation Library as described in Reassignments Add/Modify Window.

Reassignments Summary Window--

When Reassignments is selected from the Run Design Menu, a Reassignments Summary Window appears.

```
BIOPAK    Design a Run    Reassignments

+------------------- Reassignments Summary---------------------------+
|        L Plt G S -Parameter 1- -Parameter 2- -Parameter 3- P #     |
| SPP    F Cmp A S Cde Min Max Cde Min Max Cde Min Max L S           |
+--------------------------------------------------------------------+
|                                                            0       |
| ABIES T BAT                                                1       |
|                                                                    |
+--------------------------------------------------------------------+

+--------------------------------------------------------------------+
| SPP     = Species               Cde = Parameter Code               |
| LF      = Lifeform              Min = Minimum Parameter Value      |
| Plt Cmp = Plant Component       Max = Maximum Parameter Value      |
| GA      = Geographic Area       PL = Primary Lifeform Default      |
| ss      = Seral Stage           #S = Number of Substitutions       |
+--------------------------------------------------------------------+
<Ctrl-S> Save/Exit   <Ctrl-Del> Delete Record <Ctrl-Q> Cancel/Exit
 D:\BIOPAK\TESTDATA\UNTITLED.RD   <Enter> Add/Modify    <F1> Help
```

Reassignments that were previously specified are shown. The information shown on the screen may include the Species, Lifeform, Plant Component, Geographic Area, Seral Stage, and Parameter codes and ranges, the Primary Lifeform Default, and the Number of Substitutions.

The full Reassignments can be viewed and modified, and new Reassignments can be added in the Reassignments Add/Modifv Window. To view or modify an existing reassignment, highlight it and press <Enter>. To add a Reassignment, move the cursor to the blank line at the top of this window and press <Enter>. These actions bring you to the Reassignments Add/Modifv Window.

Reassignments Add/Modify Window--

This window shows the Reassignment Criteria, Substitutions and Primary Lifeform Default. Edit by moving the cursor to the relevant cell and typing in the new data. Criteria, Substitutions and Primary Lifeform Default are discussed below. When the modifications are complete, press <Ctrl-S> to save the changes and return to the Reassignment Summarv Window, or <Ctrl-Q> to cancel changes.

```
 BIOPAK    Design a Run    Reassignments    Add/Modify
                         Add/Modify
   Criteria
  Species         ABIES    Parameter1 Parameter2 Parameter3
  Lifeform         T
  Plant Component BAT      Code        Code        Code
  Geographic Area          M i n       Min         Min
  Seral Stage              Max         Max         Max

   Substitutions
  # Species Lifeform PlantComp GeoArea SerStage LoclEqn#
  1   ABCO       T        BAT

  3
  4
  5
  6
  7
  8
  9

    Primary Lifeform Default
<Ctrl-S> Save/Exit    <Ctrl-Del> Delete Line   <Ctrl-Q> Cancel/Exit
D:\...\TESTDATA\UNTITLED.RD <F3> Eqn Library <F10> Codes <F1> Help
```

Keys to use when editing in the Add/Modify Window

Key	Function
<Fl>:	Help
<F3>:	Access Equation Library
<FlO>:	Displays list of valid units and codes
<Tab>:	Moves cursor to next cell in row
<Shft-Tab>:	Moves cursor to previous cell in row
<RightArrow>:	Moves cursor to next character
<LeftArrow>:	Moves cursor to previous character
<Delete>:	Deletes a character
<Ctrl-Del>:	Deletes a line
<Ctrl-Q>:	Quits without saving changes and exits to the Run Design Menu.
<Ctrl-S>	Saves changes and exits to Run Design Menu (need to press it more than once).

Criteria--
The list of Reassignment Criteria is necessary to execute reassignments. BIOPAK will execute a reassignment only if a record can be found that matches the Reassignment Criteria you listed. A datum matches a criterion when the criterion is an identical value or a blank. If all values for one case from the input data file match their respective criteria, then the data case matches the reassignment and a reassignment will occur. Species is the only criterion that must be included in a reassignment.

As an example, suppose you want to reassign an equation for a plant component of a particular tree species, the species and component (and any other relevant criteria needed to identify the specific plant(s) or data record(s) to be reassigned) would need to be entered in the reassignment criteria list. BIOPAK will check each case from the input data file to see if it matches the criteria. For each case that matches a reassignment will occur.

Plants within a specified size range of a given parameter can be reassigned differently. For example, the smaller sizes of a particular tree species can be reassigned to the same species with a shrub lifeform. To view a list of the Parameter codes, move the cursor to a parameter cell and press <F10>. Select codes from this list by scrolling to the desired parameter, and pressing <Enter>; or type the codes directly onto the screen *(see Appendix: Codes* for a list of valid parameter codes).

Substitution keys--

The Substitution Keys allow you to specify what should replace the information in the Original Equation Request when forming the Request to Library (for more information *see Appendix: Selecting Equations and Summations).* BIOPAK will use this new request when searching for an equation in the Equation Library.

If there is more than one equation in the Library that matches the Request to Library, one of two things will happen. (1) You can specify the particular equation to be used by including the Local Equation Number in the Substitution line. If you do, you must fill in all other fields on that Substition line. (2) If you do not include the Local Equation Number, the equation BIOPAK chooses cannot be predicted.

You can select equations directly from the Equation Library. Press <F3> to access the Library Editor from the Add/Modifv Window. To select only one equation, move the cursor to the desired equation and select Reassignment selection from the Edit Library Menu. To select more than one equation, mark the desired equations, then select Reassignment selection. Details on how to use the Library Editor can be found in *Reference: Library Editor.*

The Primary Lifeform Default--

The Primary Lifeform Default can serve two purposes:

1. It can replace missing lifeform data: When lifeform is a variable in your Input Data File, but is missing in some records, BIOPAK will substitute the Primary Lifeform Default in the missing records. The steps used to find a lifeform are described in *Appendix: Lifeform.*
2. It can assign output to strata in reports: If lifeform is a variable in your Input Data File, and is not missing in any records, the Primary Lifeform Default will assign the output to a community stratum in reports. [Note: by default, trees are assigned to the Tree Stratum; shrubs and coppice to the Shrub Stratum; herbs, grasses, and sedges to the Herb Stratum; mosses, lichens, and bryophytes to the Moss Stratum.]

   As an example, assume that lifeform is a variable in your Input Data File. There are no missing Lifeform codes in your Input Data File. You, however, would like the smaller salix trees to be assigned to the Shrub Stratum in the report output. In the Reassiqnment Add/Modifv Window, type in SALIX as the species in the Criteria and Substitutions, include the parameter range for the size of the willows to be assigned to the Shrub Stratum, and type in S as the Primary Lifeform Default.

Library Editor

```
         Main Menu
Design a run
edit equation Library
Calculate plant components
Generate reports
View reports or data
goto dos Shell
Quit
```


Many users will need to use different equations than those supplied with BIOPAK. When working with large numbers of equations, it becomes difficult to document sources of equations, make unit conversions, and enter equations correctly. We have tried to facilitate this by providing an Equation Library

Editor that allows you to add new equations to the existing Library, create a new Library, or locate, sort, modify, and generate documentation for equations in a Library.

Equation Library size is limited by only disk storage capacity. The maximum number of equations that can be used at one time to calculate plant components is limited as described below in Library *Editor: Edit Library Menu:* **File--.**

The Library Editor is invoked from the Main Menu by selecting:

edit equation Library

Several items on the Edit Library Menu will be available. Menu choices that have no use at this point, however, are not selectable.

Equation Keys

BIOPAK selects equations primarily by using the Equation Key of each equation as described in *Appendix: Selecting Equations* **and subsequent sections. Thus, it is important that each equation have a unique Equation Key in a library. The following items make up an Equation Key:**

- **Species code**
- **Lifeform code**
- **Plant Component code**
- **Geographic Area code**
- **Seral Stage code**
- **Local Equation number**

The definitions of each code in the Library and in the BIOCODES file shipped with BIOPAK are given in *Appendix: Codes.* **Species codes are flexible; you can use any code no longer than six characters. The codes for lifeform are fixed; that is, you cannot use Lifeform codes other than those listed in** *Appendix: Codes.* **The codes for Plant Component, Geographic Area, and Seral Stage must be in BIOCODES; if an unlisted code is used** *(see Appendix: Codes* **for a list), add this new code to the BIOCODES file as described in** *Appendix: Customizing BIOPAK.* **If all the codes in the Equation Key are identical, for two or more equations, give them different Local Equation numbers to make the Equation Keys unique.**

Duplicate equation keys may occur when one Equation Library File is appended to equations already in the Library Editor. Check for duplication and modify the Local Equation Numbers (or other parts of the Keys) to make the Equation Keys unique. To do this, first sort the Library by the elements of the Equation Key as given above. Second, search by eye for duplicate Equation Keys. Third, change the Equation Keys as needed after selecting View/Modify from the Edit Library Menu.

Be sure that the Species codes chosen for Equation Keys are the same as those that will come from your data; otherwise Equation Reassignments will have to be made *(see Reference: Design* **a** *Run: Reassignments).*

Requirements, assumptions, and possibilities for BIOPAK equations

Equation Numbers--

The Equation Number (as well as the Equation Key) should be unique for every equation in an Equation Library. Unique Equation Numbers provide an easy way to identify and search for individual equations.

Plant components (dependent variables)--

Components in the Library are the dependent variables in the equations. Every equation must calculate a value for only ONE plant, except when cover percent (COV) is a parameter (predictor variable), as described in this section, below.

Codes--

The Component codes used to represent the dependent variables in the equations in the Library must conform to the codes listed in the BIOCODES file. The Component codes in BIOCODES, as shipped with BIOPAK, can be found in *Appendix: Codes.*

Units--

The units associated with the Component codes must conform with the units listed in the BIOCODES file. The Component units in BIOCODES, as shipped with BIOPAK, can be found in *Appendix: Units.*

Parameters (predictor variables)--

Parameters in the Library are the predictor or independent variables in the equations. For many of the equations in the Library, there is more than one parameter used to calculate the components. For a given component, some equations may use one parameter, and other equations may use another. The parameter ranges for each equation usually are included.

Cover, handled differently--

Each time the parameter COVER is used in the computation of a component, the result is multiplied by the area (in square meters) of the plot. To conform with this computation rule, for all equations that use COVER as a parameter, the coefficients installed in the Library must be calibrated so that the equation gives the plant component on a l.O-square-meter-plot, regardless of the size of the plots used to develop the equations. For component calculations based on cover data, when possible, select library equations based on a plot size equal to the plot size of your input data.

Number of plants, handled differently--

When the parameter, number of plants (NP) is available, BIOPAK considers that line in the Input data File to represent NP plants. When NP is greater than 1: the number of plants, tree basal area and calculated plant component(s) and are multiplied by NP; and average values for the parameters are weighted by NP. This occurs whether or not NP is a parameter in the equation(s) used. This feature is provided so several plants of one species and size can be recorded on one line of a field form.

We recommend against including NP as an equation parameter because it could easily cause confusion. Number (NUM) can be used instead for number of stems, fronds, et cetera.

New Predictor variable needed--
Occassionally, users may want to use an input parameter not included here, for example, plant density (for example, number of plants per square meter). Such parameters can be read in using one of the above names. Plant density, for example, can be read in as NUM. When this is done it is very important to be sure equations are not used that include that parameter with a different meaning. You could guard against this by building a new library in which all equations (for the species involved) that use the NUM parameter are expecting density in the same units as in the Input Data File.

Codes--
The Parameter codes used to represent the independent variables in the equations must conform to the Parameter codes listed in *Appendix: Codes.* **These are the same parameters that can be specified in the Data Input Format Window of Design a Run** *(see Reference: Design a Run: Data Input Format).*

Units--
The units associated with the parameters must conform to the units listed in *Appendix: Units.*

Coefficients--
Coefficients are the values estimated by regression or other methods. There can be a maximum of four in an equation.

Equation types allowed--
The equation types in table 1 are currently built into BIOPAK. Only these types can be used. We have found most equations can be put in a library using one of these forms. Sometimes specifying a coefficient as 0.0 will allow a simpler equation to be entered using a more comples equation type. Sometimes a new equation will need to be fit in a form allowed by BIOPAK.

Table l--Equation types and corresponding codes recognized by BIOPAK Equations are often shown here with a dependent variable that is log-transformed, for example, lnY for clarity of presentation and to be consistent with documentation in Biolib. The dependent variables are always untransformed, that is, Y, in BIOPAK. For logarithms: ln = natural logarithm, log = base 10 logarithm. These equation type codes should be used when a new equation is entered in an Equation Library.

Code	Equation type
1	$Y = C_1 + C_2P_1$
2	$\ln Y = C_1 + C_2 \ln P_1$
3	$\log Y = c_1 + C_2 \log P_1$
4	$Y = C_1 + C2P_l^2$
5	$Y = c_1 + c_2P_1$

6 $$Y = C_1 \frac{e^{(C_2 + C_3P_1)}}{1 + e^{(C_2 + C_3P_1)}}$$

7 $$Y = C_1 + C_2e^{P_1}$$

8 $$Y = C_1 + C_2(P_1^2P_2) + C_3(P_1^2P_2)^2$$

9 $$Y = C_1 + C_2(P_1^2P_2)$$

10 $$\ln Y = C_1 + C_2P_1 + C_3P_2^2 + C_4\sqrt{P_2}$$

11 $$Y = C_1 + C_2P_1 + C_3\sqrt{P_1}$$

12 $$Y = C_1 + C_2\ln P_1$$

13 $$\ln Y = C_1 + C_2P_1$$

14 $$Y = e^{(C_1 + C_2P_1)}P_2$$

15 $$Y = C_1 + C_2(P_1P_2)$$

16 $$\ln Y = C_1 + C_2\ln P_1 + \ln P_2$$

17 $$\ln Y = C_1 + C_2\ln P_1 + C_3\ln P_2$$

18 $$\ln Y = C_1 + C_2P_1 + C_3\ln P_2$$

19 $$\ln Y = C_1 + C_2P_1 + C_3\ln P_1 + C_4\ln P_2$$

20 $$\log Y = C_1 + C_2\log P_1 + C_3P_2 + C_4(\log P_1)P_2$$

21 $$\log Y = C_1 + C_2\log P_1 + C_3\log P_2 + C_4\log P_1\log P_2$$

22 $$\log Y = C_1 + C_2\log(\tfrac{1}{4}\pi P_1^2P_2)$$

23 $$\log Y = C_1 + C_2\log P_1 + C_3\log P_2$$

24 $$Y = C_1 + C_2P_1^3 + C_3P_1^2P_2$$

25 $$\ln Y = C_1 + C_2\ln(P_1P_2)$$

26 $$Y = C_1 + C_2P_1^2 + C_3P_1^2P_2 + C_4P_1P_2$$

27 $$Y = C_1 + C_2P_1^3 + C_3P_1^2 + C_4P_1P_2$$

28 $Y = C_1 + C_2P_1^3$

29 $Y = C_1 + C_2P_1 + C_3P_1^3$

30 $Y = C_1 + C_2(P_1P_2) + C_3P_2$

31 $\ln Y = C_1 + C_2\ln P_1 + C_3P_2 + C_4\ln P_2$

32 $Y = C_1 + C_2P_1 + C_3P_1^2$

33 $Y = C_1 + C_2P_1 + C_3P_1^2 + C_4P_1^2P_2$

34 $Y = C_1 + C_2P_1^3 + C_3P_1^2$

35 $\ln Y = C_1 + C_2\ln(P_1+P_2)$

36 $\ln Y = C_1 + C_2\ln(P_1^2+P_2)$

37 $Y = C_1 + C_2P_1^2P_2 + C_3P_1^2 + C_4P_1P_2^3$

38 $Y = C_1 + C_2(P_1^2P_2)^{\frac{1}{3}} + C_3(P_1^2P_2)^{\frac{2}{3}} + C_4P_1^2P_2$

39 $Y = C_1 P_1^2 [C_2 + C_3P_2 + \frac{C_4P_1P_2}{(P_2-137.16)}] \frac{P_2^3}{(P_2-137.16)^2}$

40 $Y = e^{(C_1 + C_2\ln(P_1^2P_2))} - e^{(C_3 + C_4\ln(P_1^2P_2))}$

41 $Y = C_1 + C_2P_1^2 + C_3P_1^4$

42 $\ln Y = C_1 + C_2\ln P_1 + C_3\ln P_2 + C_4\ln P_3$

43 $\ln Y = C_1 + C_2\ln P_1 + C_3\ln(P_2^2 + P_3^2)$

44 $\log Y = C_1 + C_2\log P_1 + C_3\log P_2 + C_4\log P_3$

45 $\ln Y = C_1 + C_2\ln P_1 + C_3(\ln P_1)^2$

46 $Y = C_1 + C_2P_1 + C_3P_2$

47 $Y = C_1 + C_2P_1 + C_3P_2 + C_4P_3$

48 $\ln(Y+C_1) = C_2\ln(P_1+C_3) + C_4$

49 $\ln Y = C_1 + C_2\ln(P_1+C_3)^2$

50 $\ln Y = C_1 + C_2 \ln P_1 + C_3 \ln(P_2 + C_4)$

51 $Y = C_1 + C_2 P_1^{C_3} + C_4 P_2 P_3$

Modifying and creating equation libraries

Your first step when using the Library Editor will be to add one or more equations (see *Add* equation-- below in this section), or retrieve an existing library (see File--: *Retrieve library* below in this section). Once you have done one of these, one line of documentation for each equation in the Library Editor can be seen in the Eauation Summary Window. File maintenance and many other jobs can be done with the Edit Library Menu. Equations and copies of equations can be modified. These steps are described in the following sections.

Equation Summary Window

```
 BIOPAK    Edit Equation Library                        Rec:1/252
 Eqn        L Plnt G S LE T Eq --Parameter-- --Parameter--
 n"  Spp    F Comp A S #  L Tp Code min max Code min max N    R^2
                                ---- Edit Library Menu ----
 24  ABAM   T BBL  W O 1  T  2 DBH | File                    | 9   0.9
 23  ABAM   T BFT  W 0 1  T  2 DBH |-------------------------| 9   0.9
 320 ABAM   T BST  W 0 1  T  2 DBH | Sort equations          | 75  0.9.
 25  ABAM   T BSW  W 0 1  T  2 DBH | Locate equation(s)      | 14  0.9'
 708 ABCO   T VSW  C M 1  T 37 DBH | Delete equation(s)      | 378 0.9
 323 ABMAS  T BST  W 0 1  T  2 DBH |-------------------------| 17  0.9'
 321 ABMAS  T BSW  W 0 1  T  2 DBH | Add equation            | 17  0.9'
 707 ABMAS  T VSW  C M 1  T 37 DBH | Copy & edit equation    | 65  0.9
 28  ABPR   T BBL  W M 1  T  2 DBH | View or modify equation | 6   0.9
 27  ABPR   T BFT  W M 1  T  2 DBH |-------------------------| 6   0.9
 30  ABPR   T BSB  W M 1  T  2 DBH | display mode            | 6   0.9
 253 ABPR   T BST  W M 1  T  2 DBH | Mark/unmark equation    | 310 0.9
 29  ABPR   T BSW  W M 1  T  2 DBH | Browse equation(s)      | 6   0.9
 77  ACCI   S AFT  W M 1  S  2 DBA |-------------------------| 19  0.9
 80  ACCI   K AFT  W Y 1  S  2 DBA | Reassignment selection  | 19  0.9
 82  ACCI   K BBD  W Y 1  S  2 DBA |-------------------------| 8   0.3
 78  ACCI   S BBL  W M 1  S  2 DBA | Exit library editor     | 11  0.9
 81  ACCI   K BBL  W Y 1  S  2 DBA |-------------------------| 6   0.9
 76  ACCI   S BFT  W M 1  S  2 DBA 0.6   13.1                 31  0.9
 D:\BIOPAK\TESTDATA\ADLIB                 <F10> Menu off <F1> Help
```

Column headings--

For each equation in the Library, the Equation Summary Window will display the following:

- **Eqnt: Equation number (unique number used to identify equations).**
- **spp: Species of plants in source data.**
- **LF: Lifeform of plants in source data.**
- **Plnt Comp: Plant Component code (dependent variable).**

- **GA:** Geographic Area of plants in source data
- **SS:** Seral Stage of plants in source data
- **LE#:** Local Equation number (number used to distinguish equations with identical equation keys).
- **TL:** Taxonomic Lifeform. "True" lifeform of species.
- **Code:** Code for parameter (independent variable) used to calculate component. Up to two components are displayed.
- **min:** Minimum value of parameter used to construct equation.
- **max:** Maximum value of parameter used to construct equation.
- **N:** Number of plants in sample.
- **R^2:** Value for R-square of equation.

Special keys--

Key	Function
<Esc>	Removes the Edit Library Menu (necessary before scrolling through the one-line equation summaries)
<PgUp>, <PgDn>	Shows the previous or next page of equation summaries
<Arrows>	Move the highlight bar through the equation summaries and highlight a particular equation
<FlO>	Toggles the Edit Library Menu
<F1>	Provides entry to help screens
<+>	Marks an equation and moves the highlight bar to the next equation (+ and - work like Mark/unmark equation on the Edit Library Menu)
<->	Unmarks an equation and moves the highlight bar to the next equation
<Enter>	Shows the documentation of the highlighted equation summary in the <u>Original and Final Equations Window</u>--same as View/Modify on the Edit Library Menu

Edit Library Menu

When there are equations in the Library Editor, any item on the Edit Library Menu can be chosen (if you have entered the Library Editor from the Main Menu); Otherwise, the editing functions are not selectable. The following sections describe how to use the functions of this menu. Instructions for editing an individual equation are in *Editing an Equation.*

File--

lIf File is selected from the menu, a File Menu will be displayed with the following selections:

Retrieve library: Retrieve an existing Equation Library (*.DBF file). You can select a file from the <u>File Selection Window</u>.

Save equations: Save the Equation Library currently in BIOPAK. When Save is selected from the File Menu, a File Type Menu appears. The current library can be saved and renamed as one of three file types:

- equation library Database (*.DBF),
- Equation list file (*.EQN), or
- Text documentation (*.TXT).

When saved as a Database, the file can be read into the Equation Library Editor for future browsing and editing; it can be used for selecting equations from the <u>Reassignments Add/Modify Window</u> of Design a Run and to create Text documentation or an Equation List File (needed for calculating plant components).

The Equation List File (*.EQN) can be saved only after saving as a Database. If the file has not been saved as a database file, Equation list file will not be selectable. The Equation List File is needed to calculate plant components. A maximum of 4,000 equations may be in an Equation List File, with a maximum of 600 for any given species.

The Equation Documentation Text File (*.TXT) is a flat ASCII file. If changes have been made to the current Equation Library Database, save the database file before saving text documentation. Depending on the number of equations in the Database File, this may be very large (with two equations per page). The file can be used in word processing documents or for reference purposes.

Keep the original Library (BIOLIB.DBF and BIOLIB.FPT) in the BIOPAK directory, and save new and modified Libraries in the directory containing any test data or report files generated. This will avoid confusion about which Library to use and reduce the likelihood of accidently overwriting the original Library.

Retrieve can bring in an initial Equation Library to work on or append one or more additional libraries.

You can read in an Equation Library when equations are already in the Library Editor, but you must be careful. BIOPAK checks the incoming Library for equations with equation numbers the same as those already in the Library Editor. You will be given the choice of allowing them in or deleting them. BIOPAK does not check for equations with duplicate equation keys. This will not affect the selection of equations by BIOPAK unless they have identical Equation Keys.

If two or more equations have identical keys it will be impossible for BIOPAK or you to differentiate them when making calculations--any might be used.

When using Save, after choosing the file type, you will be asked to specify the equations to save in the Scope Menu.

Items that can be saved:
- Marked equation(s) if any are marked.
- Current equation (equation indicated by the highlight bar).
- Range of equations (range of Equation Numbers, not range of record numbers in the file).
- All equations in the Library Editor.

Next, specify the name of the output file in a File Selection Window.

Sort equations--
Allows sorting of the equations in the Library Editor. Sorting can be done by one sort key (Single key sorting) or by several keys simultaneously (Multiple key sorting).

Single key sorting allows sorting by one of the following:
- equation Number
- Plant species
- Lifeform
- plant Component

- Geographical area
- Seral stage
- equation Type

Multiple key sorting allows sorting by any combination of the above, in any order. Enter the number, or rank, to be associated with the element in the key when sorted.

Sort, combined with Locate, can be helpful in finding all equations with the same species, geographic area, or plant component.

Locate equation(s)--

Displays a Locate Equation(s) Menu with the following selections:

- equation Number
- equation Key
- next match
- Quit

When equation Number is selected, the cursor moves to an open space above the field of Equation Numbers. Type in the number to be searched for. After it is entered, it will be right-justified. Therefore, there is no need to include leading zeroes, blanks, or wild cards (?); they would invalidate the search. Pressing <Enter> completes the search.

When equation Key is selected, the cursor moves to an open space above the first element in an Equation Key (Species). You must type in the characters in the Equation Key (codes for Species, Lifeform, Plant Component, Geographic Area, Seral Stage, and the Local Equation Number) to be searched for. Typing a wild card (?) matches any character in that column, thereby allowing you to search for a certain Plant Component or Equation Type, for example. Pressing <Enter> completes the search.

After completing a search for an Equation Number or Equation Key, the Locate Equation(s) Menu reappears so another search can be made. The Edit Library Menu leaves the screen when finding equations so that more information about the equations can be seen. Whenever Next match is a selectable menu item, it can be used; for example, after locating and editing an equation, the Next match to the last search key can be found.

Delete equation (s)--

The following may be deleted:

- Marked equation(s) if any are marked,
- Current equation (equation indicated by the highlight bar),
- Range of equations (range of Equation Numbers, not range of record numbers in the file),
- All equations in the Library Editor. This clears all the equations currently in BIOPAK, but does. not affect the Equation Library File that was read into the Library Editor.

You will be asked to confirm delete commands.

Add equation--

Displays an Original and Final Equations Window from which you will be able to fill in documentation for the equation being added as described in *Editing an*

Equation. This new equation will be given an equation number that is one greater than the greatest in the Library Editor.

Copy and edit equation--

Makes a copy of the equation identified by the highlight bar and displays it in the Original and Final Equations Window so its documentation can be edited as described in *Editing an Equation.* This new equation will be given an equation number one greater than the greatest in the Library Editor. Change at least one element in the Equation Key so it is not the same as that of the equation copied.

View or modify equation--

Displays the Original and Final Equations Window for the highlighted equation, allowing it to be viewed or edited as described in *Editing an Equation.*

Display mode--

Displays a menu of three video modes (lines per screen):

- 25-line mode (default)
- 43-line mode
- 50-line mode

Depending on the mode(s) supported by your PC, 43 or 50 lines allows viewing more equation summaries; however, editing documentation may be harder.

Mark/unmark equation--

This feature functions like t and - on the Equation Summary Window.

- M⁻marks an unmarked equation or unmarks a marked equation, and moves the highlight bar to the next equation.

Browse equation(s)--

There are several ways to browse the Library: Pressing <FlO> will toggle the menu off; Pressing <Esc> also will remove the menu; and Browse equation(s) also will turn the menu off and allow you to browse the equations.

Reassignment selection--

This option is available only when accessing the Library from Design a Run. While in the Reassignments Add/Modifv Window of Design a Run, this feature allows the selection of one or more equations. The equation(s) selected will then appear as Substitutions in the Reassignments Add/Modify Window (see *Reference: Design a Run: Reassignments).*

If selecting only one equation, highlight the equation, press <FlO> to bring back the Edit Library Menu, and select Reassignment selection. To select more than one equation, mark the equations and select Reassignment selection.

Exit library editor--

When exiting, BIOPAK will prompt you to save the equations in the Editor if changes may have been made since the equations were retrieved or saved (that is, if you used <PgUp> of <Ctrl-S> to exit from an editing window). You can select File to save changes.

Editing an equation

The documentation for an equation can be edited n three windows. The Original

and Final Equations Window contains identifying information (including Equation Number, genus, species, and Equation Key), the equation as in the original source and the equation as used by BIOPAK. The Source(s) of Equation Window shows the same identifying information, the location of the raw data (if known), and the source of the equation (literature reference, person, or unpublished report). The Source(s) of Data Window shows the sources of the raw data used to build the equation, including literature citation(s), site and vegetation descriptions, and important characteristics of the samples. The content and function of these windows are described in more detail below.

Document equations as fully as possible, but realize that it often is not possible to fully document some equations, even from published sources. Information deemed important for which there is no specific location in these windows can be put in the Source(s) of Data Window.

Original and Final Equations Window--

This window is reached by highlighting the one-line summary of the desired equation on the Equation Summarv Window and either pressing <Enter> or selecting View/Modify from the Edit Library Menu. In this window, <Tab> and <Shift-Tab> move the cursor between fields, pointing and clicking the left button on the mouse will position the cursor anywhere in any field, and <Ctrl-Home> will allow you to change the Equation Number.

Avoid duplicate Equation Keys and Equation Numbers, and choose appropriate Species codes, as described in *Equation* **Keys and** *Equation Numbers,* **above.**

```
BIOPAK     Edit Equation Library    View/Modify                    Rec:1/252
Ctrl-Home>: Change EQN #   ORIGINAL AND FINAL EQUATIONS
EQN #: 24   LIFEFORM: T SPP: ABAM    Abies amabilis
LANT COMP: BBL GEOG AREA: W SERAL'STAGE: 0 LOCAL EQN #: 1   TAX LIFE: T

    EQUATION AS IN BIOPAK:  Parameters (where measured):     MIN   MAX UNIT
DEP. VAR: Live branch biomass
PARl: DBH Stem dia. @ breast ht                              11.7  90.4  cm
AR2:
AR3:
OEFS: 1> 1.6708       2> 2.6261                    4>             EQ F:
QN FORM: ln(BBL) = 1.6708 + 2.6261 * ln (DBH)

    EQUATION AS IN ORIGINAL SOURCE:
ARAMETERS: (name, where measured on plant):                  MIN   MAX  UNI
EP VAR: Live branch biomass                                             kg
NDEP VAR1: DBH                                               11.7  90.4  cm
NDEP VAR2:
NDEP VAR3:
QN FORM: ln(BBL) = -5.2370 + 2.6261 * ln(DBH)

AMP SIZE: 9    R^2: 0.96 MSE: 0.163      SEE: 0.404      LOG BIAS CORR:

 <Ctrl-PgUp>: Previous equation        <Ctrl-PgDn>: Next equation
 <PgUp>: Save/Page up                  <PgDn>: Edit Sources of Eqn and Data
 <Ctrl-S>: Save/Exit                   <Ctrl-Q>: Cancel changes/Exit
D:\BIOPAK\TESTDATA\ADLIB.DBF                                      <F1> Help
```

Equation as in BIOPAK--

Information from the subsection EQUATION AS IN BIOPAK is used to calculate plant components. The fields contain the following:

- **LIFEFORM: Lifeform code for this Equation. May be any shown in Appendix: Codes, including K (Coppice) so equations with this unique growth form can be distinguished.**
- **TAX LIFE: Taxonomic Lifeform code. Should not be K (Coppice). This is the first Lifeform Code BIOPAK looks for if Lifeform did not come in from the Input Data File.**
- **DEP. VAR: Name or description of the dependent variable. This should match the Plant Component code. Its units must match those given in Appendix:** *Units: Component Units* **for this plant component. Give the range if known.**
- **PAR1, PAR2, PAR3: These are the independent variables in the equation, or parameters. Their codes must match those built into BIOPAK, described in** *Appendix: Codes.* **The units must match the standard metric units in** *Appendix: Units: Parameter Units.* **Name the parameter and describe any unique characteristics, for example: "DBA Diam. @ base, 10 cm aboveground". Parameters may be in any order; BIOPAK is not sensitive to order. New codes cannot be added, but other data can be used under these codes, as described in** *Appendix: Codes.*
- **EQ T: Equation type number must correspond to one of the equation types in table 1. This is used in calculating plant components.**
- **COEFS: Coefficients of the equation form given on the next line. These are used in calculating plant components.**
- **EQN FORM: This is the form and coefficients of the prediction equation after all transformations to units required by BIOPAK and algebraic manipulations needed to get it to match one of the forms in table 1.**

Eauation as in Original Source--

Information from the window subsection EQUATION AS IN ORIGINAL SOURCE is used to document the original algebraic form, coefficients, units, and statistics. This makes it easier to check for mistakes in transformations and units conversions should estimates from the equation come into question. Information in this subsection is not used in calculations. The MSE is the mean squared error, and SEE is the standard error of the estimate of the equation fit to the data.

Hot keys at the bottom of the Original and Final Equations Window make it easy to move to the Sources of Eauation Window for this equation, this window for the previous and next equations, and the Eauation Summarv Window.

Sources of Equation Window--

This window is reached from the Original and Final Equations Window by pressing <PgDn>. In this window, <Tab> and <Shift-Tab> move the cursor between fields, pointing and clicking the left button on the mouse will position the cursor anywhere in any field, and <Ctrl-Home> will allow you to change the Equation Number. No information in this window is used in calculations.

The window subsection RAW DATA LOCATIONS can include information helpful in finding the data used to build the equation, including person(s), location, computer, storage device, file name(s), and methods of access.

```
BIOPAK     Edit Equation Library    View/Modify                Rec:1/252
Ctrl-Home>: Change EQN #   SOURCES OF EQUATION
QN #: 24   LIFEFORM: T SPP: ABAM    Abies amabilis
LANT COMP: BBL GEOG AREA: W SERAL'STAGE: 0 LOCAL EQN #: 1  TAX LIFE: T
AMP SIZE: 9    R^2: 0.96 MSE: 0.163      SEE: 0.404      LOG BIAS CORR: Y
    RAW DATA LOCATIONS (person, file name & line nos.):

    SOURCE OF EQUATION (lit. ref or person):
holz et al. 1979. Equations for estimating... Res Pap 41, For Res Lab, Ore
tate Univ.
-------------------------------<SOURCES OF DATA>-----------------------------
1. Krumlik, J G 1974. Biomass.. M.S. thesis, Univ. B.C., Vancouver. 87 p. 12
ees 32.0-76.2 cm dbh, near Squamish B.C., 1500 m elevation, south aspect 2
ujimori et al. 1976. Biomass.. J Jpn. For Soc 58(10):360-373. Wildcat Mtn.
A, Ore 2 trees 11.7 cm and 19.4 cm dbh , 1300 m elevation.

 <Ctrl-PgUp>: Previous equation        <Ctrl-PgDn>: Next equation
 <PgUp>: Save/Page up                  <PgDn>: Edit Equation Data Source
 <Ctrl-S>: Save/Exit                   <Ctrl-Q>: Cancel changes/Exit
D:\BIOPAK\TESTDATA\ADLIB.DBF                                      <Fl> Help
```

The window subsection SOURCE OF EQUATION should include the authority for the equation; for example, a literature citation, description of how to find an unpublished report, or the person responsible for the validity of the equation.

Source(s) of Data Window--

This window is below the Sources of Eauation Window. To make changes, it is reached from this window by pressing <PgDn>. When it is active, the cursor appears inside and is surrounded by a double line. Text wraps automatically when typed in or deleted. There is no cut-and-paste capability. The following keys have special functions:

Key	Function
<Ins>	Toggles insert mode
<Home>	Moves cursor to beginning of line
<End>	Moves cursor to end of line
<UpArrow>, <DnArrow>	Scrolls text lines so more lines can be seen than fit in window at one time
<PgUp>	Exit to Sources of Equation Window and save changes.

This window can be used to document the location and growth environment of the plants sampled to build the equation. This may include geographic location(s), climatic factors, soil characteristics, vegetation age(s), seral stage(s), sample sizes and size ranges from these places, important details of the sampling procedure, and important or unconventional aspects of plant measurements.

This information should include environmental factors thought to significantly influence plant growth form so potential users can judge the appropriateness to plants in the environments of their sites. It also should include elements of the selection of study sites and plant samples and measurements of plant part that may restrict the utility of the equation.

Calculate Plant Components

```
 ────────── Main Menu ──────────
│ Design a run                  │
│ edit equation Library         │
│ Calculate plant components    │
│ Generate reports              │
│ View reports or data          │
│ go to dos Shell               │
│ Quit                          │
 ───────────────────────────────
```

Section

To calculate plant components, first Design the Run and save the Run Design File, know which Equation List File will be used, and have the Data File available to BIOPAK. Start this process by selecting at the Main Menu:
 Calculate plant components

The <u>Calculate Plant Components Window</u> will appear. Now select the Run Design File (*.RD), Equation List File (*.EQN), and Input Data File (*.DAT) used for calculations and the Intermediate Binary File to receive output (*.IBF). Calculations go to the Intermediate Binary File; and reports are generated from this file. These relations are shown in figure 1.

```
BIOPAK     Calculate Plant Components

 ────────── Main Menu ──────────
│ Design a run                  │
│ edit equation Library         │
│ Calculate plant components    │
│ Generate reports              │
│ View reports or data          │
│ g ────────── Calculate Plant Components ──────────
│ Q│ Title: BIOPAK TITLE
   │ Run design file:    D:\BIOPAK\TESTDATA\T2.RD
   │ Equation list file:  D:\BIOPAK\TESTDATA\ADLIB.EQN
   │ input Data file:    D:\BIOPAK\TESTDATA\T2.DAT
   │ Intermediate binary file:  D:\BIOPAK\TESTDATA\T2.IBF
   │──────────────────────────────────────────────────
   │ Diagnostic Reports:
   │   summarized equation Use report : YES
   │   detAiled equation use report   : YES
   │   errOr report                   :  NO
Mos│──────────────────────────────────────────────────
   │>>>>>>>>         Go         <<<<<<<<<<
 E  ──────────────────────────────────────────────────
 Input Data File          :  D:\BIOPAK\TESTDATA\T2.DAT
 Intermediate Binary File :  D:\BIOPAK\TESTDATA\T2.IBF
```

Title

With the highlight bar on this line, press <Enter>. The title entered will appear in all reports produced from this run.

Files to be used

To change a file shown on the Calculate Plant Components Window, move the highlight bar to the file name and press <Enter>. Then select a file from the File Selection Window as described in Getting Started: Overview *of* **Features:** *File Selection Window.*

NOTE: If your Input Data File does not have .DAT extension, rename the file and give it the .DAT extension so it will appear in the File Selection Window.

To make multiple runs and save the Intermediate Binary File produced from each run, change the name of the Intermediate Binary File each time.

Diagnostic Reports

Diagnostic Reports also are selected on the Calculate Plant Components Window. These reports are described in *Reference: Reports and Other Output: Diagnostic Reports.* **Highlight a report title, and then press <Enter> to select and deselect the report (Yes/No). File names for Diagnostic Reports are given the root name of the Intermediate Binary File and the extension .USE, .DET, .ERR, as described in** *Reference: Reports and Other Output: Diagnostic Reports.* **They can be viewed through the View Reports Window.**

Go

When appropriate files and reports have been selected, select GO to make the calculations that put them in the Intermediate Binary (.IBF) File. Give the file a new name to avoid overwriting the existing one.

Reports can now be generated. For a description of reports, *see Reference: Reports and Other Output: Reports for People* **and** *Reference: Reports and Other Output: Machine-readable Reports.* **The .IBF file may be saved after the first series of reports have been generated from it so that additional reports can be generated later.**

Generate Reports

```
──────── Main Menu ────────
Design a run
edit equation Library
Calculate plant components
Generate reports
View reports or data
go to dos Shell
Quit
```

Section

After plant components are calculated, Reports for People and Machine-readable Reports can be made from the Intermediate Binary File (.IBF). To do this, select from the Main Menu:

Generate reports

The <u>Generate Reports Window</u> will appear. From here select the plant, plot, and stand summary reports to be generated and the output units preferred.

```
BIOPAK     Generate Reports

  ──────── Main Menu ────────
  Des ──────── Generate Reports ────────
  edi  Intermediate Binary File:
  Cal    D:\BIOPAK\TESTDATA\T2.IBF
  Ger
  Vie  Reports for People:
  go     Individual plant report :     YES
  Qui    Plot summary report     :     YES
         Stand summary report    :      NO
         D:\BIOPAK\TESTDATA\T2.RPT
       Machine-readable reports:
         iNdividual plant report :      NO
          D:\BIOPAK\TESTDATA\T2.IND
         pLot summary report     :      NO
          D:\BIOPAK\TESTDATA\T2.PLT
         sTand summary report    :      NO
          D:\BIOPAK\TESTDATA\T2.STA
Most
  Rur  Output (Metric or English):     METRIC    ED.RD
  Equ                                             EQN
  Inp  >>>>>>>>         Go          <<<<<<<<<<
  Int
```

By default, the file names will be given the same root as the .IBF File. Names can be changed if desired, as described below. You cannot, however, change the extension of the file name.

Intermediate Binary File

The Intermediate Binary File shown is the last one created or used in this directory. It can be changed by selecting intermediate Binary file, and then selecting a different . IBF File in the <u>File Selection Window</u>.

Reports to be generated

Select and deselect appropriate reports by typing the capitalized hot key or by moving the menu bar to the report and pressing <Enter>. A file name can be changed by highlighting the file name with the menu bar, pressing -<Enter>, and then changing the name in the <u>File Selection Window</u>. The different reports are described in *Reference: Reports and Other Output.*

Output units

Toggle the output units by pressing <Enter>. If metric is toggled, output will be in standard metric units. If English is selected, output will be in standard English units. *See Appendix: Units* **for a list of BIOPAK standard units.**

Go

Once the desired files and reports are specified, select Go to generate the reports.

View Reports

```
Main Menu
Design a run
edit equation Library
Calculate plant components
Generate reports
View reports or data
go to dos Shell
Quit
```

Section

All reports and data files, except the Intermediate Binary File, can be examined by selecting, from the Main Menu:

View reports or data

The View Reports Window will appear. From here you can view the reports shown on the screen or change the name of the reports to be viewed. By default, the file names appearing are those last viewed or produced.

```
BIOPAK     View Reports or Plant Data

  Main Menu
 Des     View Reports
 edi Reports for people
 Cal   D:\BIOPAK\TESTDATA\T2.RPT
 Gen pLant data (or DOS text file)
 Vie   D:\BIOPAK\TESTDATA\T2.DAT
 go  Diagnostic Reports:
 Qui   Summarized equation use report
        NONE
       Detailed equation use report
        NONE
       Error Report
        NONE
     Machine-readable reports:
       Individual plant report
        NONE
       Plot summary report
Most    NONE
 Run   sTand summary report
 Equ    NONE                                 EQN
 Inp
 Intermediate Binary File : D:\BIOPAK\TESTDATA\T2.IBF
```

Changing a name

On the View Reports Window find the title of the appropriate report. The file name of the last report of this type, created or viewed, is shown just below its title.

You can select another file name by moving the highlight bar to the file name (for example, MACK1.RPT), and pressing <Enter>. A File Selection Window will appear, thereby allowing selection of an existing file as described in *Getting Started: Overview of Features: File Selection Windows.*

Viewing the report

After the file has been selected, move the highlight bar up to the, report title (for example, Reports for People) and press <Enter>. The selected file will be displayed. To scroll through the files and reports, use the arrow keys and <PgUp> or <PgDn>. Press X to return to the View Reports Window. Some reports are wider than the screen; use the right arrow keys to view the right half of these reports.

Reports and files to be viewed

- Reports for people. These reports, which include the Individual Plant Report, Plot Summary Report, and Stand Summary Report, were produced in Generate Reports. The file has the extension .RPT.
- Plant Data (or DOS text file). This View Reports selection can be used to view the Input Data File (*.DAT), the Run Design Report (*.RDR), or any file with an ASCII format. By default, whenever you enter View Reports, the Input Data File (if it has extension .DAT) is the file shown under Plant Data (or DOS text file). This file name can be changed as described above.
- Diagnostic Reports. These reports were produced in Calculate Plant Components. The reports have the extensions .DET, .USE, and .ERR.
- Machine-readable Reports. These reports were produced in Generate Reports. These reports have the extensions .IND, .PLT, and .STA.

For more detailed information on the reports, *see Reference: Reports and Other output.*

Using

View Reports uses a program called LIST made by Buerg Software. When viewing a file in LIST, pressing H displays the help screen--it is self-explanatory and easy to use. LIST will work outside of BIOPAK.

Reports and Other Output

Section

BIOPAK produces several reports and output that are briefly described here. If more information is needed, it usually can be found by examining the reports. Reports can be examined by selecting View Reports from the Main Menu, by printing the file, or by using a text editor or word processor.

Run Design Report

This report is a flat ASCII file that documents the Run Design File contents. It can be produced by selecting run Design report from the File Menu of Design a Run. The report will be given an .RDR extension.

The report contains headings and contents for each of the Run Design sections; that is, Default Settings, Data Input Format, Components to Output, and Reassignments. It can be useful for future reference.

See Tutorial: Lesson One for an example of a Run Design Report.

Diagnostic Reports

Diagnostic Reports specify the equations used to make calculations and the errors detected by BIOPAK during calculations. They can be requested when Calculate Plant Components is selected from the Main Menu.

Summarized Equation Use Report (*. USE)--

This report presents a summary of the equations used for calculations. Species are ordered alphabetically in two sections. The first section contains Equation Requests (if any) for which a component was calculated. It lists all combinations of Original Equation Request, Request(s) to Library, Equation(s) Actually Used and the number of times each combination was used during calculations. The lowest Equation Selection Penalty associated with each combination also is reported. Equations used in summations specified by you or selected by BIOPAK are shown. Sequence numbers provided are sequential indices of the items in the report.

The second section contains Requests (if any) for which no suitable equation was found. If a component could not be calculated, there are no equations actually used. If all information needed to make a Request to the Library is not found, this Request is not shown. This is usually caused by lack of a lifeform code resulting from absence of any equation for this species in the library.

The file name of this report is the root of the Intermediate Binary File with a .USE extension. The list is not linked to individual input records, as in the case of the Detailed Equation Use Report.

Column headings in Summarized Equation Use Report--

- Seq: Indicates sequence number of unique Original Requests.
- Original Request: Equation Key before Reassignment, if any. See *Glossary.*
- Seq: Indicates sequence number of Equation(s) Actually Used used to satisfy each unique Original Request.
- Best ESP: The lowest Equation Selection Penalty resulting from use of the Equation(s) Actually Used Key shown. This differs by record. See *Glossary.*
- Use Count: Number of uses of this Equation(s) Actually Used.
- NoCal Count: Number of times this Request to Library was not satisfied.
- RA: Indicates this Original Request matched any Reassignment Criteria.
- Request to Library: Equation Key representing the Request to Library. See *Glossary.*
- Equation(s) Actually Used: Keys of equations actually used to calculate the requested component. May be a summation. See *Glossary.*

Detailed Equation Use Report (*.DET)--

For every component requested for each input record (plant), this report lists the Original Equation Request, the Request(s) to Library, the Equation(s) Actually Used, and the Equation Selection Penalty for the equation (or summation) used. Each Case number corresponds to an individual input record and an individual plant and equal their line numbers in the Input Data File. The Case number is the same as that in the Error Report and the Individual Plant Report of the Reports for People. Sequence numbers provided are sequential indices of the items in the report. Information is presented for all Original Equation Requests, whether or not a component value could be calculated.

Its file name is the root of the Intermediate Binary File and a .DET extension. Multiple equation keys indicate that the component value is the sum of values obtained from these equations.

Column Headings in Detailed Equation Use Report--

* **Seq: Indicates sequence number for all Original Requests.**
* **Case: Represents the record number in Input Data File.**
* **ESP: The Equation Selection Penalty value associated with the Equation(s) Actually Used (or Request to Library if not suitable equation was found).**
* **Original Request: See Reference:** *Reports and Other Output: Summarized Equation Use Report (*.USE),* **above.**
* **RA: See Summarized Equation Use Report** *(*.USE),* **above.**
* **Request to Library:** *See Summarized Equation Use Report (*.USE),* **above.**
* **Equation(s) Actually Used:** *See Summarized Equation Use Report (*.USE),* **above.**

Error Report (.ERR)--*

This report lists codes for the two most serious errors and warnings detected by BIOPAK during selection of an equation or group of summed equations and computation of a component value. For every error and warning it provides (1) the Original Equation Request; (2) the values and variable names of Date, Locale, Stand, Plot, and Plant ID; and (3) the values and variable names of the parameters. Each case number corresponds to an individual input record, that is, an individual plant. This case number is the same as that in the Detailed Equation Use Report and the Individual Plant Report of the Reports for People.

The Error Report file name is the root of the Intermediate Binary File and the extension .ERR. Definitions for error and warning codes are listed in *Appendix: Troubleshooting: Error Messages.*

Column headinas in Error Report--

Note that headings in parentheses may be changed by the user in the Data Input Format Window of Design a Run.

* **Case: Corresponds to the record in the Input Data File and to case number in the Individual Plant Report and Detailed Equation Use Report.**
* **Site Identifications: These five headings can be changed by the user in the Data Input Format Window of Design a Run. They are:**
  * **(DATE): Date identifier from Input Data File.**
  * **(LOCALE): Locale identifier from Input Data File.**
  * **(STAND): Stand identifier from Input Data File.**
  * **(PLOT): Plot identifier from Input Data File.**
  * **(PLANT ID): Plant identifier from Input Data File.**
* **ORIGINAL REQUEST:** *See Reference: Reports and Other Output: Summarized Equation Use Report* **(*.USE), above.**
* **Data/Default:**
  * **Spp: Species code from Input Data File.**
  * **LGS: Lifeform, Geographic Area, and Seral Stage codes. Also indicates whether codes come from Data: Input Data File, or Default: Default Settings Window of Design a Run and Lifeform substitution procedures (as described in** *Appendix: Lifeform).*
* **Parameters: Values are listed for each of the parameters specified in the Data Input Format Window of Design a Run.**
* **Errors: Error codes are given for each component requested for calculation. These codes are explained in** *Appendix: Troubleshooting: Errors in Reports.*

Printing Diagnostic Reports--

These reports contain 132 characters per line or more, so printing must be done on printers or using fonts that allow this or both. We suggest you print all BIOPAK reports on continuous paper because page breaks and headings occur only

once at the top of each report, not every 60 or 80 lines.

Intermediate Binary

This file contains the calculated plant components and all other information used to generate reports. It is produced when Calculate Plant Components is selected from the Main Menu. This file name can be specified in the Calculate Plant Components Window; it is given the extension .IBF. Information in it is used to produce Reports for People and Machine-Readable Reports. Saving this file will allow additional reports to be produced later without recalculation.

Because the Intermediate Binary File (*.IBF) is not an ASCII file, it cannot be viewed in the View Reports Window or with a text editor.

Reports for People (*.RPT)

These reports present calculated values of plant components formatted with titles and column headings so people can understand them. Each of the three reports (Individual Plant, Plot Summary, and Stand Summary) can be requested when Generate Reports is selected from the Main Menu. They are all put in a file that, by default, has the same root as the Intermediate Binary File, and an extension .RPT. The file can be given a different root name. In the Plot Summary and Stand Summary Reports, species are assigned to the strata shown in *Appendix: Codes* by using the Taxonomic *Lifeform* code from the Equation List File when this code is available. If you need more details on assigning a lifeform to a species (most users will not), *see Appendix: Lifeform.*

individual Plant Report--

This report lists up to five input parameters (predictor variables) and the calculated components for each input record (individual plant). Parameters with codes in capital letters were used in one or more calculation; parameters with codes in lower case letters were not used in calculations. When requested, an Individual Plant Report is generated for each plot within each stand in the Input Data File. Codes for the two "most important" errors or warnings detected are listed next to individual component values.

Plot Summary Report--

This report gives averages of all input parameters and the per-hectare values for components by species and by vegetation strata for each plot within each stand. For these numbers to be meaningful, data for all plants in each plot must be contiguous in the Input Data File. This report is written after the Individual Plant Report. The correct size and slope (if this plot needs slope correction) must be provided as discussed under *Reference: Design a Run.* A code for the "most serious" error or warning detected is listed next to each value.

Stand Summary Report--

This report gives averages and standard errors of all input parameters and the per-hectare values for each component by species and vegetation strata over all plots within each stand. For this to occur, data for all plants in each plot must be contiguous in the Input Data File and data for all plots within each stand must be contiguous in the Input Data File. Correct size and slope specifications are necessary as discussed under *Reference: Design a Run.* These values are not weighted by plot areas. The "most serious" error or warning detected is listed next to each average value.

Information in Reports for People (.RPT)--*

Headings listed in parentheses can be changed by the user in the Data Input Format Window of Design a Run.

- REQUESTED REPORTS: Indicates which of the reports for people were requested and whether the output will be in metric or English units.
- TITLE: Title given to run in Calculate Plant Components Window is shown at top of every page.
- MAXIMUM EQUATION SELECTION PENALTY (ESP): Level set by user in Default Settings Window of Design a Run.
- THRESHOLD LEVEL: Level set by user in Default Settings Window of Design a Run.
- SUMMATION LEVEL: Level set by user in Default Settings Window of Design a Run.
- DATA FILE: Input Data File specified in Calculate Plant Components Window.
- RUN DESIGN FILE: Run Design File specified in Calculate Plant Components Window.
- IBF FILE: Intermediate Binary File specified in Calculate Plant Components Window.
- EQUATION LIBRARY: Equation Library (*.DBF) used to produce the Equation List File specified in Calculate Plant Components Window.
- EQUATION LIST: Equation List File specified in Calculate Plant Components Window.
- (PLOT): Plot value from Input Data File.
- (STAND): Stand value from Input Data File.
- (LOCALE): Locale value from Input Data File.
- FIRST (PLANT ID): First Plant value in this Plot from Input Data File.
- (DATE): First Date value from Input Data File.
- Slope: Value for plot slope from Input Data File, or as specified by user in Default Settings Window of Design a Run.
- Area Conversion Factor: Incorporates the effects of plot size and slope, with units l/area, so multiplication gives component values per hectare (or acre).
- Fixed Plot Area Size: Value for plot area from Input Data File, or as specified by user in Default Settings Window of Design a Run.
- Prism Basal Area Factor: Value from Input Data File, or as specified by user in Default Settings Window of Design a Run.

Information in Individual Plant Report--

Headings listed in parentheses can be changed by the user in the Data Input Format-Window of Design a Run.

- CAS: Corresponds to the record number (case) of the Input Data File.
- (PLANT ID):Plant identifier from Input Data File.
- LF: Lifeform code of plant.
- SPECIE: Species code of plants in Input Data File.
- PARAMETERS: Plant measurements from Input Data File which were specified in Data Input Format Window of Design a Run.
- GA: Geographic Area code. Comes from Input Data File or Default Settings Window of Design a Run.
- SS: Seral Stage code. Comes from Input Data File or Default Settings Window of Design a Run.
- (COMPONENTS): Abbreviations for components requested for calculation. Comes from the BIOCODES file. The component estimates are reported. Codes for the two most serious errors, if any, are included.

- **ERROR MESSAGES: Each of the error codes, indicated next to the component estimates, are defined here.**

Information in Plot Summary Report--

- **PLOT SUMMARY REPORT, (PLOT) = (plot-value):**
  - **(PLOT): Plot value in Input Data File.**
- **LF:** ifeform **codes of plants.**
- **SPECIE: Species codes of plants from Input Data File.**
- **NUMBER PLANTS IN (PLOT): Number of plants in plot for a given species and lifeform.**
- **PARAMETER(S) / (PAR1 . ..) / --AVERAGE--: Average value of the specified parameter for a given species and lifeform.**
- **NUMBER OF PLANTS -- per (area) --: Calculated number of plants per hectare (or acre).**
- **TREE BA (units) -- per (area) --: The tree basal area per hectare (or acre).**
- **(COMPONENTS) (units) -- per (area) --: Component estimates per hectare (or acre) for each component requested in the <u>Components to Output Window</u> of <u>Design a Run</u>.**

Information in Stand Summary Report--

@ STAND SUMMARY REPORT FOR (LOCALE) (locale-name), (DATE) (date-value):
  - **(LOCALE): Locale value from Input Data File.**
  - **(DATE): Date value from Input Data File.**
- **AVERAGES FOR (STAND) (stand-name), SAMPLE SIZE = (n):**
  - **(STAND): Stand value from Input Data File.**
  - **LF:** Lifeform **codes of plants.**
  - **SPECIE: Species codes of plants from Input Data File.**
  - **NUMBR PLNTS IN TALLY: Total number of plants in all plots for a given species and lifeform.**
  - **NUMBR PLNTS PER (PLOT): Average number of plants per plot.**
  - **PARAMETER(S)--AVERAGE: Average of all the measured values in the stand, not the average of the plot averages.**
  - **NUMBER OF PLANTS -- per (area) --: Calculated number of plants per hectare (or acre), not weighted by plot area.**
  - **TREE BA (units) -- per (area) --: The tree basal area per hectare (or acre), not weighted by plot area.**
  - **(COMPONENTS) (units) -- per (area) --: Average over all plots in the stand (per hectare or per acre) not weighted by plot area.**
- **STANDARD ERRORS FOR (STAND) (stand-name), SAMPLE SIZE = (n): These are the standard errors corresponding to the averages above, except for:**
  - **NUMBR PLNTS IN TALLY: Total number of plants in all plots for a given species and lifeform.**
  - **A value of -1.0 indicates the standard error could not be calculated because sample size was 0 or 1.**

Error codes--

Code(s) for the "most important" error(s) or warning(s) are next to the calculated values. Error rankings by importance are based on our consideration of a wide range of potential circumstances and will not reflect their importance for many particular circumstances. Definitions for error codes are at the end of the report and explanations and possible solutions are in *Appendix: Troubleshooting: Error Messages.*

Printing Reports for People--

Depending on the number of plant components requested, these reports may be more than 80 characters across, and so must be printed with narrow characters or on wide paper or both. We suggest you print all BIOPAK reports on,continuous paper since page breaks and headings occur only once at the top of each report, not every 60 or 80 lines.

Machine-Readable

These reports can be requested when Generate Reports is selected from the Main Menu. They contain several lines at the top specifying the variables and their columns. These lines can be removed with a text editor if needed for reading by other programs.

Individual Plant Report (.IND)--*

It is put in a file with a root defined by you and a .IND extension. It contains all the information in the Individual Plant Report for People; see the preceding section, *Reports for People: Individual Plant Report,* for more details.

Plot Summary Report (.PLT)--*

It is put in a file with a root defined by you and a .PLT extension. It contains all the information in the Plot Summary Report for People; see the preceding section, *Reports for People: Plot Summary Report,* for more details.

Stand Summary Report (.STA)--*

It is put on a file with a root defined by you and an extension .STA. It contains all the information in the Stand Summary Report for People; see the preceding section, *Reports for People: Stand Summary Report,* for more details.

Information in Machine-Readable Reports--

The lines of heading information at the tops of these reports specify, in order, the information in each field in the report. Some of the codes in these lines are defined in *Reports for People: Information in Reports for People,* above. Other codes include:

- STRATA: Community Stratum, for example, T, S, G, M (Tree, Shrub, Grass, Moss, respectively).
- SPP: Species codes of plants from Input Data File.
- BIO, CIR, COV, CR, DBA, DBH, FC, HT, LEN, NP, NUM, SAP, SPA, VOL, WID: Parameter codes.
- COMPONENTS: Three-character plant component codes.
- RECORDS: Number of records from the Input Data File that are summarized by this line.
- AREA (units): Plot area in (units).
- PRISM (units): Prism factor in (units) for this plot.
- SLOPE: Slope of this plot.
- # PLANT: Number of plants per unit area. Unit area is defined following AREA; see above.
- BA: Basal area of trees in the units requested (m2/ha or ft2/ac)
- VSW, BAE, BFT, AFT and many others: Three-character plant component codes.
- PlotCnt: Number of plots in this Stand.
- TotPlnts: Total number of plants (that is, records) read from Input Data File summarized in this line.

- **Plnts**: Number of plants per unit area, average or standard error.
- **Av**: Average. For parameters this is the average over all observations of this parameter. For plant components this is the average per unit area in the units requested, /m2 or /ac.
- **SE**: Standard error (standard deviation of the mean). For parameters this is the SE over all observations of this parameter. For plant components this is the SE of the average per unit area in the units requested, /m2 or /ac.

TUTORIALS

This chapter includes six tutorials that gradually introduce BIOPAK features.

Introduction to the Tutorials

The six tutorials included in the BIOPAK users guide build on each other. Therefore, it would be best to start with Lesson One and work through to Lesson Six. If unfamiliar terms or concepts are encountered, refer to the appropriate section, *Glossary,* or *Index* of this users guide for further explanation.

For information on how to make menu selections and select files from a <u>File Selection Window</u>, see Getting *Started: Overview of Features.*

The steps in these tutorials are numbered and lettered sequentially from beginning to end because they must be done sequentially. Numbering and lettering do not start over with each subsection.

The Tutorial Dataset

For all the tutorials, we will use a given Input Data File (TUTOR.DAT). The data were collected from a riparian plot in a stand of trees in the Mack Creek drainage found within the H.J. Andrews Experimental Forest. For the purposes of this tutorial, assume that as part of a long-term study on site productivity, estimates of standing biomass are needed.

Here are some lines of data from the Input Data File:

```
TP9801MACKriparian830623TSHE5478 4.52 0.15 18.3 5.9 86 86NF
TP9801MACKriparian830623TSHE5477 4.69 0.16 44.9 21.1 88 88NF
TP9801MACKriparian830623TSHE 467 3.04 0.17 41.8 23.4 106 87F
TP9801MACKriparian830623TSHE5481 3.03 0.21 20.3 11.3 94 86F
TP9801MACKriparian830623TABR 469 4.13 0.28 5.7 3.0 39 30NF
TP9801MACKriparian830623CONU 463 1.40 0.34 5.8 7.1 273 49NF
TP9801MACKriparian830623ACMA 468 3.76 0.40 9.4 14.8 20 81F
```

This particular dataset has 61 characters per line. Columns 1-6 are the code for the research site. Columns 7-10 represent the name of the stand of trees. Columns 11-18 indicate the particular plot within the stand from which the data were collected. Columns 19-24 show the date the measurements were taken. The plant species codes are found in columns 25-28, and the plant ID numbers are found in fields 29-32. The remaining numbers to the right of the plant ID are the values for measured parameters; for example, d.b.h and d.b.a.

Lesson One--Introduction to Design a Run and View Reports

In this lesson you will:

- **Use Design a Run to modify a given Run Design File (TUTOR.RD). Sections involved:**
  - **Default Settings**
  - **Data Input Format**
  - **Components to Output**
- **Save Run Design File as a different file name (TUTORl.RD).**
- **Save Run Design Report (TUTORl.RDR) to be viewed later.**
- **Choose View reports from the Main Menu.**
  - **See how files are selected and viewed.**
  - **View the Run Design Report (TUTORl.RDR).**

1. **Go to the TESTDATA directory where the tutorial files are located. Type: BIOPAK (If you are on a network system, you will need to type BIOPAKN D: where "D" represents the temporary directory. See Installation:** *Installation on a Network.)*

Modify an Existing Run Design File

2. **Select Design a run at the Main Menu.**

3. **Select File from the Run Design Menu.**
   a. **Then select Read existing run design file from the File Menu. A & Selection Window will appear. Functioning of the FoxPro windows for selecting an existing file (like this window) and opening a new file are described in** *Getting Started: File Selection Windows.*
   b. **Now select the file TUTOR.RD by highlighting it then pressing <Enter>. Press <Esc> and the File Menu will disappear and the screen will return to the Run Design Menu. The selected file will show up as the current file at the bottom of the screen.**

Modify Default Settings--

4. **Select Default settings. This editing window allows you to add the default values you want to use in calculating plant components. Tab keys move between fields.**

Areal default settings--

You can specify the default values for either Fixed Plot Area or Prism Basal Area Factor, but NOT both.

a. **Fixed Plot Area: If plot size were not included in your Input Data File, the size of your fixed plots areas would now have to be specified. If plot size is in your Input Data File but is missing in some records, this would be the value used to replace the missing values.**

Type: 2

b. **Units: Specify the units associated with the plot area. The <FlO> key will display a list you can select from.**

Type: ha (or select from list)

c. **Prism Basal Area Factor: This is where you would specify the prism**

basal area factor used to tally trees in sample.

Type: <Tab>

d. **Units: This is where you would specify the units associated with the orism basal area factor.**

Type: <Tab>

e. **Plot Slope Correction: Specify the slope to be used if it. was not included in your Input Data File. This reference stand has a projected area of 2 hectares..**

Type: 0

f. **Units: Specify the units to be associated with the slope. The <FlO> key will display a list you can select from.**

Type: % (or select from list)

Equation Kev default settings--

g. **Geographic Area default: Here you may select a code for the geographic area of the data to be used. The default code is <blank>. The Geographic Area code selected for the TUTOR.RD file was W (west side of the Cascades).**

Type: **<Tab>**

h. **Seral Stage default: Here you choose the seral stage of the data to be used. The default code is <blank>. The Seral Stage code selected in TUTOR.RD was 0 (oldgrowth).**

Type: **<Tab>**

Equation Selection Penalty default settings--

The ESP levels must be included, otherwise BIOPAK cannot select equations from the Library.

i. **Maximum ESP Level: This determines the poorest but still acceptable equation match (that is, highest acceptable ESP). For BIOPAK to have as much flexibility as possible in selecting an equation, you would select a high number. *(See Appendix: Equation Selection Penalties* for a more detailed description.) The default value, 79999, was selected in TUTOR.RD.**

Type: **<Tab>**

j. **Threshold ESP Level: This value determines the level at which a Candidate Equation is considered acceptable. An assigned Threshold ESP of zero will assure selection of the best equations. Zero was the value selected for TUTOR.RD.**

Type: **<Tab>**

k. **Summation ESP Level: If BIOPAK cannot find an individual equation to calculate a specified plant component with a lower ESP value than the assigned Summation ESP, it will begin to consider default equation summation (see figures 2-4). If no equation summation is found that has an ESP value less than the Threshold ESP, the summation with the next highest value is selected. Zero was the value selected for TUTOR.RD.**

Type: **<Tab>**

Select only Reassigned species--

1. **If Y is selected, BIOPAK performs computations only on those species specified in Equation Reassignments (see lesson four). The default setting is N (No), the option selected for TUTOR.RD.**

Type: **<Tab>**

Save changes to default settings--

m. **To save the changes to the Default Settings, press <Ctrl-S>. You will be returned to the Run Design Menu.**

Modify Data Input Format--

5. **Select Data Input Format from the Run Design Menu. A list of input variables, their units and the variable information already entered will appear. This section of the program is where you tell BIOPAK how to find certain variables, and other important information in your data file, needed for calculation and output of reports.**
   a. **To start, <DnArrow> to the second variable, named "LOCALE."**
   b. **Now you are ready to add information.**
      (1) Var Name: Name used to identify this variable in output reports. For the first five variables, this name can be changed. (The next column, Label/Description can never be changed and is only for descriptive purposes.)

   Type: **Basin**

      (2) Units: This is not relevant for this variable, therefore the cursor will skip over this column.
      (3) Type: Data Type is required for variables l0-27 only: I = integer, F = floating point (real), and E = exponential format. Other variables are character strings (A). Not applicable for this variable, therefore, cursor will skip over this column.
      (4) pos: (required) Indicates first column position of variable in Input Data File.

   Type: **1**

      (5) Len: (required) Total number of columns occupied by the particular data field (maximum is 6 for species, prism basal area factor, and plot slope correction; 8 for date, locale, stand, plot and plant ID; and 10 for all others).

   Type: 6

      (6) Dec: Number of decimal places in an F or E data type (any decimal point occurring in the data input record as a missing value will override this default). Not applicable for this variable, therefore, cursor will skip over this column.
      (7) Missing: Indicates how missing data are represented for this variable.

   Type: **<Tab> (leave blank)**

   c. **After the information for the input variable has been entered, press <Ctrl-S> to save the additions and exit Data Input Format. You will be returned to the Run Design Menu.**

Modify Components to Output--

6. **Select Components to Output. Notice that the plant component "BAT Biomass, aboveground, total" has been specified for output. For all species in the tree and shrub strata, the BAT calculation will be attempted.**

   There are two ways to enter components. You can either type in the Component codes, if you know them, or select them from the code list as follows:
   a. **Move the highlight bar to the blank line below BAT. Press <FlO> for a list of Component codes. Move up and down by using either the arrow keys or the mouse.**

b. Move highlight bar to BFT. Select by pressing <Enter>. You will be returned to the Component to Output Window. Notice that BFT has been entered under the heading Code.

c. Choose strata to be computed for BFT. Put a Y in the T (tree) column, and a Y in the S (shrub) column so that total foliar biomass will be calculated only for trees, shrubs, and coppice lifeforms. An N in both the H (herb) and M (moss) columns will prevent calculation of BFT for lifeforms in these strata.

d. Press <Ctrl-S> to exit and save additions.

Save changes to existing Run Design File--

7. Now, to save the changes to the Run Design File, select File.
   a. Select Save run design file. A File Selection Window will appear, thereby allowing you to rename the file.
   b. Name the file TUTORl. It will be given the extension .RD. Now <TAB> to the <Save> option and press <Enter>. You will be returned to the File Menu.

Make Run Design Report--

8. Select run Design report to save the run specifications in a report format (ASCII). A File Selection Window will appear and you will be prompted to name the file. We suggest TUTOR1 so it is identified with the TUTORl.RD file it represents. It will be given the extension .RDR. After saving this, press <Esc> to return to the Run Design Menu.

9. To exit the Run Design Menu, select Exit run design. You will be returned to the Main Menu.

View Reports: view a Run Design Report

10. Select View' Reports from the Main Menu. A View Reports Window will be displayed.
    a. Move the highlight bar down to the line under Plant data (it should currently either say NONE or show the Input Data File name). Select this by either pressing <Enter> or clicking it with the mouse. A File Selection Window will appear. Press <TAB> to get to the file box and <Scroll> the highlight bar to the newly created .RDR file, then either press <Enter> or <Tab> and select <Open>. You will be returned to the View Reports Window.
    b. Move the highlight bar up to Plant data. Select it by pressing <Enter> and the Run Design Report will appear for viewing.
    c. BIOPAK uses LIST, shareware, for viewing files. When in LIST, type H to see the help screen.

Example of Run Design Report (TUTOR1.RDR)

11. The sections of the Run Design Report are numbered l-4. Each represents a section of Design a Run; that is, Default Settings, Data Input Format, Components to Output, and Reassignments. Entries made in these sections of Design a Run will be reported here. When you are done viewing the report press X to return to the View Reports Window. Press <EsC> to return to the Main Menu. Plant component calculations now can be made.

(today's date)

Run Design Report for File D:\BIOPAK\TESTDATA\TUTOR1.RD

1. Default Settings of File

Maximum Equation Selection Penalty	79999
Threshold Equation Selection Penalty	0
Equation Selection Penalty	0
Select Species	N
Geographic Area default	W
Seral Stage default	0
Fixed Plot Area	2
Plot Units	ha
Prism Basal Area Factor	
Prism Basal Units	
Fixed Plot Slope	0
Fixed Plot Units	%

2. Data Input Format Specification

Variable Name	Label/Description	Units	Type	Pos	Len	Dec	Mis
YEAR	Date		A	19	2		
BASIN	Locale		A	1	6		
STAND	Stand		A	7	4		
PLOT	Plot		A	11	8		
TREE #	Plant ID		A	29	4		
SPECIES	Species		A	25	4		
			A				
GEO AREA	Geographic Area		A				
SERSTAGE	Seral Stage		A				
BIO	Biomass		F				
CIR	Circumference		F				
COV	Cover		F				
CR	Crown ratio		F				
DBA	Diameter near base		F				
DBH	Diameter breast height	cm	F	43	5	1	
FC	Form Class		F				
HT	Height	m	F	49	5	1	
LEN	Length		F				
NP	Number of plants		F				
NUM	Number fronds, stems		F				
SAP	radial thickness		F				
SPA	x-sect area		F				
	Volume		F				
	Width		F				
	Fixed plot area		F				
PRISMFAC	Prism basal area factor		F				
PLTSLOPE	Plot slope correction		F				

3. Component Values to Output

Code	Definition of Plant Component Code	--Strata-- T	S	H	M
BAT	Biomass, aboveground, total	Y	Y	N	N
BFT	Biomass, foliage, total	Y	Y	N	N

4. Reassignments

*** No reassignments exist ***

Exiting

From the View Reports Window press **<Esc>** to return to the Main Menu. From there press **Q** to quit. You will be asked if you want to erase the C:\BIOENV error check file. You can erase it since it does not concern you at this point.

Lesson Two--Introduction to Plant Component Calculations and Generating Reports

In this lesson you will:

- Use the given Equation List File (BIOLIB.EQN)
- Use Run Design File previously created (TUTORl.RD)
- Calculate some plant components
  - Name the run
  - Select files to be used for calculations
  - Name the Intermediate Binary File (TUTORl.IBF)
  - Produce Diagnostic Reports (TUTORl.USE, TUTORl.DET, TUTORl.ERR)
- Use Generate Reports
  - Reports for People (TUTORl.RPT)
- View reports
  - Reports for People

Calculate Plant Components with Diagnostic Reports

1. Select Calculate plant components from the Main Menu. The Calculate Plant Components Window will appear. Now you will be able to give a title to this particular run, select the files to be used in the calculations, name the Intermediate Binary File, and select the Diagnostic Reports to be produced.
   a. The highlight bar should appear on the first line with the heading Title. Select this by pressing <Enter>. You will be able to give a title to this particular run; for example, "Test run from Tutorial: Lesson Two." After naming the run, press <Enter>.
   b. If the newly created Run Design File (TUTORl.RD) is not shown on the Calculate Plant Components Window, move the highlight bar to the line titled Run design file and press <Enter>. A File Selection Window will appear where the Run Design File to be used for the calculations can be selected. Select TUTORl.RD. The file TUTORl.RD will now appear in the Calculate Plant Components Window.
   c. Now move the highlight bar to Equation list file. Select file BIOLIB.EQN using the File Selection Window as you selected TUTOR.RD. This will supply the equations to be used for the calculations.
   d. To select the Input Data File to be used in the calculations, move the highlight bar to input Data file, and select the file TUTOR.DAT, as described above.
   e. By executing the calculations, an Intermediate Binary File (*.IBF) will be produced. To name this output file, move the highlight bar to the line titled Intermediate binary file and press <Enter>. A File Selection Window will appear where you can name the .IBF file. We suggest TUTORl.IBF. Then, select <Save>.
   f. Below the Intermediate Binary File name, select each of the Diagnostic Reports to be generated by moving the cursor to each line and pressing <Enter> to toggle the YES option.
   g. Now that you have named all the relevant files, select <Go> to execute the calculations.

Generate Reports

2. Select Generate reports. By default, the files listed are given the same root name as the .IBF. You can change these names by highlighting the file name and pressing <Enter>. A File Selection Window will appear thereby allowing you to rename the file.
   a. Under the heading Reoorts for PeoPle, select the three reports either by highlighting each line and pressing <Enter> or by using the relevant hot key--this will toggle the Yes/No selection to the YES position. The machine-readable reports can be generated at a later time.
   b. Toggle the metric/English option for report output by either pressing <Enter> or using the 0 hot key. Select METRIC.
   c. Now select <Go> to generate the specified reports.

View Reports

3. Select View Reports or data from the Main Menu. The files that have recently been generated will appear as the file names under each heading. In the case of the pLant data (or DOS text file), the Input Data File used in the calculations should be the file that appears.
   a. While the highlight bar is on the first line, titled Reports for People, press <Enter> to view this report.
   b. By scanning the Reports for People, which includes an Individual Plant Report, Plot Summary Report, and Stand Summary Report, notice that there were no BAT values calculated for the Species codes CONU (Cornus nuttalli, Pacific dogwood) and TABR (Taxus brevifolia, Pacific yew). The error codes indicate that TABR was not found in the Equation Library. For CONU, the specific equation requested is not in the Library. For further investigation, browse the Diagnostic Reports (TUTORl.USE, TUTORl.DET, TUTORl.ERR), which were generated when you calculated plant components.
   c. Press X when you are done viewing a file and you will be returned to the View Reports Window.

Printing Reports

4. Exit BIOPAK from the Main Menu. All BIOPAK output must be printed from within a text editor or word processor, or with the DOS PRINT command or another printing utility because BIOPAK does not print files. All printable BIOPAK files are flat ASCII files except for the form feed character at the tops of pages. You may want to print all BIOPAK reports on continuous paper because page breaks and headings occur only once at the top of each report, not every 60 or 80 lines.

Printing a Report for People--

5. If you choose, print the file TUTORl.RPT on a printer or with a font that can print at least 132 characters per line and that is not proportionally spaced.

Example of Reports for People (TUTOR1.RPT)

To save space, most cases (records) from the Input Data File are not included in the Individual Plant Report below.

```
* * * * * BIOPAK Reports for People * * * * *   Date:      Time:     Page  1
                                                04/19/94   12.28.08

Requested reports:    Individual Plant, Plot Summary, Stand Summary
                      in metric units

USER TITLE:     Test run for tutorial, Lesson Two

Biomass values calculated on 04/19/94 at 12.24.14

Max. Equation Selection  Data File =                 D:\BIOPAK\TUTOR\TUTOR.DAT
  Penalty (ESP) = 79999  Run Design File (.RD) =     D:\BIOPAK\TUTOR\TUTOR.RD
Threshold Level =     0  Intermed. Bin. File (.IBF) = D:\BIOPAK\TUTOR\TUTOR.IBF
Summation Level =     0  Equation Library (.DBF) =   D:\BIOPAK\BIOL\BIOLIB8.DBF
                         Equation List (.EQN) =      D:\BIOPAK\TUTOR\TUTOR.EQN


TITLE: Test run for tutorial, Lesson Two                              Page  2

RIPPLOT  RIPSTAND LOCALE   FIRST TREE #  YEAR      Slope Area Conversion Factor
-------- -------- -------- ------------- --------  ----- ----------------------
riparian MACK                  5478        83        .0%             .50

Fixed Plot Area Size = 20000.00   (m2)

Prism Basal Area Factor =      .00 (m2/ha)

--------------INDIVIDUAL PLANT REPORT--------------------------------

Case TREE #   L Specie ----Parameter(s)---- G S   BIO TOT    BIO TOT
              F                             A S   FOLIAGE    ABOVGRND
                                                   (gm)        (gm)

   1 5478     T TSHE      18.3DBH  590.0ht  W 0  7814.10  131604.80
   2 5477     T TSHE      44.9DBH 2110.0ht  W 0 52767.14   1287830.
   3  467     T TSHE      41.8DBH 2340.0ht  W 0 45315.46   1085451.
   4 5481     T TSHE      20.3DBH 1130.0ht  W 0  9743.94  171625.00
   5 5479     T THPL       8.5DBH  320.0HT  W  0  7754.90h  17781.74h
   6  469       TABR       5.7dbh  300.0ht  W  0      .00CM      .00CM
   7  463     S CONU       5.8dbh  710.0ht  W 0       .   00MN   .00MN
   8 5480       TABR       7.2dbh  430.0ht  W 0       .   00CM   .00CM
   9  468     T ACMA       9.4DBH 1480.0ht  W 0   867.82  22487.61
  10  466     T ACMA      24.2DBH      .0   W 0  4004.17  257186.60

==/\/\/\/\==  cases 2 - 75 would be included here ==/\/\/\/\/\/\==

  76 5569     T TSHE      12.0DBH  540.0ht  W  0  3183.32h  45052.95h
  77 5191     T TSHE      43.5DBH  2030.0ht  W  0  49327.42  1193603.
  78  474     T ACMA       6.7DBH  890.0ht  W  0   501.93h   9715.53h

Error messages:
C NO EST: No LF in data. No Reass w/ match spp, GA & SS. Spp not in .EQN file.
M NO EST: One or more parameters are missing for all candidate equations.
N NO EST: No match for Request to Lib in .EQN since Spp/LF/Comp not found at any ESP.
V WARNING: Over extrapolation occurred.
c WARNING: Equation used lacks parameter range, so no extrapolation test was done.
h WARNING: Under extrapolation occurred.


-------- PLOT SUMMARY REPORT, RIPPLOT = riparian--------------------

L  Specie  Number     Parameter(s)    Number   Tree   BIO TOT   BIO TOT
F          Plants     DBH     HT        of      BA    FOLIAGE   ABOVGRND
             in     -----average-----  plants  (m2)    (kg)      (kg)
           RIPPLO                    ----------- per hectare.-----------

  TABR         3     9.4   453.3       2       .0       .00C      .00C
  All          3     9.4   453.3       2       .0       .00       .00

T ACMA         7    15.2  1352.0       4       .1      8.56V    700.36V
```

T PSME	5	148.3	6212.0	3	4.4	519.94	54110.07V
T THPL	16	54.5	2554.4	8	3.3	7473.59V	31532.84V
T TSHE	45	39.6	2172.2	23	4.4	6987.88c	48784.12V
T All	73	48.0	2485.1	37	12.3	14989.98	135127.40
S CONU	2	7.1	830.0	1	.0	.00M	.00M
S All	2	7.1	830.0	1	.0	.00	.00
Grand Tot	78	45.4	2361.3	39	12.3	14989.98	135127.40

Error messages:
See individual plant report above

TITLE: Test run for tutorial, Lesson Two Page 3

==
STAND SUMMARY REPORT for LOCALE , RIPSTAND MACK , YEAR 83

NOTE:
In this case values in the Stand Summary Report (not shown) are the same as in the Plot Summary Report because the data are for one plot.

Lesson Three--Introduction to Diagnostic Reports

In this lesson you will:

- **Use Diagnostic Reports generated in Calculate Plant Components (TUTORl.USE, TUTORl.DET, TUTORl.ERR)**
- **View reports**
  - **Summarized Equation Use Report (TUTORl.USE)**
  - **Detailed Equation Use Report (TUTORl.DET)**
  - **Error Report (TUTORl.ERR)**

In the previous tutorial, we found that the specified plant components were not calculated for two species in the Input Data File--CONU and TABR. We will now view the Diagnostic Reports to determine the reasons for this omission. Use the <RtArrow> key to see the portions of the reports that are off the screen.

Interpretation of Diagnostic Reports

1. **Select View reports or data from the Main Menu. Reference: Reports and** *Other* **Output contains more complete information on each report.**
   a. **Under the heading Diagnostic Reports, the three diagnostic reports generated when we calculated plant components in Lesson Two should be shown (TUTORl.USE, TUTORl.DET, TUTORl.ERR).**

Summarized Equation Use Report--

b. **Select Summarized equation use report. TUTORl.USE will appear on the screen. A summary of the equations used to calculate each component for each species will be displayed. This is the most useful diagnostic report. For all species where calculations were possible in this run, more than one equation (or summation) was used to calculate BAT. The Use Count column shows that no records for CONU or TABR were used in calculations. The NoCal Count column indicates how many records were not used (no calculations). Note that in the Equation(s) Actuallv Used column, CONU and TABR are blank. When more than one Equation Key is present under Equation(s) Actuallv Used, the values from each of these equations were summed to estimate the value for the Original Request. Press X to return to the View Reports Window.**

Detailed Equation Use Report--

c. **Select Detailed equation use report. This report displays every equation used to calculate BAT for each of the 78 records in the Input Data File. The Original Equation Request (explained more fully in** *Appendix: Selecting Equations and Summations)* **for TABR, does not include a lifeform or component because these could not be found in the Equation Library. The Geographic Area and Seral Stage codes were found in the Default Settings which we modified in** *Tutorial: Lesson One.* **The Oriqinal Request for CONU is complete, thereby indicating that there are equations in the Library for this species. For some species, for example ACMA, some of the Equations Actually Used were summations. If an equation does not exist for a specified component, a summation of lesser components will be attempted within the user-specified ESP constraints** *(see Appendix: Selecting Equations and Summations).* **Press X to return to the View Reports Window.**

Error Report--

d. **Select Error report. This report includes the errors associated with attempts to calculate components for each line of data in the Input Data File. For the species TABR, the codes indicate that the species is not in the Library** *(see Appendix: Troubleshooting: Error Messages).* **For CONU, the error code indicates that the specific equation requested is not in the Library. Press X to return to the View Reports Window.**

e. **Press <Esc> to return to the Main Menu.**

Printing output

2. **Exit BIOPAK from the Main Menu. All BIOPAK output must be printed from within a text editor or word processor or with the DOS PRINT command or another printing utility because BIOPAK does not print files. All printable BIOPAK files are flat ASCII files except for the form feed character at the top of pages.**

Printing a Summarized Equation Use Report--

3. **Print the file TUTORl.USE on a printer or with a font that can print at least 132 characters per line and that is not proportionally spaced. Other diagnostic reports can be printed in this way.**

Lesson Four--Introduction to Equation Library and Reassignments

In this lesson you will:

- **Use the given Equation List File (BIOLIB.EQN)**
- **Edit Equation Library (BIOLIB.DBF)**
  - **Locate equations, Equation key**
  - **Browse equations**
- **Modify the Run Design File** (TUTOR1.RD)
  - **Modify default settings**
  - **Reassignments**
  - **Save Run Design File as new name** (TUTOR2.RD)

In the previous tutorials, we found that the specified plant components were not calculated for two species in the Input Data File--CONU and TABR. We will now use the Equation Library to locate the equations for CONU. Because the error codes in Reports for People indicated that there are no equations for TABR, we have decided to substitute equations for TSHE (Tsuoa heterophvlla, western hemlock). In a real application you could choose a different species. We will therefore locate the equations in the Library for TSHE to see if they are appropriate.

Edit Equation Library

1. **Select edit equation Library-from the Main Menu.**
   a. **Select File from the Edit Library Menu.**
   b. **Select Retrieve from the File Menu. A File Selection Window will appear. Select BIOLIB.DBF from the list of .DBF files in the box. (If BIOLIB.DBF does not show up in your current directory, select the first line in the file box, [..], the parent directory. This will move you up to the next higher directory. From there, select the directory your Equation Library database was installed in.) It will take a while for BIOPAK to copy the Equation Library.**

Locate equation--

   c. **When the Library has been copied, select Locate equations(s) from the Edit Library Menu. Then select equation Key, from the Locate Menu. The cursor will appear under the heading Spp (Species). Type in CONU. The first equation for CONU will be seen at the top of the list. Unneeded lines have been cut from the following screen for brevity.**

```
BIOPAK   Edit Equation Library   Locate, <Enter>: when done   Rec:116/973
Eqn          L Plnt G S LE T Eq ---Parameter--- ---Parameter---
 #     Spp   F Comp A S  # L Tp Code min  max   Code min  max    N  R^2
      CONU
 101  CONU   K AFT  W E  1 S  2 DBA 0.4  3.2                    25  0.77
 102  CONU   K BBL  W E  1 S  2 DBA 0.4  3.2                    25  0.84
 100  CONU   K BFT  W E  1 S  2 DBA 0.4  3.2                    25  0.84
 103  CONU   K BST  W E  1 S  2 DBA 0.4  3.2                    25  0.78
 552  CONU   K PFT  W E  1 S  2 DBA 0.4  3.2                    25  0.77
D:\BIOLIB\TESTDATA\BIOLIB.DBF                               <F1> Help
```

Notice that all CONU equations are for lifeform K (coppice). Because BIOPAK will not substitute lifeform--unless specified by you--these equations were not used. The equations are also for Geographic Area W (west side of the Cascades) and Seral. Stage E (Early). BIOPAK would have substituted this Geographic Area and Seral Stage, given the ESP constraints you had specified in Default Settings, if the lifeform had been correct. Although the Mack Creek dataset (TUTOR.DAT) is from an old-growth stand, we have decided to use these equations for CONU in this tutorial. Equations for noncoppice shrubs would certainly be more appropriate. For BIOPAK to substitute these equations, however, the coppice lifeform will need to be specified in an equation reassignment.

Browse equation--

d. <Backspace> over CONU. Still using the Equation Key, type in TSHE. There are several equations for TSHE, many of which would be appropriate for our calculations. Press <Enter> to terminate the Equation Key search, and then select Quit. You will be returned to the Edit Library Menu. To browse through the Library, either select Browse equation(s), or press <FlO> to toggle the Menu off. By using the arrow keys, or <PgDn>, you can scroll through the equations.

e. To view more detailed documentation, highlight the equation summary line and type <Enter> to go to the <u>View Modifv Window</u>. From here <PgDn> and <PgUp> show documentation for this equation. When finished viewing, <PgUp> until you reach the <u>Browse Equations Window</u>.

f. To exit the Equation Library Editor, press <FlO> to toggle the Menu on. Then select Exit library editor. If no changes have been made to the Library, you will be returned to the Main Menu (unless you selected View or modify equation and saved by using <PgUp>).

Modify an Existing Run Design (.RD) File

2. **Select Design a run at the Main Menu.**

a. Select File from the Run Design Menu.

b. Select Read existing run design file from the File Menu. A File <u>Selection Window</u> will appear. Use the <u>Drive Box</u> and <u>Directory Box</u> to go to the directory where you stored TUTORliRD. Highlight TUTORl.RD and press <Enter>. You will return to the File Menu. Press <Esc> and the -program will return to the Run Design Menu, and the selected file will appear as the current file at the bottom of the screen.

Modify Default Settings--

3. **Select Default Settings from the Run Design Menu. This editing window allows you to modify the default values in BIOPAK that were used in calculating plant components.**

a. Use <Tab> to get through the cells in the window to the last line, <u>Select Only Reassigned Species?</u>

Type: Y

b. Press <Ctrl-S> to save the change and exit to the Run Design Menu.

Modify Reassignments--

4. **Select Reassignments at the Run Design Menu. You will be in a <u>Reassignment Summary Window</u>.**

a. To add a reassignment:

Type: **<Enter>.**

A Reassignment Add/Modify Window will appear which allows you to enter the reassignment criteria and substitution information.

b. In the first data entry field, following the heading Criteria, enter the Species code for Pacific dogwood:

Type: **CONU.**

The rest of the reassignment criteria can be left blank because we are planning to reassign all occurrences of CONU, not selected ones that fit given parameters.

c. <Tab> to the bottom half of the screen. Under the heading Substitutions, again enter the Species code in the first column:

Type: **CONU.**

In the second column,

Type: **K** (or select from <FlO> list)

This represents the coppice lifeform. The rest of the Substitution Key can be left blank.

d. Now, for the species CONU, BIOPAK will substitute the equations in the Library with the coppice lifeform. That resolves the CONU problem. Press <Ctrl.-S> to save changes and return to the Reassignment Summary Window. Now for TABR.

e. To add another reassiqnment, with the cursor on a blank line in the Reassionment Summary Window; press <Enter>.

f. In the Criteria Box enter the Species code to be reassigned:

Type: **TABR**

g In the Substitution Key, enter the species name:

Type: **'TSHE.**

h. Now, for all occurrences of the species TABR in the Input Data File, equations for the species TSHE will be substituted. Press <Ctrl-S> to save the new reassignment and return to the Reassiqnment Summary Window. Press <Ctrl-S> again to save all changes to Equation Reassignments and return to the Run Design Menu.

Save Run Design changes--

5. To save the changes made to the Run Design File, select File from the Run Design Menu. Then select Save. Name the file TUTOR2. It will be given the extension .RD.

6. To save the information in the Run Design File in an easily understood format, select run Design report. A File Selection Window will appear and will prompt you to name the file. It will be given the extension .RDR. We suggest naming the file TUTOR2 so it is identified with the TUTOR2.RD file it represents. Then press <Esc> to return to the Run Design Menu.

7. To exit the Run Design Menu, select Exit run design and press <Enter>. You will be returned to the Main Menu.

Lesson Five--Plant Component Calculations with Reassignments

In this lesson you will:

- Use the given Equation List File (BIOLIB.EQN)
- Use modified Run Design File (TUTOR2.RD)
- Calculate Plant Components
- Generate Reports
  - Reports for People
- View Reports
  - Run Design Report (TUTOR2.RDR)
  - Reports for People (TUTOR2.RPT)
  - Diagnostic Reports (TUTOR2.USE, TUTOR2.DET, TUTOR2,ERR)
- Use Equation Library Editor
  - Locate equations
  - Browse equations

Calculate Plant Components

1. Select Calculate plant components from the Main Menu. You will be shown a <u>Calculate Plant Components Window</u>.
   a. Give a new title to this run, for example, "Second Run, w/ CONU and TABR Reassignments."
   b. Select TUTOR2.RD as the Run Design File, if it is not already shown. If BIOLIB.EQN is not selected as the Equation List File, select it now.
   d: Verify that TUTOR.DAT is the Input Data File.
   e. Name the Intermediate Binary File: TUTOR2.IBF.
   f. If N appears next to the names of the Diagnostic Reports, toggle on the Y options to select all reports.
   g. Select <GO> to execute the calculations.

Generate Reports

2. Select Generate reports. A <u>Generate Reports Window</u> will appear. If all three reports under Reports for People are toggled Y (Yes), select <GO> to generate the reports, otherwise toggle the reports to the Y selection before executing <GO>.

View Reports

3 Select View reports. View the Reports for People and Diagnostic Reports, as described in earlier tutorials.
   a. Reports for People and the Summarized Equation Use Report show that the component calculations for species TABR were executed by using equations for the species TSHE, as you specified in the Equation Reassignment.
   b. Component calculations for the species CONU, however, still were not executed. We will check to see whether we overlooked something regarding CONU in the Equation Library.

Edit Equation Library

4. Select edit equation Library from the Main Menu. At the Edit Library Menu:
   a. Select File.
   b. Select Retrieve. Again select the file BIOLIB.DBF from the list of .DBF files.
   c. Select Locate equations(s), then select equation Key. Type in CONU. Then press <Enter> and Quit from Locate Equations Menu. Press <Esc> or <FlO> to remove the Edit Library Menu.
   d. You can view the documentation for the equation summarized on the highlighted line by pressing <Enter> or selecting View/modify equation from the Edit Library Menu. The three pages of documentation are fairly self-explanatory and are fully described in *Reference: library Editor.*

Resolving the problem of two parameters in one

e. We will now examine the information more closely. All equations for the species CONU use DBA as one of the parameters. In our Input Data File, DBA and DBH occupy the same data fields. We did not specify DBA in the Data Input Format Window of Design a Run. Therefore, because BIOPAK cannot read the DBA from the data, it cannot use the CONU equations in the Library. Two approaches are possible to resolve this problem.
f. You can modify the Input Data File by using a text editor or data management program to move the values for DBA to different data fields than those for DBH. We recommend this approach because it avoids possible errors.
g. Another way, NOT usually recommended, is to specify DBA as being in the same location as DBH in the Data Input Format. Care is needed, however, because a serious problem may occur. There are many species in the Library that have some equations using DBA and others using DBH. Take PSME, for example. If the data you collected are for the DBH of PSME, and if both parameters are specified as being in the same data field, when BIOPAK encounters equations using DBA, it may use these thinking that DBA was a measured parameter. BIOPAK then will use the DBH values in your Input Data File as DBA values in its calculations. Such potential errors can be avoided if you create a new Equation Library for the Input Data File, in which all equations are deleted that use parameters not measured. In other words, if you measured the DBH of THPL, delete all equations for THPL having DBA as a parameter; if you measured the DBA of PSME, delete all equations with DBH as a parameter; and so on for all species with equations using either parameter.
h. We will not step through either approach, but leave the choice and implementation to the user as an additional learning experience.

Resolving the problem of no total biomass equation

i. Also, notice that for the species CONU, there are no equations for the plant component BAT. If you believe several existing component equations in the Library would be a reasonable estimate of BAT if summed, you canspecify that a summation be done in Equation Reassignments (for details *see Appendix: Selecting Equations and Summations).* To do this, while in the Substitution Key, specify species CONU, lifeform K, and one of the components from a CONU equation in the Library. Below this first line in the Substitution Key, continue to list the species, lifeform, and other components to be used in the summation.

Exit Library Editor

j. If you are not in the Eouation Summary Window, press <Esc> one to three times to return to this window. If the Edit Library Menu is not shown, toggle it on by pressing FlO. Select Exit to return to the Main Menu.

Lesson Six--Editing the Equation Library

In this lesson you will:

- **Use given Equation Library (BIOLIB.DBF and BIOLIB.FPT)**
  - **Sort equations**
  - **Mark equations**
  - **Save subset of equations as new Equation Library**
- **Save Equation Library as database file (*.DBF)**
- **Save Equation Library as an Equation List File (*.EQN)**
- **Save partial Equation Library as Equation Documentation Text File (*.TXT)**

Before starting this tutorial, be sure to make a backup of the Equation Library files (BIOLIB.DBF, BIOLIB.FPT).

The Equation Library Editor allows you to modify documentation for equation(s), add and delete equations and make new equation libraries. These capabilities and others are described in *Reference: Library Editor.* **Some of them are illustrated in this tutorial.**

1. Select edit equation Library from the Main Menu. At the Edit Libraryz Menu.,

> **Se1ect Retrieve. Then select the file BIOLIB.DBF from the list of database files.**
> **Use <FlO> to toggle the menu off.**

Vie wing Documentation for an Equation

2. Each line in the Equation Summary Window summarizes one equation that predicts a plant component. Information here includes species, lifeform, plant component code, geographic area code, seral stage code, the first two parameters (when both present) and their ranges.

a. Use PgUp and PgDn to move through this table. Note equations are available for many plant components for some species and for one or a few components for others.

b. Use PgUp, PgDn, and the arrow keys or a mouse to highlight one line (equation) in the Equation Summary Window that may interest you.

c. For the highlighted equation, view the first screen of documentation by pressing <Enter> when the Edit Library Menu is not shown or selecting View/Modify equation from this menu. The Original and Final Equations Window shows the form, units and fit statistics (when available) of the equation as in the original source, and the equation number, equation key, form, units and parameters of the equation as used by BIOPAK.

d. Press <PgDn> to view the Sources of Equation Window. This includes raw data locations, source of equation (for example, literature citation) and sources of field data.

e. Press <PgDn> to view the Sources of Data Window more clearly. Information here is often abbreviated.

f. Press <PgUp> to return to the Sources of Equation Window.

g. From the Sources of Equation Window or the Original and Final Equations Window you can press <Ctrl-PgUp> and <Ctrl-PgDn> to move to the documentation for the previous and next equation (as ordered in the Equation Summary Window).

h. Press <PgUp> to return to the Equation Summary Window.

Sorting the Equation Library

3. Press <F10> to toggle on the Edit Library Menu.
   a. Select Sort equations and then Multiple key sorting to get to the Enter Sort Order Window.
   b. Set the sort order by putting a 1 in front of Lifeform and 2 in front of Plant Species. Note for the future that each sort key must have a different sort order (not including those with 0 that are not used in the sort).
   c. Press <Ctrl-S> to sort the Equation Library.

Marking and saving equations

3. Now save a subset of the BIOLIB.DBF Library that includes only tree species. First, browse through the Library.
   a. Select Browse equations.
   b. There are many more equations of tree species than of other lifeforms, so mark the equations that are not trees. With the highlight bar at the first nontree equation, press + to mark it. A small bullet appears at the far left of each marked equation. Pressing - unmarks an equation. Mark all the equations with lifeform C (sedge), G (grass), and H (herb). When you get to the K (coppice) and S (shrub) lifeforms, for this tutorial, refrain from marking the species with T (tree) taxonomic lifeform. Stop marking when the T (Tree) species are reached.

Making a new Equation Library (.DBF) and Equation List (.EQN)

4. A new library can now be made that includes only marked equations. Toggle the Menu back on by pressing <F10>.
   a. Select File from the Edit Library Menu.
   b. Select Save from the File Menu.
   c. Select equation library Database.
   d. Select Marked equation(s).
   e. In the File Selection Window, select the drive and directory you are using for tutorial files.
   f. At the bottom of this window name the file something like NONTREES. Do not retain the name BIOLIB, otherwise the original BIOLIB will, be overwritten with the smaller subset Library.
   g. Select <Save> to create the new library NONTREES.DBF.
   h. You will then be given a chance to save an Equation List file with the same root name containing these equations. The Equation List File is required for Calculating plant components.

Deleting marked equations and saving the remainder

5. Delete the equations for nontree species..
   a. Select Delete equation(s) from Edit Library Menu.
   b. Select Marked equations.

   The original Equation Library, BIOLIB, is still alive and well because BIOPAK is always working with copies of the Library files.

6. Now save the remaining equations, all for tree species.

a. Select File.
b. Select Save.
c. Select equation library Database.
d. Select All equations.
e. In the File Selection Window, name the file something like TREES. It will be given a .DBF extension.

Remember, before being able to use the Library in calculations, you also must save it as an Equation list file.

NOTE: If you want to save a subset of the Library based on something other than lifeform (for example, geographic area, plant component), it would be helpful to sort the Library by these factors first.

Creating text documentation of equations

7. You also may want a printout of the text documentation for selected equations. We will save the documentation for equations used. to calculate BAT (total aboveground biomass) for the tree species PSME, in an earlier tutorial. Refer to the printout of the Summarized Equation Use Report (TUTORl.USE) you made in Lesson Four.
   a. Select Browse equations. At least two different summations were used to compute BAT. By looking at the equation keys in the Equation(s) Actually Used column of the Summarized Equation Use Report, you can match their keys with those of equations in the Library. In the Equation Summarv Window the codes Spp, LF, Plant Comp, GA (geographic area), SS (seral stage) and LE# (local equation number) comprise the equation key.
   b. One summation used equations for BCL, BCD, and BST. Another used equations for BFT, BBL, BST, and BBD. Locate the equation keys for these in the Equation Library and use + to mark each.
   c. Select File from the Edit Library Menu.
   d. Select Save equations.
   e. Select Text documentation.
   f. Select Marked equation(s).
   g. In the File Selection Window, name the Equation Documentation Text File something like PSME. It will be given a .TXT extension. If this tutorial were an exercise with your own Input Data File, this file could be saved or printed as documentation of the equations used to calculate the total aboveground biomass of your Douglas-fir data.

LITERATURE CITED

Alaback Paul B. 1986. Biomass regression equations for understory plants in coastal Alaska: effects of species and sampling design on estimates. Northwest Science. 60(2): 90-103.

Alaback Paul B. 1987. Biomass-dimension relationships of understory vegetation in relation to site and stand age. In: Estimating tree biomass regressions and their error: Proceedings of the workshop on tree biomass regression functions and their contribution to the error of forestry inventory estimates; 1986 May 26-30; Syracuse, NY. Gen. Tech. Rep. NE-GTR-117. Broomall, PA: U.S. Department of Agriculture, Forest Service, Northeastern Forest Experiment Station: 141-148.

Alemdag, I.S. 1980. Manual of data collection and processing for the development of forest biomass relationships. Information Rep. PI-X-4. Chalk River, ON: Canadian Forestry Service, Petawawa National Forestry Institute. 38 p.

Brix, H.; Mitchell, A.K. 1983. Thinning and nitrogen fertilization effects on sapwood development and relationships of foliage quantity to sapwood area and basal area in Douglas-fir. Canadian Journal of Forest Research. 13: 384-389.

Buech, Richard R.; Rugg, David J. 1989. Biomass relations of shrub components and their generality. Forest Ecology and Management. 26: 257-264.

Daubenmire, Rexford. 1968. Plant communities: a textbook of plant synecology. New York: Harper and Row. 300 p.

Dean, T.J.; Long, J.N. 1986. Variation in sapwood area-leaf area relations within two stands of lodgepole pine. Forest Science. 32(3): 749-758.

Espinosa-Bancalari, M.A.; Perry, D.A.: Marshall, John D. 1987. Leaf area-sapwood area relationships in adjacent young Douglas-fir stands with different early growth rates. Canadian Journal of Forest Research. 17(2) 174-180

Garrison, G.A.; Skovlin, J.M.; Poulton, C.E.; Winward, A.H. 1976. Northwest plant names and symbols for ecosystem inventory and analysis. Gen Tech. Rep. PNW-46. Portland, OR: U.S. Department of Agriculture, Forest Service, Pacific Northwest Forest and Range Experiment Station. 263 p.

Gholz, H.L.; Grier, C.C.; Campbell, A.G.; Brown, A.T. 1979. Equations for estimating biomass and leaf area plants in the Pacific Northwest. Res. Pap. 41. Corvallis, OR: Oregon State University, School of Forestry. 39 p.

Grier, Charles C.; Logan, Robert S. 1977. Old-growth <u>Pseudotsuga menziesii</u> communities of a western Oregon watershed: biomass distribution and production budgets. Ecological Monographs. 47: 373-400.

Koerper, Greg J.; Richardson, Curtis J. 1980. Biomass and net annual primary production regressions for Populus grandidentata on three sites in northern lower Michigan. Canadian Journal of Forest Research. 10(l): 92-101.

Long, J.N.; Smith, F.W. 1988. Estimating leaf area of Abies lasiocarpa across ranges of stand density and site quality. Canadian Journal of Forest Research. 19(7): 930-932.

Madgwick, H.A.I. 1970. Biomass and productivity models of forest canopies. In: Reichle, David E., ed. Ecological studies: analysis of temperate forest ecosystems. Berlin, Germany: Springer-Verlag: 47-54. Vol. 1.

Marshall, J.D.; Waring, R.H. 1986. Comparison of methods of estimating leaf-area index in old-growth Douglas-fir. Ecology. 67(4): 975-979.

Pearson, John A.; Fahey, Timothy J.; Knight, Dennis H. 1984. Biomass and leaf area in contrasting lodgepole pine forests. Canadian Journal of Forest Research. 14: 259-265.

Pieper R.D. 1978. Measurement techniques for herbaceous and shrubby vegetation. Las Cruces, NM: New Mexico State University, Department of Animal and Range Science. 145 p.

Sachs, Donald. 1983. Management effects on nitrogen nutrition and long-term productivity of western hemlock stands: an exercise in simulation with FORCYTE. Corvallis, OR: Oregon State University. 63 p. M.S. thesis.

Schlaegel, Bryce E.; Kennedy, Harvey E., Jr. 1984. Do different young plantation-grown species require different biomass models? In: Saucier, Joseph R., ed.: Proceedings of the 1984 Southern forest biomass workshop; 1984 June 5-7; Athens, GA. Asheville, NC: U.S. Department of Agriculture, Forest Service, Southeastern Forest Experiment Station: 23-35.

Standish, J.T.; Manning, G.H.; Demaerschalk, J.P. 1985. Development of biomass equations for British Columbia tree species. Vancouver, BC: Pacific Forestry Centre, Canadian Forestry Service. 47 p.

Stanek, W.; State, D. 1978. Equations predicting primary productivity (biomass) of trees, shrubs and lesser vegetation based on current literature. Victoria, BC: Canadian Forestry Service, Pacific Forest Research Centre. 58 p.

Thompson, Dan C. 1989. The effect of stand structure and stand density on the leaf area-sapwood area relationship of lodgepole pine. Canadian Journal of Forest Research. 19: 392-398.

Tritton, Louise M.; Hornbeck, James W. 1982. Biomass equations for major tree species of the Northeast. Gen. Tech. Rep. NE-GTR-69. Durham, NH: US Department of Agriculture, Forest Service, Northeastern Forest Experiment Station. 46 p.

Valentine, Harry T.; Tritton, Louise M.; Furnival, George M. 1984. Subsampling trees for biomass, volume, or mineral content. Forest Science. 30(3): 673-681.

Waring, R.H.; Schroeder, P.E.; Oren, R. 1982. Application of the pipe model theory to predict canopy leaf area. Canadian Journal of Forest Research. 12(3): 556-560.

Weiner, Jacob; Thomas, Sean C. 1992. Competition and allometry in three species of annual plants. Ecology. 73(2): 648-656.

Wharton, Eric H.; Cunia, Tiberius, comps. 1987. Estimating tree biomass regressions and their error. In: Proceedings of the workshop on tree biomass regression functions and their contribution to the error of forest inventory estimates; 1986 May 26-30; Syracuse, NY. Gen. Tech. Rep. NE-GTR-117. Broomall, PA: U.S. Department of Agriculture, Forest Service, Northeastern Forest Experiment Station. 303 p.

Whittaker, R.H.; Bormann, F.H.; Likens, G.E.; Siccama, T.G. 1974. The Hubbard Brook ecosystem study: forest biomass and production. Ecological Monographs. 44: 233-254.

Whittaker, R.H.; Woodwell, G.M. 1968. Dimension and production relations of trees and shrubs in the Brookhaven Forest, New York. Journal of Ecology. 56: l-25.

Woods, Kerry D.; Feiveson, A.H.; Botkin, Daniel B. 1991. Statistical error analysis for biomass density and leaf area index estimation. Canadian Journal of Forest Research. 21: 974-989.

APPENDICES

Appendices include more detail and start with complete contents.

Section

Codes

There are six types of codes; four codes can be modified by the user (Geographic Area, Seral Stage, Plant Component, and Species), and two cannot be changed (Lifeform and Parameter). All codes, except Parameter, are part of the Equation Key and affect selection of equations from the Library.

Geographic Area codes and Seral Stage codes now in BIOPAK

Geographic Area and Seral Stage codes either must be included in the Input Data File or be specified in the Default Settings Window of Design a Run. The codes can be modified as described in Appendix: Customizing *BIOPAK.* They are part of the Equation Key. The following Geographic Area and Seral Stage codes fit ecosystems (primarily forests) in our area.

Code	Meaning
Geographic Area codes:	
A	Southeast Alaska
C	Coast Ranges (BC, WA, OR, N. CA)
E	East side of the Cascades and eastern OR and WA
R	Rocky Mountains
S	Sierra Nevada
W	West side of the Cascades
G	General (Combination of several areas, or unknown)
Seral Stage codes:	
E	Early (recently disturbed sites; reorganizational stage of succession; self-thinning not important; herbs and/or shrubs are usually dominant in our area)
Y	Young (site approaching full occupancy, or site fully occupied; self-thinning occurring; no or little establishment by later-seral species)
M	Mature (significant establishment and growth of later-seral species; canopy of early seral species breaking up)
O	Old-growth (Original canopy well broken up; late-seral species very common and dominating understory)
G	General (combination of several stages, or unknown)

Lifeform codes allowed by BIOPAK

Lifeform codes either must be included in the Input Data File or be substituted by the user or BIOPAK. The following are the only Lifeform codes recognized by BIOPAK. They cannot be changed by the user. Lifeform code is part of the Equation Key.

Code	Lifeform	Strata used in reports
C	Sedge, rush	Herb
	Grass	Herb
H	Herb	Herb
K	Coppice	Shrub
	Lichen	Moss
M	Bryophyte	Moss
	Shrub	Shrub
T	Tree	Tree

Parameter codes allowed by BIOPAK

The following Parameter codes are used in the Data Input Format Window of Design a Run and in the Equation Library; they are not included in the Input Data File. In the Data Input Format Window, the codes represent the measured parameters in the Input Data File. In the Equation Library, Parameter codes represent the independent variables used to calculate the plant components, except that codes marked by asterisks cannot be used in equations. These codes are the only Parameter codes recognized by BIOPAK. They cannot be changed by the user. Be sure to look at the documentation for each equation to be used to see where and how these parameters were measured.

Code	Description
BIO	Biomass
CIR	Circumference
c o v	Canopy cover
CR	Crown ratio
DBA	Diameter at or near base
DBH	Diameter at breast height
	Form class
HT	Height
LEN	Length (for example, along stem, projected crown length)
	Number of plants
NUM	Number (for example, of fronds, stems, or flowers)
*PLOTAREA	Fixed-plot area
*PRISMFAC	Prism basal area factor
*PLTSLOPE	Plot slope correction
SAP	Sapwood radial thickness
SPA	Sapwood cross-sectional area
VOL	Volume (for example, of bole, or crown)
WID	Width (for example, projected crown width)

Plant Component codes currently built into BIOPAK

Plant Component codes come into play when components are requested for calculation. Component codes are part of the Equation Key. The definitions are ordered by derivation of the code. This list can be modified as described in *Appendix: Customizing BIOPAK: BIOCODES File.* Note: Equations are not available in the Library for every component listed below.

Code	Definition
Leaves and flowers:	
AFN	All-sided area, foliage, new
AFO	All-sided area, foliage, old
AFT	All-sided area, foliage, total
BFF	Biomass, foliage (fronds), fertile
BFN	Biomass, foliage, new
BFO	Biomass, foliage, old
BFT	Biomass, foliage, total
BFV	Biomass, foliage (fronds), vegetative
BIT	Biomass, inflorescence, total
PFN	Projected (one-sided for broad leaves) area, foliage, new
PFO	Projected (one-sided for broad leaves) area, foliage, old
PFT	Projected (one-sided for broad leaves) area, foliage, total
Branches:	
BBD	Biomass, branches, dead
BBL	Biomass, branches, live
BBS	Biomass, branches, small
BBT	Biomass, branches, total (live + dead)
Stems:	
BSB	Biomass, stem, bark (may or may not include top and/or stump)
BST	Biomass, stem, total (bark plus wood)
BSW	Biomass, stem, wood (may or may not include top and/or stump)
CSB	Cross-sectional area, stem, at base of the stem
CSD	Cross-sectional area, stem, at d.b.h.
CZB	Cross-sectional area, sapwood, at base of the stem
CZD	Cross-sectional area, sapwood, at d.b.h.
HST	Height, stem, total
LSL	Length of longest stem
VQW	Volume, top, wood
VSB	Volume, stem, bark (may or may not include top and/or stump)
VST	Volume, stem, total (wood plus bark)
VSW	Volume, stem, wood (may or may not include top and/or stump)
VSZ	Volume, stem, sapwood
VYl	Volume, boardfoot, Scribner
VY2	Volume, boardfoot, International
Crown (wood + bark + foliage):	
BCD	Biomass, crown, dead (may or may not include top of stem)
BCL	Biomass, crown, live (may or may not include top of stem)
BCT	Biomass, crown, total (live plus dead)
PCH	Projected area, crown, projected onto the horizontal plane
PCS	Projected area, crown, projected onto the sloping ground surface
VCT	Volume, crown, total
Underground:	
BKC	Biomass, coarse roots, root crown
BKL	Biomass, coarse roots, live

BLL Biomass, rootlets (fine), live
BLM Biomass, rootlets (fine), mycorrhizal
BLU Biomass, rootlets (fine), unmycorrhizal
BRD Biomass, roots, dead
BRL Biomass, roots, live
BRT Biomass, roots, total
BUD Biomass, underground, dead
BUL Biomass, underground, live
BUN Biomass, underground, nodules
BUT Biomass, underground, total

Groups of components (relations shown graphically in figures 2-4):
BAE Biomass, aboveground, entire (live and dead, wood plus bark)
BAL Biomass, aboveground, live (wood t bark t foliage)
BAP Biomass, aboveground, plus (live, wood plus bark)
BAT Biomass, aboveground, total (live and dead, wood t bark t foliage)
BTT Biomass, total (aboveground and underground), total
VAE Volume, aboveground, entire (live and dead, wood t bark)

Species codes in current Equation Library

The Species codes in the library as of December 1993 are listed by lifeform groups. The letters in parentheses after the lifeform group names represent the Taxonomic Lifeform codes associated with the species in the Equation Library.

Code	Scientific name	Common name
Sedges (C):		
LUCA2	*Luzula campestris*	Smooth woodrush
LUZUL	*Luzula* spp.	Woodrush
Grasses (G):		
AGROS	*Agrostis* spp.	Bentgrass
CARU	*Calamagrostis rubescens*	Pinegrass
FEAR	*Festuca arizonica*	Arizona fescue
FESTU	*Festuca* spp.	Fescue
Gramin	*Graminoides* spp.	Any grass species
POFE	*Poa fendleriana*	Muttongrass
Herbs, Forbs (H):		
ADBI	*Adenocaulon bicolor*	American adenocaulon
ADPE	*Adiantum pedatum*	Northern maidenhair fern
ANMA	*Anaphalis margaritacea*	Common pearl everlasting
ARCA3	*Aralia californica*	California aralia
ATFI	*Athyrium filix-femina*	Ladyfern
BLSP	*Blechnum spicant*	Deerfern
CASC2	*Campanula scouleri*	Bellflower
CIRSI	*Cirsium* spp.	Thistle
CIVU	*Cirsium vulgare*	Bull thistle
CLUN	*Clintonia uniflora*	Queencup beadlily
COAS	*Coptis aspenifolia*	Spleenwort-leaved goldthread

COCA	*Cornus canadensis*	**Bunchberry dogwood**
COCA2	*Conyza canadensis*	**Horseweed**
COHE	*Collomia heterphyla*	**Varied-leaf colomia**
COLA	*Coptis laciniata*	**Cutleaf goldthread**
DRAU2	*Dryopteris austriaca*	**Mountain woodfern**
EPAN	*Epilobium angustifolium*	**Fireweed**
EPPA	*Epilobium paniculatum*	**Autumn willow-weed**
EPWA	*Epilobium watsonii*	**Watson's willow-weed**
EQUIS	*Equisetum* **spp.**	**Horsetail**
GATR	*Galium triflorum*	**Sweetscented bedstraw**
GNMI	*Gnaphalium microcephalum*	**Cudweed**
GOOB	*Goodyera oblongifolia*	**Rattlesnake-plantain**
GYDR	*Gymnocarpium dryopteris*	**Oak-fern**
HIAL	*Hieracium albiflorum*	**White hawkweed**
LAPO	*Lathyrus polyphyllus*	**Pacific peavine**
LIBO2	*Linnaea borealis*	**Twinflower**
LOCR	*Lotus crassifolius*	**Big lotus**
LOOB	*Lotus oblongifolius*	**Lotus specie**
LULA	*Lupinus latifolius*	**Broadleaf lupine**
MADIA	*Madia* **spp.**	**Tarweed**
MADI2	*Maianthemum dilatitum*	**May-lily**
MIGU	*Mimulu guttatus*	**Common monkeyflower**
MOUN	*Moneses uniflora*	**Woodnymph**
MUMO	*Muhlenbergia montana*	**Mountain muhly**
OXOR	*Oxalis oregana*	**Oregon oxalis**
PEFR2	*Petasites frigidus*	**Sweet coltsfoot**
PERA	*Pedicularis racemosa*	**Sickletop pedicularis**
POMU	*Polystichum munitum*	**Pacific coast swordfern**
PTAQ	*Pteridium aquilinum*	**Braken fern**
PYSE	*Pyrola secunda*	**Sidebells**
RUPE	*Rubus pedatus*	**Five-leaved bramble**
SEJA	*Senecio jacobaea*	**Tansey ragwort**
SESY	*Senecio silvaticus*	**Woodland groundsel**
SETR	*Senecio triangularis*	**Arrowleaf groundsel**
SILO2	*Sitanion longifolium*	**Squirreltail**
SMST	*Smilacina stellata*	**Starry solomonplume**
STC04	*Stachys cooleyae*	**Cooley's hedge-nettle**
THOC	*Thalicrum occidentale*	**Western meadowrue**
TITR	*Tiarella trifoliata*	**Foamflower, coolwort**
TRLA	*Trifolium latifolium*	**Twin clover**
TRLA2	*Tridentalis latifolia*	**Western starflower**
VISE	*Viola sempervirens*	**Redwoods violet**
WHMO	*Whipplea modesta*	**Whipplevine**
XETE	*Xerophyllum tenax*	**Beargrass**

Coppice (K):

ACCI	*Acer circinatum*	**Vine maple**
ACMA	*Acer macrophyllum*	Bigleaf **maple**
ARME	*Arbustus menziensii*	**Pacific** madrone
CONU	*Cornus nuttalli*	**Pacific dogwood**
LIDE	*Lithocarpus densiflorus*	Tanoak
QUKE	*Quercus kelloggii*	**California black oak**
RHMA	*Rhododendron macrophyllum*	**Pacific rhododendron**

Bryophytes (M):

EUOR	*Eurhynchium oreganum*	**Moss**
HYCI	*Hypnum circinale*	**Moss**
HYSP	*Hylocomium splendens*	**Feather moss**
JULA	*Jungermannia lanceolata*	**Liverwort**
PLUN	*Plagiothecium undulatum*	**Moss**
POMA4	*Pogonatum macounii*	**Moss**
PTCR	*Ptilium crista-castransis*	**Moss**
RHGL	*Rhizomnium glabrescens*	**Moss**
RHLO	*Rhytidiadelphus lorens*	**Feather moss**

Shrubs (S):

ACCI	*Acer circinatum*	**Vine maple**
ACGL	*Acer glabrum*	**Mountain maple**
ALSI	*Alnus sinuata*	**Sitka alder**
AMAL	*Amelanchier alnifolia*	**Serviceberry**
ARC03	*Arctostaphylos columbiana*	**Manzanita**
ARPA	*Arctostaphylos patula*	**Greenleaf manzanita**
ARTR	*Artemisia tridentata*	**Big sagebrush**
ARUV	*Arctostaphylos uvi-ursi*	**Kinnikinnick**
ARVI	*Arctostaphylos viscida*	**Whiteleaf manzanita**
BENE	*Berberis nervosa*	**Cascade hollygrape**
BERE	Berberis repens	**Creeping hollygrape**
CACH	*Castanopsis chrysophylla*	**Golden chinkapin**
CASE	*Castanopsis sempervirens*	**Sierra chinkapin**
CECO	*Ceanothus cordulatus*	**Mt. whitethorn ceanothus**
CEIN	*Ceanothus integerrimus*	**Deerbrush ceanothus**
CESA	*Ceanothus sanguineus*	**Redstem ceanothus**
CEVE	*Ceanothus velutinus*	**Snowbrush ceanothus**
CEVEL	*Ceanothus velutinus* **var.** *laevigatus*	*Greasewood*
CEVEV	*Ceanothus velutinus* **var.** *velutinus*	
CHNA	*Chrysothamnus nauseosus*	**Rubber/gray rabbitbrush**
CHUM	*Chionophila umbellata*	**Common princes-pine**
COCOC	*Corylus cornuta var. californica*	**California hazel.**
COCA2	*Corylus cornuta*	**Hazel**
COST	*Cornus stolonifera*	**Western dogwood**
GASH	*Gaultheria shallon*	**Sal al**
HABL	*Haplopappus bloomeri*	**Rabbitbrush goldenweed**
HODI	*Holodiscus discolor*	**Creambush rockspirea**
JUCO	*Juniperus communis*	Common juniper
LIDE	*Lithocarpus densiflorus*	**Tanoak**
LOUT	*Lonicera utahensis*	**Utah honeysuckle**
MEFE	*Menziensia ferruginea*	Smooth menziensia
OPHO	*Oplopanax horridum*	**American devilsclub**
PAMY	*Pachistima myrsinites*	**Oregon boxwood**
PHLE2	*Philadelphus lewisii*	**Mockorange**
PHMA	*Physocarpus malvaceus*	**ninebark**
PRVI	*Prunus virginiana*	**Chokecherry**
PUTR	*Purshia tridentata*	**Antelope bitterbrush**
QUKE	*Quercus kelloggii*	**California balch oak**
RHMA	*Rhododendron macrophyllum*	**Pacific rhododendron**
RIBES	*Ribes* **spp.**	**Currant species**
RIBR	*Ribes bracteosum*	**Stink currant**

ROSA	*Rosa* **spp.**	**Rose species**
RUID	*Rubus idaeus*	**Red raspberry**
RULE	*Rubus leucodermis*	**Whitebark raspberry**
RUPA	*Rubus parviflorus*	**Western thimbleberry**
RUSP	*Rubus spectabilis*	**Salmonberry**
RUUR	*Rubus ursinus*	**California dewberry**
SAJE	*Salix jepsonii*	**A willow**
SALIX	*Salix*	**Willow species**
SASC	*Salix scouleriana*	**Scouler willow**
SASE	*Sambucus cerulea*	**Blueberry elder**
SAS12	*Salix sitchensis*	**Sitka willow**
SHCA	*Sherphedia canadensis*	**Buffaloberry**
sosc	*Sorbus scopulina*	**Mountain ash**
SPBE	*Spirea betulifolia*	**White spirea**
SYAL	*Symphoricarpos albus*	**Common snowberry**
SYMPH	*Symphoricarpos*	**Snowberry species**
VAAL	*Vaccinium alaskaense*	**Alaskan huckleberry**
VACC I	*Vaccinium* **spp.**	**Huckleberry species**
VAGL	*Vaccinium globulare*	**Blue huckleberry**
VAPA	*Vaccinium parviflorum*	**Red whortleberry**
VASC	*Vaccinium scoparium*	**Grouse whortleberry**

Trees, Tree combinations (T):

ABIES	*Abies* **spp.**	**Fir species**
ABAM	*Abies amabilis*	**Pacific silver fir**
ABCO	*Abies concolor*	**White fir**
ABGR	*Abies grandis*	**Grand fir**
ABLA2	*Abies lasiocarpa*	**Subalpine fir**
ABMA	*Abies magnifica*	**California red fir**
ABMAS	*Abies magnifica shastensis*	**Shasta red fir**
ABPR	*Abies procera*	**Noble fir**
ACMA	*Acer macrophyllum*	**Bigleaf maple**
ALRU	*Alnus rubra*	**Red alder**
ALSI	*Alnus sinuata*	**Sitka alder**
ARME	*Arbutus menziesii*	**Pacific madrone**
BEPA	*Betula papyrifera*	**White/paper birch**
CADE	*Calocedrus decurrens*	**Incense-cedar**
CACH	*Castanopsis chrysophylla*	**Golden chinkapin**
CEDAR	**CHNO & THPL**	
CHNO	*Chamaecyparis nootkatensis*	**Alaska yellow-cedar**
JUOC	*Juniperus occidentalis*	**Western juniper**
JUSC	*Juniperus scopulorum*	**Rocky Mountain juniper**
LAOC	*Larix occidentalis*	**Western larch**
LIDE	*Lithocarpus densiflorus*	**Tanoak**
PIAB	**PIMO & ABGR & PIAL**	
PIAL	*Pinus albicaulus*	**Whitebark pine**
PICO	*Pinus contorta*	**Lodgepole pine**
PIEN	*Picea engelmannii*	**Engelmann spruce**
PIJE	*Pinus jefferyi*	**Jeffrey pine**
PILA	*Pinus lambertiana*	**Sugar pine**
PIMO	*Pinus monticola*	**Western white pine**
PINUS	*Pinus*	**Pine species**
PIP0	*Pinus ponderosa*	**Ponderosa pine**
PISI	*Picea sitchensis*	**Sitka spruce**

POTR	*Populus tremuloides*	**Quaking aspen**
POTR2	*Populus trichocarpa*	**Black cottonwood**
PPPA	**PSME & PIPO & PIEN & ABLA 2**	
PREM	*Prunus emarginata*	**Bitter cherry**
PSME	*Pseudotsuga menziesii*	**Douglas-fir**
QUAG	*Quercus agrifolia*	**Coast live oak**
QUCH	*Quercus chrysolepsis*	**Canyon live oak**
	Quercus douglasii	**Blue oak**
QUEN	*Quercus engelmannii*	**Engelmann oak**
QUGA	*Quercus garryana*	**Oregon white oak**
QUKE	*Quercus kelloggii*	**California black oak**
QULO	*Quercus lobata*	**Valley oak**
QUWI	*Quercus wislizeni*	**Interior live oak**
SEGI	*Sequoiadendron giganteum*	**Giant sequoia**
THLAPI	**THPL & LAOC & PICO**	
THPL	*Thuja plicata*	**Western redcedar**
THPSPI	**THPL & PSME & PIPO**	
TSHE	*Tsuga heterophylla*	**Western hemlock**
TSME	*Tsuga mertensiana*	**Mountain hemlock**
UMCA	*Umbellularia californica*	**California-laurel**

Customizing BIOPAK

Section

BIOPAK was designed to meet the needs of our ecology research group at the Pacific Northwest Research Station in Corvallis, Oregon. We have bu-ilt some flexibility into the system, however, by allowing users to customize some key elements of the software.

Equation Library

The Equation Library shipped with BIOPAK contains about 1,000 equations. Most equations were developed in the Pacific Northwest. The Equation Library Editor allows for both modifying the existing Library, and for creating a new one. *Reference: Library Editor* contains full information on adding new equations and *Appendix: Equation Library* gives more information on the Equation Library shipped with BIOPAK.

For your particular needs, you will probably modify the Equation Library. For example, if BIOPAK will be used in a limited geographic area, you may want to save a subset of the existing library and add more equations from a particular region. If BIOPAK will be used outside the Northwest of the United States of America you will probably want to build a library of new equations.

BIOCODES File

BIOCODES is a flat ASCII file that can be modified with a text editor. The file contains all Plant Component codes and units, Geographic Area codes, Seral Stage codes, and Equation Selection Penalties (ESPs). The BIOCODES file provides a great deal of flexibility in applying BIOPAK, but user beware! The format and function of the file must be understood before it can be modified; otherwise, invalid results or a nonfunctional program may result. Before starting any modifications, make a backup copy of the, BIOCODES file.

The BIOCODES file is used for several purposes in the software:

1. Data verification in the Run Design module. The Plant Component, Geographic Area and Seral Stage codes, as specified in BIOCODES, are the only valid entries when designing a run. The NO VALUE CALCULATED Equation Selection Penalty level is also the upper limit for ESP Levels in the Default Settings Window.
2. Selection of equations. The ESP values associated with each mismatch

affect the selection of equations from the Library. For a given record from the Input Data File, BIOPAK will select an equation with the lowest total ESP.

3. Column headings in reports. The abbreviated component descriptions entered under the columns "Titlinel" and "Titline2" are used as column headings for the component output in reports.

Lines beginning with an asterisk (*) denote lines read directly by the software. The text in the lines directly following the asterisk must not be changed, or the program will not run.

Lines beginning with an ampersand (&) are comments and may be inserted anywhere in BIOCODES. In this case, the ampersand was used to insert column headings so that the file is easier to interpret.

Because the file is read directly by the software, be sure to retain the file format. Be careful in modifying BIOCODES, no error checking is done. If the structure is not correct, the program may crash or give invalid results.

Here is a sample BIOCODES File:

```
*COMPONENT CODES (LEXICAL ORDER)
&Co Unit TitLinel TitLine2 Definition
AFN cm2 AREA NEW FOLIAGE Area, foliage, new
AFO cm2 AREA OLD FOLIAGE Area, foliage, old
AFT cm2 AREA TOT FOLIAGE Area, foliage, total
BAE gm   BIO ENTR ABOVGRND Biomass, aboveground, entire (live&dead, wood+bark)
BAL gm   BIO LIVE ABOVGRND Biomass, aboveground, live, total
BAP gm   BIO W+BK ABOVGRND Biomass, aboveground, wood t bark
BAT gm   BIO TOT ABOVGRND Biomass, aboveground, total
BBD gm   BIO DEAD BRANCHES Biomass, branches, dead
BBL gm   BIO LIVE BRANCHES Biomass, branches, live
BBS gm   BIO SMAL BRANCHES Biomass, branches, small
BBT gm   BIO TOT BRANCHES Biomass, branches, total (live t dead)
BCD gm   BIO DEAD CROWN   Biomass, crown, dead
BCL gm   BIO LIVE CROWN   Biomass, crown, live
BCT gm   BIO  TOT  CROWN   Biomass, crown, total
BFF gm   BIO FERT FRONDS Biomass, foliage (fronds), fertile
BFN gm   BIO NEW FOLIAGE Biomass, foliage, new
BFO gm   BIO OLD FOLIAGE Biomass, foliage, old
BFT gm   BIO TOT FOLIAGE Biomass, foliage, total
BFV gm   BIO VEG FRONDS Biomass, foliage (fronds), vegetative
BIT gm   BIOMASS INFLORES Biomass, inflorescense, total
BKC gm   BIO CRWN COARSRTS Biomass, koarse roots, root crown
BKL gm   BIO LIVE COARSRTS Biomass, koarse roots, live
BLL gm   BIO LIVE ROOTLETS Biomass, rootlets (fine), live
BLM gm   BIO MYC ROOTLETS Biomass, rootlets (fine), mycorrhizal
BLU gm   BIO UNMY ROOTLETS Biomass, rootlets (fine), un-mycorrhizal
BRD gm   BIO DEAD ROOTS   Biomass, roots, dead
BRL gm   BIO LIVE ROOTS   Biomass, roots, live
BRT gm   BIO TOT   ROOTS   Biomass, roots, total (live t dead)
BSB gm   BIO STEM   BARK   Biomass, stem, bark
BST gm   BIO STEM TOTAL   Biomass, stem, total
BSW gm   BIO STEM WOOD Biomass, stem, wood
BTT gm   BIO TOT   TOTAL   Biomass, total (above and below ground), total
```

```
BUD gm   BIO DEAD UNDRGRND Biomass, underground, dead
BUL gm   BIO LIVE UNDRGRND Biomass, underground, live
BUN gm   BIO NOD UNDRGRND Biomass, underground, nodules
BUT gm   BIO TOT UNDRGRND Biomass, underground, total
CSB cm2 AREA STM   BASE   Cross-sectional area, stem, at base of the stem
CSD cm2 AREA STM BREAST Cross-sectional area, stem, at d.b.h.
CZB cm2 AREA SAP   BASE   Cross-sectional area, sapwood, at base of the stem
CZD cm2 AREA SAP BREAST Cross-sectional area, sapwood, at d.b.h.
HST m    HT STEM   TOTAL   Height, stem, total
LSL m    LEN LONG STEM Length of the longest stem
PCH cm2 PROJ CRN HORIZONT Projected area, crown, onto the horizontal plane
PCS cm2 PROJ CRN SLP GRND Projected area, crown, onto the sloping ground surface
PFN cm2 PROJ NEW FOLIAGE Projected area, foliage, new
PFO cm2 PROJ OLD FOLIAGE Projected area, foliage, old
PFT cm2 PROJ TOT FOLIAGE Projected area, foliage, total
VAE m3   VOL ENTR ABOVGRND Volume, aboveground, entire (live & dead wood t bark)
VCT m3   VOL TOT   CROWN   Volume, crown, total
VQW cm3 VOL WOOD   TOP    Volume, top, wood
VSB cm3 VOL STEM   BARK Volume, stem, bark
VST cm3 VOL STEM TOTAL   Volume, stem, total (top and stump)
VSW cm3 VOL STEM   WOOD   Volume, stem, wood
VSZ cm3 VOL STEM SAPWOOD Volume, stem, sapwood
VY1 bdft VOL BDFT SCRIBNER Volume, boardfoot, Scribner
VY2 bdft VOL BDFT INTERNAT Volume, boardfoot, International

*GEOGRAPHIC AREA CODES
G General
A Southeast Alaska
C Coast Ranges
W Western Cascades and High Cascades
E East side of Cascades and eastern Oregon and Washington
R Rocky Mountains
S Sierra Nevada

*GTABLE
& Codes in top line are for candidate equations
& Codes in 1st row are for Request to Library
        G     A     c     w     E     R     S
'G'     0   515   511   510   513   512   514
'A'   510     0   110   111 10012 10010 10011
'C'   510   111     0   110  1012  1011  1013
'W'   510   111   110     0  1012  1011  1013
'E'   510 10000  1011  1010     0   110   111
'R'   510 10000  1011  1010           0   111
'S'   510 10000  1011  1010   110           0

*SERAL STAGE CODES
G General
E Early vegetation in reorganizational stages of succession
Y Young vegetation in early stages of succession
M Mature vegetation in middle stages of succession
O Old-growth vegetation in late stages of succession
```

```
  *STABLE
& Codes in top line are for candidate equations
  & Codes in 1st row are for Request to Library
          G
  'G'      0  1003  1001  1000  1002
  'E'   1001      0 1000 10001 10000
  'Y'   1000 1001          100  1002
  'M'   1000 10000   101     0   100
  'O'   1000 10000 1001    100     0

  *UNDER-EXTRAPOLATION:
  150

  *OVER-EXTRAPOLATION:
  20050

  *PARAMETER RANGE UNKNOWN:
  3000

  *COPPICE CHANGED -TO TAX LIFE:
  4000

  *BFT CHANGED TO BAT FOR HGS:
  5000

  *NO VALUE CALCULATED:
  80000
```

Modifying Plant Component codes-

The Plant Component codes recognized by BIOPAK may be added, changed, or deleted. There may be a total of 150 Plant Component codes, and they must be in alphabetical order. For each Plant Component code added, the units associated with them also must be included. Only the metric units in *Appendix: Units* are valid because these units must match those in the Equation Library. When modifying Component codes, stay within the section of BIOCODES following the line:
*COMPONENT CODES (LEXICAL ORDER)

The format is as follows:

Columns:	Contents:
1-3	Component code, all capital letters
4	Blank
5-8	Units (must be metric, as in *Appendix: Units*)
9	Blank
10-17	Column heading in reports, line 1
	Blank
19-26	Column heading in reports, line 2
	Blank
28-80	Descriptive label (used in Components to Output)

A system was developed to construct the list of codes shipped with BIOPAK. Table 2 illustrates the system and the meaning of the characters used in their construction. Use of all these characters is encouraged so that all Plant Component codes have a consistent interpretation.

Table 2--BIOPAK system for deriving Plant Component codes[a]

Character	Meaning(s)
First character:	
A	All-sided surface or leaf area
P	Projected surface or leaf area
C	Cross-sectional area
B	Biomass
H	Plant height
L	Length of longest stem
V	Volume
Second character:	
A	Aboveground
B	Branch
C	Crown (branches and foliage)
F	Foliage or fronds
I	Inflorescence
Z	Sapwwod
S	Stem
Y	Board feet
Q	Top
T	Total (aboveground and underground)
U	Underground
R	Roots
L	Little roots (generally < 2 mm diameter)
K	Coarse roots (generally > 2 mm diameter)
W	Current year twigs
N	Current year twigs and foliage
X	Aboveground woody without current year twigs, with bark.
Third character:	
B	Bark; or Base of stem
W	Wood
P	Wood plus bark, live
E	Entire: live and dead, wood and bark
L	Live; or Longest
D	Dead; or DBH
N	Nodules; or New
0	Old
F	Fertile (reproductive)
V	Vegetative (not reproductive)
C	Crown (canopy crown or root crown)
T	Total
S	Small; Or Projected onto the sloping ground surface
M	Mycorrhizal
U	Unmycorrhizal
Z	Sapwood
1	Scribner
2	International

[a] Each Plant Component code is made of 3 characters with the meanings given here

Modifying Geographic Area codes--

Most of the equations shipped with BIOPAK were developed in the Pacific Northwest. You may want to use BIOPAK outside this region, or add more specific geographic areas than those found in the current version of BIOCODES.

If more equations from other regions are added, the new Geographic Area codes and their associated ESPs need to be added. There also may be reason to split up the geographic areas currently found in BIOCODES. Again, the new codes and their associated ESPs must be added.

Codes and their meanings can be added, modified, or deleted after the line:
***GEOGRAPHIC AREA CODES**

Any letter may be used as a Geographic Area code; therefore there may be a total of up to 26 codes. After settling on a new set of codes, the codes and ESPs immediately following the line:
***GTABLE**
must be revised. The codes on the top and side of the *GTABLE must be in the same order as those following *GEOGRAPHIC AREA CODES. The codes on the left side must start in column 1 and be enclosed in single quotes. Values on each line in this square matrix are delimited by white spaces (a blank or several blanks -in row). Lining up values in the same column will facilitate interpretation by inserting multiple blanks. The codes across the top line represent those of candidate equations in the Library, and the codes in the first column represent those in the Request to the Library (from data or <u>Default Settinqs Window</u>). Refer to *Modifying Equation Selection Penalties* **for guidelines on setting ESPs.**

Modifying Seral Stage codes--

The'seral stages shipped with BIOPAK reflect a particular plant ecology. perspective. The equations in the L brary use these Seral Stage codes. If working from a different perspective you may want to change the given codes. The Seral Stage codes and their meanings can be added, changed, or deleted after the line
***SERAL STAGE CODES**

Any letter may be used as a Seral Stage code; therefore there may be a total of up to 26 codes. After a new set of codes is settled on, the codes and ESPs immediately following the line
***STABLE**
must be revised. The codes on the top and side of the *STABLE must be in the same order as those following *SERAL STAGE CODES. The codes on the left side must start in column 1 and be enclosed in single quotes, for example, 'G'. Values on each line in this square matrix are delimited by white spaces (a blank or several blanks in a row). We suggest lining up values in the same column to facilitate interpretation by inserting multiple blanks. The codes across the top line represent those of candidate equations in the Library, and the codes in the first column represent those in the Request to the Library (from data or <u>Default Settinqs Window</u>). Refer to *Modifying Equation Selection Penalties* **for guidelines on setting ESPs.**

Modifying Equation Selection Penalties--

The major feature of BIOPAK is its ability to link vegetation Input Data Files with a library of equations. In many instances, the plants used to construct

the equations in the Library will closely match the plants in the Input Data File. There also will be instances, however, when the plant sizes, geographic areas, or seral stages will not match. With each mismatch, there is an associated Equation Selection Penalty.

The severity of the mismatch will depend on the particular situation; for example, if the Input Data File were from southeast Alaska, but an equation is used from coastal Oregon, a slight geographic mismatch will occur. If the equation were from the Sierras, however, the mismatch would be more severe. The ESPs assigned to each mismatch should reflect these severities.

In the BIOCODES file shipped with BIOPAK, we used four levels of magnitude (100, 500, 1000, and 10000) for geographic area and seral stage mismatches. On some lines in the geographic area and seral stage tables, there is more than one ESP of the same magnitude. In these cases, we ranked the ESPs in order of preference, for example, for an Input Data File from the west side of the Cascades (W), we preferred C (Oregon and Washington Coast Ranges) over A (southeast Alaska).

Keep in mind the purpose of the ESPs. For each record in the Input Data File, BIOPAK will consider equations for a given species and plant component. If there is an equation that matches the input record exactly (same species, lifeform, geographic area, seral stage, and plant size), the resultant ESP would be zero. Although the species and lifeform must match, there may be some geographic area and seral stage mismatches, or plant size extrapolations. BIOPAK will sum the ESPs for each potential equation and select an equation that will result in the lowest ESP value.

File

When an equation for a specific species and plant component is not present in the Equation Library, BIOPAK may perform a summation of lesser components. See *Appendix: Selecting Equations and Summations: BIOPAK Selects Summations* **for more details.**

These default summation trees, as shown in figures 2 to 4, are specified in a flat ASCII file called BIOSUMM. These summation trees may be modified, within strict guidelines; however, great care should be taken when doing this. It is easy to make mistakes that will be difficult to detect. Refer to *Appendix: Selecting Equations and Summation: BIOPAK Selects Summation* **for the roles of Equation Selection Penalty weights.**

Any line that begins with a dollar sign ($) or an ampersand-(&) is considered a comment, and may be placed anywhere in BIOSUMM. In this case, we used an ampersand to insert column headings and a dollar sign to insert column numbers. Any "+" sign in the first column indicates that an alternative summation is available; for example, for BAT, either BFT and BAE can be summed, or BCT and BST can be summed.

Here is an example of a BIOSUMM File:

```
& Tree-Shrub-Coppi Herb-Grass-Sedge Moss-Lichen-Bryo
&Co SummStruct1 ESP1 SummStruct2 ESP2 SummStruct3 ESP3

$23456789012345678901234567893012345678901234567890
AFN
AFO
AFT AFN+AFO          AFN+AFO          AFN+AFO
BAE BAP+BBD
BAP BBL+BST
BAT BFT+BAE          BFT+BST          BFT
+   BCT+BST
BBD             0.1
BBL             0.1
BCD
BCL
BCT BCL+BCD.
BFN
BFO
BFT BFN+BFO     0.1  BFN+BFO          BFN+BFO
BKC
BKL
BLL BLU+BLM          BLU+BLM
BLM
BLU
BRL BKC+BKL+BLL      BKL+BLL
BSB             0.1
BST BSB+BSW
BSW
BTT BAT+BUT          BAT+BUT          BAT+BUL
BUD
BUL  BRL+BUN         BRL+BUN
BUN             0.1
BUT BULtBUD          BULtBUD
PFN
PFO
PFT PFN+PFO          PFN+PFO          PFN+PFO
VSB             0.1
VST VSB+VSW
VSW
```

Modifyjng the Default Summation Trees--

The Component codes are in the first three columns of the BIOSUMM File, The Component codes from the BIOCODES File must be included in BIOSUMM if they are either:

1. A parent component of a summation (that is, it can be computed by summing two or more components), or
2. A subcomponent in a summation (that is, it is used in a summation to. compute another component).

All Plant Component codes in BIOSUMM must be in the BIOCODES file described under *BIOCODES* File. Component codes must be all capital letters. Parent' codes must be in alphabetical order.

There are separate summation tree structures for three groups of lifeforms, as can be seen in the preceding example of a BIOSUMM File. Subcomponents cannot be repeated within a given summation tree, except in the case of optional tree structures (see figures 2 through 4 for a graphical representation of the summation trees). For example, BST appears twice in the Default Summation Tree for tree, shrub, and coppice lifeforms--once as a subcomponent of BAP, and once as a subcomponent of BAT. This is acceptable because each usage of BST is part of separate BAT summation option. Because the optional summations are "either/or" situations, only one BAT summation is being considered at a time; therefore, only one BST is considered at one time.

The ESP value of a summation is represented by the highest ESP value of any of its subcomponents *(see Appendix: Equation Selection Penalties* **for more information on the calculation of summation ESPs). The ESP weights determine the importance of a given subcomponent to a summation. Without ESP weights, if a subcomponent were missing, the summation would not be executed. If a subcomponent were a significant contributor to the summation, then this would be acceptable (ESP weight = 1.0). If the contribution of the subcomponent to the summation were minor, however, then it should be given less weight (ESP weight < 1.0).**

Columns	Contents
l-3	Component code representing the sum (the parent code in the sum)
4	Blank
Summation for Tree, Shrub and Coppice lifeforms (optional):	
5-7	Code for first component to add
a	t sign
9-11	Code for second component to add
12	t sign (if have third component in summation)
13-15	Code for third component to add (optional)
16	
17-20	ESP weight for subcomponent in a summation, use decimal point, may be blank if = 1.0
21	Blank
Summation for Grass, Herb and Sedge lifeforms (optional):	
22-24	Code for first component to add
25	t sign
26-28	Code for second component to add
29	t sign (if have third component in summation)
30-32	Code for third component to add (optional)
33	Blank
34-37	ESP weight for subcomponent in a summation, use decimal point, may be blank if = 1.0
38	Blank
Summation for Bryophyte and Lichen lifeforms (optional):	
39-41	Code for first component to add
42	t sign
43-45	Code for second component to add
46	t sign (if have third component in summation)
47-49	Code for third component to add (optional)
50	Blank
51-54	ESP weight for subcomponent in a summation, use decimal point, may be blank if = 1.0

Occasionally you may want to specify more than one group of codes to use to calculate the value for a parent code; that is, there would be more than one potential summation for the given component. Each of these can be inserted on its own line directly following that parent code. Modify these lines by omitting the parent code and putting a "+" sign in column 1. The rest of the format is as given above. There may be at most two such additional summation lines for any parent code. The number of Plant Component codes in BIOCODES plus the number of additional summation lines in BIOSUMM must not exceed 80.

Equation Library

Section

The Library supplied with BIOPAK

The Equation Library supplied with BIOPAK was developed to meet the needs of our ecology research group in Corvallis. It includes most equations we could find from Oregon and Washington sites and has been supplemented to include many equations for species from the Sierra Nevada Mountains of California, northern Rocky Mountains, British Columbia, and southeast Alaska. The files BIOLIB.DBF and BIOLIB.FPT together make up this library and contain over 1,100 equations. The most up-to-date version of the library will be shipped with the BIOPAK software.

This library includes all the equations in Gholz and others (1979) except those with problems we could not resolve. We have corrected problems with published equations, following communication with the authors, as we encountered them. The Species codes used conform, in general, to those in Garrison and others (1976). Codes for bryophytes are comprised of the first two letters of the genus and first two letters of the species, in a manner similar to those in Garrison and others (1976), and numbers have been added when needed to distinguish them from other codes.

The equations can be edited, or new equations can be added, as described in *Reference: Library Editor.*

List of equations in BIOLIB in January 1994--

We have included a list of equations, as shown in the Eauation Summarv Window of the Library Editor *(see Reference: Library Editor).* **We periodically correct and add equations so the library shipped with BIOPAK may be different.**

The abbreviated column headings in this table, from left to right, are as follows. See the sections in parentheses for values of the codes or more information.

Eqn #	**Equation number** *(Reference: Library Editor: Requirements, possibilities and assumptions for BIOPAK equations)*
SPP	**Species** *(Appendix: Codes)*
LF	**Lifeform** *(Appendix: Codes)*
Plnt Comp	**Plant component** *(Appendix: Codes)*
GA	**Geographic area** *(Appendix: Codes)*
SS	**Seral stage** *(Appendix: Codes)*
LE #	**Local equation number** *(Reference: Library Editor: Equation keys)*
TL	**Taxonomic lifeform (Same codes as lifeform;** *see Appendix: Codes)*
Eq Tp	**Equation type** *(Reference: Library Editor,* **table 1)**
min, max	**Minimum and maximum of the parameter values used to build the equation**
	Sample size of the data set used to build the equation
R^2	**R-squared of the plant component prediction equation**

BIOPAK Edit Equation Library Browse Equations Rec:1/1145

Eqn #	Spp	L F	Plnt Comp	G A	S S	LE #	T L	Eq Tp	---Parameter--- Code	min	max	---Parameter--- Code	min	max	N	R^2
Sedges (C) and Grasses (G):																
1092	LUCA2	C	BAT	W	E	01	C	2	COV	0.2	1.5				5	0.981
833	LUZUL	C	BAT	E	Y	01	C	15	COV			HT			22	0.90
1056	AGROS	G	BAT	W	E	01	G	11	COV	0.3	20.0				14	0.886
834	CARU	G	BAT	E	Y	01	G	1	COV						34	0.70
961	FEAR	G	BAT	R	Y	01	G	2	DBA						138	0.87
962	FEAR	G	BAT	R	Y	02	G	2	DBA						138	0.87
963	FEAR	G	BAT	R	Y	03	G	2	DBA						138	0.87
964	FEAR	G	BAT	R	Y	04	G	2	DBA						138	0.87
965	FEAR	G	BAT	R	Y	05	G	2	DBA						138	0.87
966	FEAR	G	BAT	R	Y	06	G	2	DBA						138	0.87
1085	FESTU	G	BAT	W	E	01	G	1	COV	0.7	3.0				5	0.846
1086	FESTU	G	BAT	W	E	02	G	17	COV	0.7	3.0	LEN	10.0	20.0	5	0.987
810		G	BAT	W	G	01	G	1	COV	1	10				10	0.94
955	POFE	G	BAT	R	Y	01	G	2	DBA						173	0.81
956	POFE	G	BAT	R	Y	02	G	2	DBA						173	0.81
957	POFE	G	BAT	R	Y	03	G	2	DBA						173	0.81
958	POFE	G	BAT	R	Y	04	G	2	DBA						173	0.81
959	POFE	G	BAT	R	Y	05	G	2	DBA						173	0.81
960	POFE	G	BAT	R	Y	06	G	2	DBA						173	0.81
Herbs, Forbs (H):																
797	ADBI	H	BAT	W	G	01	H	1	COV	1	25.				10	0.94
134	ADPE	H	BFT	W	O	01	H	13	LEN	20.0	98.0				52	0.88
1057	ANMA	H	BAT	W	E	01	H	2	COV	0.4	7.0				15	0.87
197	ANMA	H	BAT	W	Y	01	H	1	LEN	7.	100.				17	0.87
198	ANMA	H	BAT	W	Y	02	H	1	COV	0.1	24.				144	0.80
135	ARCA3	H	BAT	W	O	01	H	13	DBA	1.2	3.9				22	0.94
169	ATFI	H	BAT	S	G	01	H	1	COV						8	
136	ATFI	H	BFT	W	G	01	H	15	LEN	45.0	160.0	NUM	2.	26.	21	0.80
207	ATFI	H	BFT	W	G	02	H	16	LEN	45.0	160.0	NUM	2.	26.	21	0.74
138	BLSP	H	BFT	W	O	01	H	15	LEN	35.0	100.0	NUM	2.	39.	28	0.92
208	BLSP	H	BFT	W	O	02	H	16	LEN	35.0	100.0	NUM	2.	39.	28	0.57
1065	CASC2	H	BAT	W	E	01	H	48	COV	0.1	3.5				12	0.97
1069	CIRSI	H	BAT	W	E	01	H	2	LEN	2.0	120.0				10	0.85
1070	CIRSI	H	BAT	W	E	02	H	2	COV	0.8	27.0				11	0.95
799	CIVU	H	BAT	W	G	01	H	1	COV	1.	8.				10	0.93
203	CIVU	H	BAT	W	Y	01	H	1	COV	1.2	17.				27	0.71
800	CLUN	H	BAT	W	G	01	H	1	COV	1.	20.				10	0.98
211	COAS	H	BAT	A	M	01	H	1	COV	2.	40.				19	0.87
224	COAS	H	BAT	A	M	02	H	2	COV	0.	10.				12	0.71
212	COCA	H	BAT	A	M	01	H	1	COV	3.	60.				22	0.90
225	COCA	H	BAT	A	M	02	H	1	COV	0.	10.				12	0.82
801	COCA	H	BAT	W	G	01	H	1	COV	1.	20.				10	0.96
1072	COCA2	H	BAT	W	E	01	H	2	COV	0.2	16.0				24	0.73
1071	COCA2	H	BAT	W	E	02	H	17	COV	0.2	12.0	LEN	39.0	165.0	22	0.92
1073	COCA2	H	BAT	W	E	03	H	2	LEN	35.0	165.0				27	0.63
1074	COCA2	H	BAT	W	E	04	H	42	COV	0.2	12.0	LEN	39.0	165.0	22	0.95
1075	COCA2	H	BAT	W	E	05	H	17	DBA	0.1	1.1	LEN	35.0	165.0	27	0.88
1076	COCA2	H	BAT	W	E	06	H	48	DBA	0.1	1.1				26	0.86
1077	COHE	H	BAT	W	E	01	H	48	COV	0.6	15.0				18	0.92
1117	COHE	H	BAT	W	E	02	H	1	COV	1.0	19.0				8	0.97
802	COLA	H	BAT	W	G	01	H	1	COV	1.	10.				9	0.99
1078	CRCA	H	BAT	W	E	01	H	2	COV	0.3	3.0				12	0.81
139	DRAU2	H	BFT	W	O	01	H	15	LEN	45.0	110.0	NUM	2.	10.	20	0.69
209	DRAU2	H	BFT	W	O	02	H	16	LEN	45.0	110.0	NUM	2.	10.	20	0.88
141	EPAN	H	AFT	W	E	01	H	2	LEN	52.0	155.0				13	0.92
143	EPAN	H	BAT	W	E	01	H	2	LEN	52.0	155.0				36	0.89
1079	EPAN	H	BAT	W	E	02	H	2	COV	0.1	72.0				32	0.94
1081	EPAN	H	BAT	W	E	03	H	50	COV	0.1	32.0	LEN	1.0	77.0	30	0.96
1118	EPAN	H	BAT	W	E	04	H	1	COV	3.0	30.0				11	0.96
1139	EPAN	H	BAT	W	E	05	H	2	LEN	1.0	77.0				26	0.94
140	EPAN	H	BFT	W	E	01	H	2	LEN	52.0	155.0				13	0.93
142	EPAN	H	BST	W	E	01	H	2	LEN	52.0	155.0				13	0.98
560	EPAN	H	PFT	W	E	01	H	2	LEN	52.0	155.0				13	0.92
144	EPPA	H	BAT	W	E	01	H	2	LEN	20.0	145.0				59	0.76

1080	EPPA	H	BAT	W	E	02	H	17	COV	0.2	22.0	DBA	0.1	1.0	25	0.929
1138	EPPA	H	BAT	W	E	03	H	17	LEN	15.0	95.0	DBA	0.1	1.0	23	0.899
1082	EPPA	H	BAT	W	E	04	H	2	COV	0.2	22.0				26	0.871
205	EPPA	H	BAT	W	Y	02	H	1	COV	0.1	24.				36	0.921
1083	EPWA	H	BAT	W	E	01	H	48	COV	0.1	8.5				11	0.886
145	EPWA	H	BAT	W	G	01	H	13	LEN	36.0	162.0				21	0.69
206	EPWA	H	BAT	W	Y	01	H	1	COV	0.1	4.				12	0.979
1084	EQUIS	H	BAT	W	E	01	H	11	COV	0.2	8.0				11	0.93;
1088	GATR	H	BAT	W	E	01	H	2	COV	0.1	4.5				24	0.911
242	GATR	H	BAT	W	Y	01	H	2	COV	1.0	20.0				9	0.85;
1089	GNMI	H	BAT	W	E	01	H	11	COV	0.1	8.0				18	0.93;
837	GOOB	H	BAT	E	Y	01	H	15	COV			HT			31	0.83
803	GOOB	H	BAT	W	G	01	H	1	COV	1.	10.				10	0.95
226	GYDR	H	BAT	A	O	01	H	2	COV	0.	100.				23	0.97
1090	HIAL	H	BAT	W	E	01	H	17	COV	0.4	7.0	LEN	2.0	110.0	21	0.901
243	HIAL	H	BFT	W	Y	01	H	1	COV	2.0	20.0				7	0.952
794	LAPO	H	BAT	W	G	01	H	1	COV	2.	20.				9	0.94
793	LIBO2	H	BAT	W	G	01	H	1	COV	1.	9.				10	0.87
244	LIBO2	H	BFT	W	Y	01	H	1	COV	1.5	80.0				6	0.995
1091	LOCR	H	BAT	W	E	01	H	2	COV	0.2	70.0				21	0.986
163	LOOB	H	BAT	S	G	01	H	1	COV						4	
170	LULA	H	BAT	S	G	01	H	1	COV						8	
1059	LULA	H	BAT	W	E	01	H	17	COV	0.1	32.0	LEN	3.0	55.0	18	0.97:
1134	LULA	H	BAT	W	E	02	H	2	COV	0.1	32.0				18	0.961
1140	LULA	H	BAT	W	E	03	H	2	LEN	3.0	55.0				16	0.881
213	MADI2	H	BAT	A	M	01	H	1	COV	1.	97.				15	0.93:
229	MADI2	H	BAT	A	M	02	H	1	COV	1.	15.				9	0.99
1135	MADIA	H	BAT	W	E	01	H	17	COV	0.6	10.0	LEN	34.0	80.0	15	0.821
172	MIGU	H	BAT	S	G	01	H	1	COV						8	
214	MOUN	H	BAT	A	M	01	H	1	COV	2.5	25.				8	0.89
230	MOUN	H	BAT	A	M	02	H	1	COV	0.0	2.5					
967	MUMO	H	BAT	R	Y	01	H	2	DBA						169	0.86
968	MUMO	H	BAT	R	Y	02	H	2	DBA						169	0.86
969	MUMO	H	BAT	R	Y	03	H	2	DBA						169	0.86
150	OXOR	H	BFT	W	O	01	H	1	COV	5.	100.				10	0.96
151	PEFR2	H	BAT	W	G	01	H	13	LEN	5.0	23.0				41	0.94
277	PEFR2	H	BAT	W	Y	01	H	2	COV	0.	100.				70	
792	PERA	H	BAT	W	G	01	H	1	COV	1.	20.				10	0.96
153	POMU	H	BFT	W	O	01	H	15	LEN	34.0	130.0	NUM	4.	70.	41	0.91
210	POMU	H	BFT	W	O	02	H	16	LEN	34.0	130.0	NUM	4.	70.	41	0.82
204	POMU	H	BFT	W	Y	01	H	1	COV	0.4	72.				66	0.78.
155	PTAQ	H	AFT	W	E	01	H	2	DBA	0.33	1.12				19	0.88
1099	PTAQ	H	BAT	W	E	01	H	2	COV	0.1	15.0				36	0.88
1141	PTAQ	H	BAT	W	E	02	H	2	LEN	5.0	65.0				58	0.86'
1122	PTAQ	H	BAT	W	E	03	H	1	COV	2.0	55.0				7	0.94,
154	PTAQ	H	BFT	W	E	01	H	2	DBA	0.33	1.12				19	0.90
156	PTAQ	H	BST	W	E	01	H	2	DBA	0.33	1.12				19	0.95
562	PTAQ	H	PFT	W	E	01	H	2	DBA	0.33	1.12				19	0.88
835	PYSE	H	BAT	E	Y	01	H	1	COV						31	0.86
235	RUPE	H	BAT	A	M	01	H	1	COV	1.	60.				10	0.72
215	RUPE	H	BFT	A	M	01	H	1	COV	1.	60.				13	0.79
1112	SEJA	H	BAT	W	E	01	H	48	COV	0.4	22.0				13	0.91
158	SESY	H	AFT	W	E	01	H	2	LEN	24.0	102.0				38	0.79
1113	SESY	H	BAT	W	E	01	H	2	COV	0.1	32.0				19	0.97
1142	SESY	H	BAT	W	E	02	H	2	DBA	0.2	1.0				17	0.56
1143	SESY	H	BAT	W	E	03	H	13	LEN	28.0	85.0				17	0.80
1144	SESY	H	BAT	W	E	04	H	17	LEN	28.0	85.0	DBA	0.2	1.0	17	0.96
157	SESY	H	BFT	W	E	01	H	2	LEN	24.0	102.0				38	0.79
160	SESY	H	BIT	W	E	01	H	2	LEN	24.0	102.0				30	0.85
161	SESY	H	BRL	W	E	01	H	2	LEN	24.0	102.0				37	0.69
159	SESY	H	BST	W	E	01	H	2	LEN	24.0	102.0				38	0.82
563	SESY	H	PFT	W	E	01	H	2	LEN	24.0	102.0				38	0.79
171	SETR	H	BAT	S	G	01	H	1	COV						a	
953	SILO2	H	BAT	R	Y	01	H	2	DBA						171	0.81
954	SILO2	H	BAT	R	Y	02	H	2	DBA						171	0.81
796	SMST	H	BAT	W	G	01	H	1	COV	1.	10.				10	0.96
162	STCO4	H	BAT	W	Y	01	H	2	LEN	40.0	140.0				37	0.79
836	THOC	H	BAT	E	Y	01	H	15	COV			HT			21	0.96
236	TITR	H	BAT	A	M	01	H	2	COV	0.	10.				11	0.83
216	TITR	H	BAT	A	M	02	H	1	COV	10.	75.				21	0.93

806	TITR	H	BAT	W	G	01	H	1	COV	2.	50.				10	0.94
1123	TRLA	H	BAT	W	E	04	H	1	COV	2.0	55.0				10	0.97
1114	TRLA2	H	BAT	W	E	01	H	11	COV	0.1	2.4				38	0.74
805	TRLA2	H	BAT	W	G	01	H	1	COV	1.	15.				10	0.97
1115	VISE	H	BAT	W	E	01	H	2	COV	0.1	5.5				12	0.97
808	VISE	H	BAT	W	G	01	H	1	COV	1.	9.				10	0.96
1116	WHMO	H	BAT	W	E	01	H	2	COV	0.2	12.0				12	0.95
1124	WHMO	H	BAT	W	E	02	H	1	COV	3.0	97.0				10	0.90
1125	WHMO	H	BAT	W	O	01	H	1	COV	2.0	25.0				10	0.85
809	XETE	H	BAT	W	G	01	H	1	COV	2.	70.				10	0.98
152	XETE	H	BFT	W	O	01	H	9	DBA	2.0	26.0	LEN	40.0	80.0	22	0.94
Coppice (K):																
80	ACCI	K	AFT	W	Y	01	S	2	DBA	0.9	3.8				19	0.91
82	ACCI	K	BBD	W	Y	01	S	2	DBA	0.9	3.8				a	0.33
81	ACCI	K	BBL	W	Y	01	S	2	DBA	0.9	3.8				6	0.97
a3	ACCI	K	BST	W	Y	01	S	2	DBA	0.9	3.8				20	0.94
547	ACCI	K	PFT	W	Y	01	S	2	DBA	0.9	3.8				19	0.91
85	ACMA	K	AFT	W	E	01	T	2	DBA	0.4	7.2				27	0.91
86	ACMA	K	BBL	W	E	01	T	2	DBA	0.7	7.2				22	0.67
84	ACMA	K	BFT	W	E	01	T	2	DBA	0.4	7.2				27	0.89
87	ACMA	K	BST	W	E	01	T	2	DBA	0.4	7.2				27	0.96
548	ACMA	K	PFT	W	E	01	T	2	DBA	0.4	7.2				27	0.91
815	ARME	K	AFT	C	Y	01	T	4	DBA	0.5	5.5				70	0.96
816	ARME	K	BAT	C	Y	01	T	4	DBA	0.5	5.5				70	0.97
814	ARME	K	PFT	C	Y	01	T	4	DBA	0.5	5.5				70	0.96
101	CONU	K	AFT	W	E	01	S	2	DBA	0.4	3.2				25	0.77
102	CONU	K	BBL	W	E	01	S	2	DBA	0.4	3.2				25	0.84
100	CONU	K	BFT	W	E	01	S	2	DBA	0.4	3.2				25	0.84
103	CONU	K	BST	W	E	01	S	2	DBA	0.4	3.2				25	0.78
552	CONU	K	PFT	W	E	01	S	2	DBA	0.4	3.2				25	0.77
812	LIDE	K	AFT	C	Y	01	T	4	DBA	0.3	4.5				78	0.94
813	LIDE	K	BAT	C	Y	01	T	4	DBA	0.3	4.5				52	0.98
811	LIDE	K	PFT	C	Y	01	T	4	DBA	0.3	4.5				78	0.94
1013	QUKE	K	BAT	S	O	01	T	2	DBA	0.1	1.7				50	0.72
1014	QUKE	K	BAT	S	O	02	T	17	DBA	0.1	1.7	HT	1.0	109.0	50	0.80
1015	QUKE	K	BAT	S	O	03	T	17	DBA	0.1	1.7	NUM	1.0	27.0	50	0.81
1016	QUKE	K	BAT	S	O	04	T	44	LEN	4.0	155.0	WI0	2.0	149.0	50	0.87
1017	QUKE	K	BAT	S	O	05	T	17	NUM	1.0	27.0	HT	1.0	109.0	50	0.87
1028	QUKE	K	BAT	S	O	06	T	44	LEN	4.0	155.0	WI0	2.0	149.0	50	0.87
1029	QUKE	K	BAT	S	O	07	T	17	LEN	4.0	155.0	WID	2.0	149.0	50	0.87
1004	QUKE	K	BAT	S	Y	01	T	2	DBA	0.075	0.55				49	0.69
1005	QUKE	K	BAT	S	Y	02	T	17	DBA	0.075	0.55	HT	3.00	47.0	49	0.82
1006	QUKE	K	BAT	S	Y	03	T	17	DBA	0.075	0.55	NUM	1.0	8.0	49	0.83
1007	QUKE	K	BAT	S	Y	04	T	17	NUM	1.0	8.0	HT	3.00	47.0	49	0.85
1008	QUKE	K	BAT	S	Y	05	T	44	LEN	5.0	57.0	WID	2.00	39.0	49	0.88
1024	QUKE	K	BAT	S	Y	06	T	44	LEN	5.0	57.0	WID	2.00	39.0	49	0.90
1025	QUKE	K	BAT	S	Y	07	T	17	LEN	5.0	57.0	WID	2.00	39.0	49	0.86
118	RHMA	K	AFN	W	E	01	S	2	DBA	0.4	1.6				20	0.63
117	RHMA	K	AFT	W	E	01	S	2	DBA	0.4	1.6				20	0.70
122	RHMA	K	AFT	W	E	02	S	2	DBA	1.6					54	0.74
119	RHMA	K	BBL	W	E	01	S	2	DBA	0.4	1.6				20	0.45
116	RHMA	K	BFN	W	E	01	S	2	DBA	0.4	1.6				20	0.72
115	RHMA	K	BFT	W	E	01	S	2	DBA	0.4	1.6				20	0.74
121	RHMA	K	BFT	W	E	02	S	2	DBA	1.6					113	0.76
120	RHMA	K	BST	W	E	01	S	2	DBA	0.4	1.6				20	0.78
557	RHMA	K	PFN	W	E	01	S	2	DBA	0.4	1.6				20	0.63
556	RHMA	K	PFT	W	E	01	S	2	DBA	0.4	1.6				20	0.70
558	RHMA	K	PFT	W	E	02	S	2	DBA	1.6					54	0.74
Bryophytes (M):																
1119	EUOR	M	BAT	W	O	01	M	1	COV	3.0	55.0				4	0.99
1121	HYCI	M	BAT	W	O	01	M	1	COV	5.0	60.0				4	0.99
218	HYSP	M	BAT	A	M	01	M	1	COV	9.	90.				30	
227	HYSP	M	BAT	A	M	02	M	1	COV	0.0	9.0					
1120	HYSP	M	BAT	W	O	01	M	1	COV	4.0	65.0				4	0.98
219	JULA	M	BAT	A	M	01	M	1	COV	30.	88.				11	0.91
228	JULA	M	BAT	A	M	02	M	1	COV	0.	30.					
220	PLUN	M	BAT	A	M	01	M	1	COV	1.	15.				17	0.81
231	PLUN	M	BAT	A	M	02	M	1	COV	0.	1.					
221	POMA	M	BAT	A	M	01	M	1	COV	3.	90.				12	0.94
232	POMA	M	BAT	A	M	02	M	1	COV	1.	3.					

217	PTCR	M	BAT	A	G	01	M	1	COV	2.	90.				8	0.86
222	RHGL	M	BAT	A	M	01	M	1	COV	1.	80.				13	0.81
233	RHGL	M	BAT	A	M	02	M	1	COV	0.	1.					
223	RHLO	M	BAT	A	M	01	M	1	COV	10.	90.				29	0.744
234	RHLO	M	BAT	A	M	02	M	4	COV	0.	10.				10	0.979
Shrubs (S):																
77	ACCI	S	AFT	W	M	01	S	2	DBA	3.8					19	0.94
78	ACCI	S	BBL	W	M	01	S	2	DBA	0.6	13.1				11	0.98
76	ACCI	S	BFT	W	M	01	S	2	DBA	0.6	13.1				31	0.97
79	ACCI	S	BST	W	M	01	S	2	DBA	0.6	13.1				11	0.99
546	ACCI	S	PFT	W	M	01	S	2	DBA	3.8					19	0.94
774	ACGL	S	BAT	R	G	01	S	2	DBA	0.4	3.7				32	0.98
981	ACGL	S	BFT	R	G	01	S	2	DBA	0.4	3.7				32	0.89
777	ALSI	S	BAT	R	G	02	S	2	DBA	0.7	6.3				30	0.95
178	ALSI	S	BFT	C	E	01	S	2	DBA	1.5	4.2				25	0.87
984	ALSI	S	BFT	R	G	02	S	2	DBA	0.7	6.3				30	0.82
1032	ALSI	S	BFT	R	G	03	S	32	BIO	15.6	1244.				30	0.805
260	ALSI	S	BRL	C	E	01	S	1	BIO						8	0.81
177	ALSI	S	BST	C	E	01	S	2	DBA	1.5	4.2				25	0.92
261	ALSI	S	BUN	C	E	01	S	1	BIO						8	0.81
773	AMAL	S	BAT	R	G	01	S	2	DBA	0.4	4.5				39	0.99
980	AMAL	S	BFT	R	G	01	S	2	DBA	0.4	4.5				39	0.83
1033	AMAL	S	BFT	R	G	02	S	2	BIO	2.64	904.9				37	0.885
1058	ARCO3	S	BAT	W	E	01	S	11	COV	0.2	1.8				13	0.956
1060	ARCO3	S	BAT	W	E	02	S	2	DBA	0.1	0.4				13	0.931
1061	ARCO3	S	BAT	W	E	03	S	17	DBA	0.1	0.4	LEN	5.0	19.0	13	0.963
294	ARPA	S	BAL	E	Y	01	S	17	DBA	0.4	11.5	LEN	7.0	298.0	150	0.96
735	ARPA	S	BAL	E	Y	02	S	2	DBA	0.4	11.5				150	0.95
620	ARPA	S	BAT	E	E	01	S	35	LEN			WID			10	0.997
630	ARPA	S	BAT	E	E	02	S	2	VOL	1.56	2104.				10	0.994
658	ARPA	S	BAT	E	Y	01	S	17	DBA	0.4	11.5	LEN	7.0	298.0	150	0.97
736	ARPA	S	BAT	E	Y	02	S	2	DBA	0.4	11.5				150	0.96
278	ARPA	S	BFT	E	Y	01	S	17	DBA	0.4	11.5	HT	20.0	230.0	150	0.79
737	ARPA	S	BFT	E	Y	02	S	2	DBA	0.4	11.5				150	0.79
279	ARPA	S	BST	E	Y	01	S	17	DBA	0.4	11.5	LEN	7.0	298.0	150	0.96
738	ARPA	S	BST	E	Y	02	S	2	DBA	0.4	11.5				150	0.95
89	ARTR	S	BAE	E	G	01	S	1	VOL	22.68	2732.				20	0.80
998	ARTR	S	BAE	E	G	02	S	3	WID	20.	119.				26	0.86
999	ARTR	S	BAE	E	G	03	S	23	LEN	20.	119.	WI0	19.	98.	26	0.87
1000	ARTR	S	BAE	E	G	04	S	44	LEN	20.	119.	WID	19.	98.	26	0.95
1001	ARTR	S	BAE	E	G	05	S	23	WID	20.	119.	HT	34.	117.	26	0.95
1002	ARTR	S	BAE	E	G	06	S	1	VOL						50	0.83
771	ARTR	S	BAT	R	G	02	S	2	DBA	0.8	6.9				22	0.92
88	ARTR	S	BFT	E	G	01	S	1	VOL	22.68	2732.				20	0.68
994	ARTR	S	BFT	E	G	02	S	3	WID	20.	119.				26	0.88
995	ARTR	S	BFT	E	G	03	S	23	LEN	20.	119.	WID	19.	98.	26	0.89
996	ARTR	S	BFT	E	G	04	S	44	LEN	20.	119.	WID	19.	98.	26	0.97
997	ARTR	S	BFT	E	G	05	S	23	WID	20.	119.	HT	34.	117.	26	0.96
978	ARTR	S	BFT	R	G	01	S	2	DBA	0.8	6.9				22	0.75
1034	ARTR	S	BFT	R	G	02	S	2	BIO	13.85	1532.				20	0.891
970	ARTR	S	PFT	E	G	01	S	1	SPA	0.2	5.5				20	0.95
971	ARTR	S	PFT	E	G	02	S	3	HT	24.	116.				20	0.64
972	ARTR	S	PFT	E	G	03	S	3	WID	16.	153.				20	0.87
973	ARTR	S	PFT	E	G	04	S	3	WID						20	0.88
744	ARUV	S	BAT	R	Y	01	S	32	COV						100	0.82
789	ARVI	S	BAT	G	G	01	S	2	DBA	0.2	14.0				60	0.98
785	ARVI	S	BFT	G	G	01	S	2	DBA	0.2	14.0				60	0.97
790	ARVI	S	BST	G	G	01	S	2	DBA	0.2	14.0				60	0.97
1062	BENE	S	BAT	W	E	01	S	11	COV	0.1	11.0				13	0.980
137	BENE	S	BFT	W	O	01	S	1	COV	5.	90.				32	0.80
621	BERE	S	BAT	E	E	01	S	35	LEN			WI0			10	0.922
631	BERE	S	BAT	E	E	02	S	2	VOL	1.152	362.5				10	0.969
993	BERE	S	BAT	R	G	01	S	2	DBA	0.3	0.9				36	0.70
726	BERE	S	BFT	R	G	01	S	2	DBA	0.3	0.9				36	0.48
1035	BERE	S	BFT	R	G	02	S	1	BIO	1.10	14.08				36	0.877
93	CACH	S	AFN	W	E	01	T	2	DBA	0.4	5.5				30	0.74
92	CACH	S	AFT	W	E	01	T	2	DBA	0.4	5.5				30	0.76
1063	CACH	S	BAT	W	E	01	S	2	DBA	0.2	0.6				23	0.845
1064	CACH	S	BAT	W	E	02	S	17	DBA	0.2	0.6	LEN	11.0	50.0	23	0.835
95	CACH	S	BBD	W	E	01	T	2	DBA	0.6	5.5				22	0.75

94	CACH	S	BBL	W	E	01	T	2	DBA	0.6	5.5				24	0.90
91	CACH	S	BFN	W	E	01	T	2	DBA	0.4	5.5				30	0.75
90	CACH	S	BFT	W	E	01	T	2	DBA	0.4	5.5				30	0.77
96	CACH	S	BST	W	E	01	T	2	DBA	0.4	5.5				30	0.96
550	CACH	S	PFN	W	E	01	T	2	DBA	0.4	5.5				30	0.74
549	CACH	S	PFT	W	E	01	T	2	DBA	0.4	5.5				30	0.76
267	CASE	S	BAP	S	G	01	S	1	COV						3	
164	CASE	S	BAT	S	G	01	S	1	COV						6	
237	CASE	S	BFT	S	G	01	S	1	COV						3	
268	CECO	S	BAP	S	G	01	S	1	COV						4	
165	CECO	S	BAT	S	G	01	S	1	COV						8	
238	CECO	S	BFT	S	G	01	S	1	COV						4	
183	CEIN	S	BAE	W	Y	01	S	2	DBA	1.03	4.79				15	0.91
784	CEIN	S	BAT	G	G	01	S	2	DBA	0.3	6.5				46	0.97
184	CEIN	S	BAT	W	Y	01	S	2	DBA	1.03	4.79				15	0.91
787	CEIN	S	BBD	G	G	01	S	32	DBA	0.3	6.5				46	0.71
788	CEIN	S	BFT	G	G	01	S	2	DBA	0.3	6.5				46	0.86
182	CEIN	S	BFT	W	Y	01	S	2	DBA	1.03	4.79				15	0.80
786	CEIN	S	BST	G	G	01	S	2	DBA	0.3	6.5				46	0.97
180	CESA	S	BAE	W	Y	01	S	2	DBA	0.46	5.7				12	0.99
1066	CESA	S	BAT	W	E	02	S	2	DBA	0.1	0.3				11	0.75
1067	CESA	S	BAT	W	E	03	S	2	LEN	2.0	17.0				10	0.94
181	CESA	S	BAT	W	Y	01	S	2	DBA	0.46	5.7				12	0.98
179	CESA	S	BFT	W	Y	01	S	2	DBA	0.46	5.7				12	0.92
928	CEVE	S	BAL	E	Y	01	S	42	DBA	0.3	11.7	HT	21.0	188.0	150	0.98
739	CEVE	S	BAL	E	Y	02	S	2	DBA	0.3	11.7				150	0.96
622	CEVE	S	BAT	E	E	01	S	35	LEN			WID			10	0.98
632	CEVE	S	BAT	E	E	02	S	2	VOL	21.92	3588.				10	0.98
296	CEVE	S	BAT	E	Y	01	S	42	DBA	0.3	11.7	HT	21.	188.	150	0.97
740	CEVE	S	BAT	E	Y	02	S	2	DBA	0.3	11.7				150	0.96
768	CEVE	S	BAT	R	G	01	S	2	DBA	0.6	2.5				30	0.92
1068	CEVE	S	BAT	W	E	01	S	1	COV	0.1	0.5				7	0.84
681	CEVE	S	BFT	E	Y	01	S	17	DBA	0.3	11.7	LEN	8.	266.	150	0.92
741	CEVE	S	BFT	E	Y	02	S	2	DBA	0.3	11.7				150	0.90
975	CEVE	S	BFT	R	G	01	S	2	DBA	0.6	2.5				30	0.67
1036	CEVE	S	BFT	R	G	02	S	45	BIO	8.04	565.0				30	0.85
694	CEVE	S	BST	E	Y	01	S	42	DBA	0.3	11.7	HT	21.	188.	150	0.97
742	CEVE	S	BST	E	Y	02	S	2	DBA	0.3	11.7				150	0.95
780	CEVEL	S	BAT	G	G	01	S	2	DBA	0.3	8.5				75	0.99
783	CEVEL	S	BBD	G	G	01	S	41	DBA	0.3	8.5				75	0.81
781	CEVEL	S	BFT	G	G	01	S	2	DBA	0.3	8.5				75	0.85
782	CEVEL	S	BST	G	G	01	S	2	DBA	0.3	8.5				75	0.99
98	CEVEV	S	AFN	W	M	01	S	11	DBA	1.0	7.0				43	0.85
97	CEVEV	S	BAT	W	M	01	S	10	LEN	100.	250.	DBA	1.0	7.0	43	0.96
99	CEVEV	S	BRL	W	M	01	S	1	BIO						24	0.84
551	CEVEV	S	PFN	W	Y	01	S	11	DBA		7.0				43	0.85
623	CHNA	S	BAT	E	E	01	S	35	LEN			WID			10	0.98
633	CHNA	S	BAT	E	E	02	S	2	VOL	1.17	1788.				10	0.99
798	CHUM	S	BAT	W	G	01	S	1	COV	3.	40.				10	0.98
1101	COCO2	S	BST	G	G	01	S	9	DBA	0.2		HT	30.48		117	
1100	COCO2	S	VST	G	G	01	S	9	DBA	0.2		HT	30.48		117	0.97
105	COCOC	S	AFT	W	M	01	S	2	DBA	0.7	2.9				20	0.81
106	COCOC	S	BAE	W	M	01	S	2	DBA	0.7	2.9				20	0.89
269	COCOC	S	BAP	S	G	01	S	1	COV						4	
166	cococ	S	BAT	S	G	01	S	1	COV						8	
239	cococ	S	BFT	S	G	01	S	1	COV						4	
104	cococ	S	BFT	W	M	01	S	2	DBA	0.7	2.9				20	0.82
553	COCOC	S	PFT	W	M	01	S	2	DBA	0.7	2.9				20	0.81
270	COST	S	BAP	S	G	01	S	1	COV						4	
778	COST	S	BAT	R	G	02	S	2	DBA	0.6	3.4				31	0.93
167	COST	S	BAT	S	G	01	S	1	COV						8	
985	COST	S	BFT	R	G	02	S	2	DBA	0.6	3.4				31	0.58
1037	COST	S	BFT	R	G	03	S	1	BIO	21.93	683.7				31	0.85
240	COST	S	BFT	S	G	01	S	1	COV						4	
148	GASH	S	AFT	W	E	01	S	1	COV	2.	60.				12	0.91
1087	GASH	S	BAT	W	E	01	S	2	COV	0.1	10.5				13	0.95
147	GASH	S	BFT	W	E	01	S	1	COV	2.	60.				12	0.97
146	GASH	S	BFT	W	O	01	S	2	COV	5.	85.				32	0.83
149	GASH	S	BST	W	E	01	S	1	COV	2.	60.				12	0.95
561	GASH	S	PFT	W	E	01	S	1	COV	2.	60.				12	0.91

624	HABL	S	BAT	E	E	01	S	35	LEN			WID			10	0.95
634	HABL	S	BAT	E	E	02	S	2	VOL	0.49	546.7				10	0.95
108	HODI	S	AFT	W	M	01	S	2	DBA	0.5	3.1				20	0.86
109	HODI	S	BAE	W	M	'01	S	2	DBA	0.5	3.1				20	0.98
767	HODI	S	BAT	R	G	01	S	2	DBA	0.7	2.2				31	0.93
974	HODI	S	BFT	R	G	01	S	2	DBA	0.7	2.2				31	0.86
1038	HODI	S	BFT	R	G	02	S	2	BIO	11.53	502.0				31	0.90
107	HODI	S	BFT	W	M	01	S	2	DBA	0.5	3.1				20	0.89
554	HODI	S	PFT	W	M	01	S	2	DBA	0.5	3.1				20	0.86
772	JUCO	S	BAT	R	G	01	S	2	DBA	0.8	2.9				23	0.92
979	JUCO	S	BFT	R	G	01	S	2	DBA	0.8	2.9				23	0.80
1039	JUCO	S	BFT	R	G	02	S	1	BIO	37.37	629.9				23	0.95
1003	LIDE	S	BAT	S	G	01	T	46	DBA			VOL			50	0.94
1145	LIDE	S	BFT	S	G	01	T	51	DBA			LEN			50	0.90
749	LOUT	S	BAT	R	G	01	S	2	DBA	0.3	1.7				32	0.96
731	LOUT	S	BFT	R	G	01	S	2	DBA	0.3	1.7				32	0.67
1040	LOUT	S	BFT	R	G	02	S	2	BIO	1.12	255.9				32	0.89
748	MEFE	S	BAT	R	G	01	S	2	DBA	0.4	2.1				37	0.98
730	MEFE	S	BFT	R	G	01	S	2	DBA	0.4	2.1				37	0.83
1041	MEFE	S	BFT	R	G	02	S	2	BIO	0.63	220.9				37	0.81
110	OPHO	S	BFT	R	M	01	S	2	DBA						38	0.82
111	OPHO	S	BST	R	M	01	S	2	DBA						38	0.94
832	PAMY	S	BAT	E	Y	01	S	15	COV			HT			77	0.95
769	PHLE2	S	BAT	R	G	01	S	2	DBA	0.5	2.9				28	0.90
976	PHLE2	S	BFT	R	G	01	S	2	DBA	0.5	2.9				28	0.71
1042	PHLE2	S	BFT	R	G	02	S	32	BIO	1.94	501.7				28	0.88
747	PHMA	S	BAT	R	G	01	S	2	DBA	0.4	3.8				38	0.94
729	PHMA	S	BFT	R	G	01	S	2	DBA	0.4	3.8				38	0.89
1043	PHMA	S	BFT	R	G	02	S	2	BIO	2.96	485.2				38	-0.93
776	PRVI	S	BAT	R	G	01	S	2	DBA	0.6	2.9				31	0.98
983	PRVI	S	BFT	R	G	01	S	2	DBA	0.6	2.9				31	0.74
1044	PRVI	S	BFT	R	G	02	S	32	BIO	4.67	549.4				31	0.90
295	PUTR	S	BAL	E	Y	01	S	2	DBA	0.3	6.9				150	0.95
626	PUTR	S	BAT	E	E	01	S	35	LEN			WID			10	0.98
636	PUTR	S	BAT	E	E	02	S	2	VOL	8.208	4349.				10	0.98
732	PUTR	S	BAT	E	Y	01	S	2	DBA	0.3	6.9				150	0.96
733	PUTR	S	BFT	E	Y	01	S	2	DBA	0.3	6.9				150	0.61
734	PUTR	S	BST	E	Y	01	S	2	DBA	0.3	6.9				150	0.94
1018	QUKE	S	BAT	S	O	01	T	2	DBA	0.1	6.35				50	0.81
1019	QUKE	S	BAT	S	O	02	T	17	DBA	0.1	6.35	HT	4.0	202.0	50	0.94
1020	QUKE	S	BAT	S	O	03	T	17	DBA	0.1	6.35	NUM	1.	9.	50	0.84
1021	QUKE	S	BAT	S	O	04	T	17	HT	4.0	202.0	NUM	1.	9.	50	0.92
1022	QUKE	S	BAT	S	O	05	T	44	HT	4.0	202.0	LEN	3.	198.	50	0.95
1030	QUKE	S	BAT	S	O	06	T	44	DBA	0.1	6.35	LEN	3.	198.	50	0.95
1031	QUKE	S	BAT	S	O	07	T	17	LEN	3.	198.	WID	3.	172.	50	0.94
1009	QUKE	S	BAT	S	Y	01	T	2	DBA	0.1	3.25				50	0.86
1010	QUKE	S	BAT	S	Y	02	T	17	DBA	0.1	3.25	HT	5.0	215.0	50	0.92
1011	QUKE	S	BAT	S	Y	03	T	17	DBA	0.1	3.25	NUM	1.0	5.0	50	0.86
1012	QUKE	S	BAT	S	Y	04	T	17	LEN	7.0	41.0	HT	5.0	215.0	50	0.91
1023	QUKE	S	BAT	S	Y	05	T	17	HT	5.0	215.0	NUM	1.0	5.0	50	0.79
1026	QUKE	S	BAT	S	Y	06	T	44	LEN	7.0	41.0	WID	4.0	104.0	50	0.95
1027	QUKE	S	BAT	S	Y	07	T	17	LEN	7.0	41.0	WID	4.0	104.0	50	0.89
113	RHMA	S	AFT	W	O	01	S	2	DBA	0.3	7.0				108	0.90
114	RHMA	S	BAE	W	O	01	S	2	DBA	0.5	4.4				12	0.99
1097	RHMA	S	BAT	W	E	01	S	2	LEN	3.0	35.0				38	0.94
1098	RHMA	S	BAT	W	E	02	S	11	DBA	0.2	0.8				38	0.69
112	RHMA	S	BFT	W	O	01	S	2	DBA	0.3	7.0				51	0.99
555	RHMA	S	PFT	W	O	01	S	2	DBA	0.3	7.0				108	0.90
627	RIBES	S	BAT	E	E	01	S	35	LEN			WID			10	0.96
637	RIBES	S	BAT	E	E	02	S	2	VOL	0.616	2308.				10	0.94
991	RIBES	S	BAT	R	G	01	S	2	DBA	0.4	1.4				37	0.90
1096	RIBES	S	BAT	W	E	01	S	2	COV	1.0	11 . .				17	0.90
1102	RIBES	S	BAT	W	E	02	S	2	DBA	0.1	0.9				16	0.87
1103	RIBES	S	BAT	W	E	03	S	2	LEN	4.0	45.0				17	0.83
1104	RIBES	S	BAT	W	E	04	S	17	DBA	0.1	0.9	LEN	4.0	45.0	16	0.98
724	RIBES	S	BFT	R	G	01	S	2	DBA	0.4	1.4				37	0.6[illegible]
1045	RIBES	S	BFT	R	G	02	S	2	BIO	2.60	165.3				37	0.90
123	RIBR	S	BFT	W	G	01	S	2	DBA	0.6	3.2				28	0.84
124	RIBR	S	BST	W	G	01	S	2	DBA	0.9	3.2				12	0.81
628	ROSA	S	BAT	E	E	01	S	35	LEN			WID			10	0.95

638	ROSA	S	BAT	E	E	02	S	2	VOL	1.001	136.5			10	0.98
990	ROSA	S	BAT	R	G	01	S	2	DBA	0.2	1.2			32	0.96
721	ROSA	S	BFT	R	G	01	S	2	DBA	0.2	1.2			32	0.88
1046	ROSA	S	BFT	R	G	02	S	2	BIO	0.32	55.54			32	0.92
746	RUID	S	BAT	R	G	01	S	2	DBA	0.3	0.9			26	0.89
728	RUID	S	BFT	R	G	01	S	2	DBA	0.3	0.9			26	0.85
1047	RUID	S	BFT	R	G	02	S	2	BIO	2.04	40.62			26	0.97
1105	RULE	S	BAT	W	E	01	S	2	COV	0.2	15.0			11	0.99
1106	RULE	S	BAT	W	E	02	S	2	LEN	5.0	85.0			12	0.91
1107	RULE	S	BAT	W	E	03	S	2	DBA	0.1	1.1			12	0.91
1108	RULE	S	BAT	W	E	04	S	17	DBA	0.1	1.1	LEN 5.0	85.0	12	0.95
745	RUPA	S	BAT	R	G	01	S	2	DBA	0.3	1.4			27	0.88
1109	RUPA	S	BAT	W	E	01	S	2	COV	0.1	21.0			29	0.93
791	RUPA	S	BAT	W	G	01	S	1	COV	5.	75.			10	0.92
201	RUPA	S	BAT	W	Y	01	S	13	COV	20.	100.			6	0.90
727	RUPA	S	BFT	R	G	01	S	2	DBA	0.3	1.4			27	0.72
1048	RUPA	S	BFT	R	G	02	S	2	BIO	1.31	59.68			27	0.87
199	RUPA	S	BFT	W	Y	01	S	13	COV	20.	100.			6	0.76
200	RUPA	S	BST	W	Y	01	S	13	COV	20.	100.			6	0.90
125	RUSP	S	BFT	W	G	01	S	2	DBA	0.5	2.5			21	0.76
126	RUSP	S	BST	W	G	01	S	2	DBA	0.5	2.5			13	0.89
1110	RUUR	S	BAT	W	E	01	S	48	COV	0.2	80.0			13	0.98
795	RUUR	S	BAT	W	G	01	S	1	COV	1.	15.			10	0.97
202	RUUR	S	BAT	W	Y	01	S	2	COV	8.	100.			16	0.84
1111	SACE	S	BAT	W	E	01	S	17	DBA	0.2	0.6	LEN 3.0	14.0	13	0.94
1136	SACE	S	BAT	W	E	02	S	17	COV	0.2	2.0	LEN 3.0	14.0	13	0.95
1137	SACE	S	BAT	W	E	03	S	11	COV	0.2	2.0			13	0.94
271	SAJE	S	BAP	S	G	01	S	1	COV					4	
168	SAJE	S	BAT	S	G	01	S	1	COV					8	
241	SAJE	S	BFT	S	G	01	S	1	COV					4	
779	SALIX	S	BAT	R	G	01	S	2	DBA	0.7	3.7			31	0.97
986	SALIX	S	BFT	R	G	01	S	2	DBA	0.7	3.7			31	0.68
1049	SALIX	S	BFT	R	G	02	S	2	BIO	6.48	525.3			31	0.74
245	SASC	S	BAT	W	Y	01	S	2	DBA	0.5	3.6			9	0.96
246	SASC	S	BFT	W	Y	01	S	2	DBA	0.5	3.6			9	0.92
127	SASI2	S	BFT	W	G	01	S	2	DBA	1.4	6.3			7	0.92
770	SHCA	S	BAT	R	G	01	S	2	DBA	0.7	2.9			30	0.89
977	SHCA	S	BFT	R	G	01	S	2	DBA	0.7	2.9			30	0.80
1050	SHCA	S	BFT	R	G	02	S	2	BIO	9.57	453.7			30	0.89
775	SOSC	S	BAT	R	G	01	S	2	DBA	1.0	4.2			29	0.95
982	SOSC	S	BFT	R	G	01	S	2	DBA	1.0	4.2			29	0.84
1051	SOSC	S	BFT	R	G	02	S	45	BIO	19.9	821.8			29	0.90
992	SPBE	S	BAT	R	G	01	S	2	DBA	0.2	0.8			31	0.84
725	SPBE	S	BFT	R	G	01	S	2	DBA	0.2	0.8			31	0.80
1052	SPBE	S	BFT	R	G	02	S	2	BIO	0.410	13.57			31	0.96
987	SYAL	S	BAT	R	G	01	S	2	DBA	0.2	1.2			31	0.88
804	SYAL	S	BAT	W	G	01	S	1	COV	1.	25.			10	0.66
720	SYAL	S	BFT	R	G	01	S	2	DBA	0.2	1.2			31	0.68
1053	SYAL	S	BFT	R	G	02	S	1	BIO	1.35	94.61			31	0.95
629	SYMPH	S	BAT	E	E	01	S	35	LEN			WID		12	0.97
639	SYMPH	S	BAT	E	E	02	S	2	VOL	4.485	590.4			12	0.97
132	VAAL	S	AFT	G	M	01	S	2	DBA	0.6	3.6			21	0.94
133	VAAL	S	BAE	G	M	01	S	2	DBA	0.6	3.6			26	0.94
131	VAAL	S	BFT	G	M	01	S	2	DBA	0.3	3.6			35	0.94
559	VAAL	S	PFT	G	M	01	S	2	DBA	0.6	3.6			21	0.94
807	VACCI	S	BAT	W	G	01	S	1	COV	1.	6.			10	0.95
988	VAGL	S	BAT	R	G	01	S	2	DBA	0.3	1.7			44	0.97
723	VAGL	S	BFT	R	G	01	S	2	DBA	0.3	1.7			44	0.84
1054	VAGL	S	BFT	R	G	02	S	1	BIO	0.53	139.9			44	0.95
186	VAPA	S	BAE	W	Y	01	S	2	DBA	0.4	3.3			7	0.97
187	VAPA	S	BAT	W	Y	01	S	2	DBA	0.4	3.3			7	0.97
185	VAPA	S	BFT	W	Y	01	S	2	DBA	0.4	3.3			7	0.96
831	VASC	S	BAT	E	Y	01	S	15	COV			HT		26	0.82
989	VASC	S	BAT	R	G	01	S	2	DBA	0.3	0.7			31	0.62
743	VASC	S	BAT	R	Y	01	S	15	COV			HT		50	0.61
722	VASC	S	BFT	R	G	01	S	2	DBA	0.3	0.7			31	0.26
1055	VASC	S	BFT	R	G	02	S	2	BIO	0.92	16.14			31	0.55
Trees (T):															
885	ABAM		BAT	G	G	01	T	9							
883	ABAM		BBL	G	G	01	T	9	DBH	4.5	30.4	HT 310.	2580.	45	0.53

24	ABAM	T	BBL	W	O	01	T	2	DBH	11.7	90.4				9	0.96
882	ABAM	T	BBS	G	G	01	T	9	DBH	4.5	30.4	HT	310.	2580.	45	0.53
884	ABAM	T	BFT	G	G	01	T	9	DBH	4.5	30.4	HT	310.	2580.	45	0.54
23	ABAM	T	BFT	W	O	01	T	2	DBH	11.7	90.4				9	0.97
881	ABAM	T	BSB	G	G	01	T	9	DBH	4.5	30.4	HT	310.	2580.	45	0.94
248	ABAM	T	BSB	W	M	01	T	2	DBH	8.1	109.3				143	0.85
361	ABAM	T	BSB	W	M	02	T	2	DBH	13.3	80.0				68	0.91
26	ABAM	T	BSB	W	O	01	T	2	DBH	11.7	90.4				14	0.99
319	ABAM	T	BSB	W	O	02	T	2	DBH	8.1	109.3				75	0.83
250	ABAM	T	BST	W	M	01	T	2	DBH	8.1	109.3				143	0.94
362	ABAM	T	BST	W	M	02	T	2	DBH	13.3	80.0				68	0.97
320	ABAM	T	BST	W	O	01	T	2	DBH	8.1	109.3				75	0.93
880	ABAM	T	BSW	G	G	01	T	9	DBH	4.5	30.4	HT	310.	2580.	45	0.96
249	ABAM	T	BSW	W	M	01	T	2	DBH	8.1	109.3				143	0.94
360	ABAM	T	BSW	W	M	02	T	2	DBH	13.3	80.0				68	0.97
25	ABAM	T	BSW	W	O	01	T	2	DBH	11.7	90.4				14	0.99
318	ABAM	T	BSW	W	O	02	T	2	DBH	8.1	109.3				75	0.93
379	ABCO	T	BSB	S	O	01	T	2	DBH	14.4	158.4				56	0.94
380	ABCO	T	BST	S	O	01	T	2	DBH	14.4	158.4				56	0.97
378	ABCO	T	BSW	S	O	01	T	2	DBH	14.4	158.4				56	0.97
708	ABCO	T	VSW	C	M	01	T	37	DBH	17.78	63.5	HT			378	0.96
890	ABGR	T	BAT	G	G	01	T	9	DBH	4.6	43.9	HT	340.	3480.	40	0.96
889	ABGR	T	BBL	G	G	01	T	9	DBH	4.6	43.9	HT	340.	3480.	40	0.45
888	ABGR	T	BBS	G	G	01	T	9	DBH	4.6	43.9	HT	340.	3480.	40	0.45
523	ABGR	T	BCD	R	G	01	T	24	DBH	2.54	50.8	HT			22	0.93
524	ABGR	T	BCD	R	G	02	T	2	DBH	2.54	45.72				22	0.93
525	ABGR	T	BCD	R	G	03	T	1	BIO							
589	ABGR	T	BCD	R	M	01	T	2	DBH	2.54	30.48				15	0.83
502	ABGR	T	BCL	R	G	01	T	2	DBH	2.54	101.6				35	0.95
577	ABGR	T	BCL	R	M	01	T	4	HT	112.8	289.6				9	0.85
588	ABGR	T	BCL	R	M	02	T	2	DBH	2.54	30.48				15	0.92
570	ABGR	T	BCL	R	Y	01	T	1	HT	94.5	426.7				12	0.79
590	ABGR	T	BCT	R	M	01	T	2	DBH	2.54	30.48				15	0.94
891	ABGR	T	BFT	G	G	01	T	9	DBH	4.6	43.9	HT	340.	3480.	40	0.46
887	ABGR	T	BSB	G	G	01	T	9	DBH	4.6	43.9	HT	340.	3480.	40	0.79
613	ABGR	T	BST	R	M	01	T	9	DBH	0.	10.16	HT			8	0.97
614	ABGR	T	BST	R	M	02	T	4	DBH	0.	10.16				8	0.87
600	ABGR	T	BST	R	Y	01	T	34	DBH	0.	10.16				12	0.99
886	ABGR	T	BSW	G	G	01	T	9	DBH	4.6	43.9	HT	340.	3480.	40	0.95
709	ABGR	T	VSW	R	M	01	T	37	DBH	17.78	58.42	HT			50	0.97
20	ABIES	T	BBL	G	M	01	T	2	DBH	8.7	111.0				26	0.95
19	ABIES	T	BFT	G	M	01	T	2	DBH	8.7	111.0				25	0.94
22	ABIES	T	BSB	G	M	01	T	2	DBH	8.7	111.0				20	0.98
21	ABIES	T	BSW	G	M	01	T	2	DBH	8.7	111.0				20	0.97
921	ABLA2	T	BAT	G	G	01	T	9	DBH	3.5	44.4	HT	220.	2790.	89	0.95
919	ABLA2	T	BBL	G	G	01	T	9	DBH	3.5	44.4	HT	220.	2790.	89	0.78
918	ABLA2	T	BBS	G	G	01	T	9	DBH	3.5	44.4	HT	220.	2790.	89	0.47
527	ABLA2	T	BCD	R	G	01	T	25	DBH	2.54	33.02	HT			16	0.93
528	ABLA2	T	BCD	R	G	02	T	2	DBH	2.54	33.02				16	0.91
529	ABLA2	T	BCD	R	G	03	T	1	BIO							
505	ABLA2	T	BCL	R	G	01	T	9	DBH	2.54	33.02	CR			16	0.95
506	ABLA2	T	BCL	R	G	02	T	4	DBH	2.54	33.02				16	0.84
568	ABLA2	T	BCL	R	Y	01	T	2	HT	76.2	301.8				13	0.90
920	ABLA2	T	BFT	G	G	01	T	9	DBH	3.5	44.4	HT	220	2790.	89	0.56
917	ABLA2	T	BSB	G	G	01	T	9	DBH	3.5	44.4	HT	220	2790.	89	0.94
409	ABLA2	T	BSB	R	O	01	T	2	DBH	15.7	46.9				11	0.64
322	ABLA2	T	BSB	W	O	01	T	2	DBH	15.6	68.7				17	0.96
397	ABLA2	T	BSB	W	O	02	T	2	DBH	15.6	68.7				21	0.88
605	ABLA2	T	BST	R	M	01	T	26	DBH	0.	10.16	HT			12	0.99
606	ABLA2	T	BST	R	M	02	T	28	DBH	0.	10.16				12	0.99
410	ABLA2	T	BST	R	O	01	T	2	DBH	15.7	46.9				11	0.98
323	ABLA2	T	BST	W	O	01	T	2	DBH	15.6	68.7				17	0.98
398	ABLA2	T	BST	W	O	02	T	2	DBH	15.6	68.7				21	0.97
910	ABLA2	T	BSW	G	G	01	T	9	DBH	3.5	44.4	HT	220.	2790.	89	0.99
408	ABLA2	T	BSW	R	O	01	T	2	DBH	15.7	46.9				11	0.95
321	ABLA2	T	BSW	W	O	01	T	2	DBH	15.6	68.7				17	0.98
396	ABLA2	T	BSW	W	O	02	T	2	DBH	15.6	68.7				21	0.97
382	ABMA	T	BSB	S	O	01	T	2	DBH	18.8	143.2				31	0.95
383	ABMA	T	BST	S	O	01	T	2	DBH	18.8	143.2				31	0.98
381	ABMA	T	BSW	S	O	01	T	2	DBH	18.8	143.2				31	0.98

707	ABMAS	T	VSW	C	M	01	T	37	DBH	17.78	63.5	HT			65	0.961
28	ABPR	T	BBL	W	M	01	T	2	DBH	18.8	111.0				6	0.94
27	ABPR	T	BFT	W	M	01	T	2	DBH	18.8	111.0				6	0.99
30	ABPR	T	BSB	W	M	01	T	2	DBH	18.8	111.0				6	0.99
251	ABPR	T	BSB	W	M	02	T	2	DBH	15.9	235.5				310	0.922
253	ABPR	T	BST	W	M	01	T	2	DBH	15.9	235.5				310	0.984
29	ABPR	T	BSW	W	M	01	T	2	DBH	18.8	111.0				6	0.99
252	ABPR	T	BSW	W	M	02	T	2	DBH	15.9	235.5				310	0.984
428	ACMA	T	BBD	W	G	01	T	2	DBH	5.1	45.7				16	0.78
33	ACMA	T	BBD	W	O	01	T	2	DBH	7.6	35.3				18	0.15
32	ACMA	T	BBL	W	O	01	T	2	DBH	7.6	35.3				18	0.88
427	ACMA	T	BCL	W	G	01	T	2	DBH	5.1	45.7				16	0.93
31	ACMA	T	BFT	W	O	01	T	2	DBH	7.6	35.3				18	0.87
35	ACMA	T	BSB	W	O	01	T	2	DBH	7.6	35.3				18	0.98
34	ACMA	T	BSW	W	O	01	T	2	DBH	7.6	35.3				18	0.99
654	ACMA	T	VAE	C	G	01	T	17	DBH	10.	90.	HT	90.	270.	61	0.944
655	ACMA	T	VSW	C	G	01	T	17	DBH	10.	90.	HT	90.	270.	61	0.924
429	ACMA	T	VSW	W	G	01	T	2	DBH	5.1	45.7				16	0.97
564	ALRU	T	AFT	C	Y	01	T	2	DBH	1.7	13.2				18	0.91
565	ALRU	T	AFT	C	Y	02	T	2	DBA	2.5	16.0				18	0.96
37	ALRU	T	BAE	C	Y	01	T	8	DBH			HT			119	0.98
653	ALRU	T	BAE	C	Y	02	T	32	HT							0.975
288	ALRU	T	BAT	C	Y	01	T	2	DBH	1.7	13.2				18	0.95
292	ALRU	T	BAT	C	Y	02	T	2	DBA	2.5	16.0				18	0.98
940	ALRU	T	BAT	G	Y	01	T	9	DBH	5.8	33.3	HT	610.	2380.	41	0.99
422	ALRU	T	BBD	W	G	01	T	2	DBH	2.54	63.5				53	0.63
273	ALRU	T	BBD	W	M	01	T	2	DBH	9.1	39.6				10	0.72
265	ALRU	T	BBL	C	M	01	T	2	DBH	6.0	20.0				12	0.91
284	ALRU	T	BBL	C	Y	01	T	2	DBH	1.7	13.2				18	0.91
285	ALRU	T	BBL	C	Y	02	T	2	DBA	2.5	16.0				18	0.96
938	ALRU	T	BBL	G	Y	01	T	9	DBH	5.8	33.3	HT	610.	2380.	41	0.35
274	ALRU	T	BBL	W	M	01	T	2	DBH	9.1	39.6				10	0.92
937	ALRU	T	BBS	G	Y	01	T	9	DBH	5.8	33.3	HT	610.	2380.	41	0.35
421	ALRU	T	BCL	W	G	01	T	2	DBH	2.54	63.5				53	0.94
652	ALRU	T	BCT	C	Y	01	T	8	DBH			HT			91	0.746
264	ALRU	T	BFT	C	M	01	T	2	DBH	6.0	20.0				10	0.85
39	ALRU	T	BFT	C	Y	01	T	9	DBH	4.83	17.53	HT	564.	1326.	66	0.64
280	ALRU	T	BFT	C	Y	02	T	2	DBH	1.7	13.2				18	0.93
281	ALRU	T	BFT	C	Y	03	T	2	DBA	2.5	16.0				18	0.97
939	ALRU	T	BFT	G	Y	01	T	9	DBH	5.8	33.3	HT	610.	2380.	41	0.02
272	ALRU	T	BFT	W	M	01	T	2	DBH	9.1	39.6				10	0.96
38	ALRU	T	BRL	C	Y	01	T	8	DBH			HT			28	
936	ALRU	T	BSB	G	Y	01	T	9	DBH	5.8	33.3	HT	610.	2380.	41	0.98
275	ALRU	T	BSB	W	M	01	T	2	DBH	9.1	39.6				10	0.985
266	ALRU	T	BST	C	M	01	T	2	DBH	6.0	20.0				12	0.98
36	ALRU	T	BST	C	Y	01	T	8	DBH			HT			91	0.99
287	ALRU	T	BST	C	Y	02	T	2	DBH	1.7	13.2				18	0.96
291	ALRU	T	BST	C	Y	03	T	2	DBA	2.5	16.0				18	0.98
935	ALRU	T	BSW	G	Y	01	T	9	DBH	5.8	33.3	HT	610.	2380.	41	1.00
276	ALRU	T	BSW	W	M	01	T	2	DBH	9.1	39.6				10	0.985
289	ALRU	T	HST	C	Y	01	T	2	DBH	1.7	13.2				18	0.84
293	ALRU	T	HST	C	Y	02	T	2	DBA	2.5	16.0				18	0.83
282	ALRU	T	PFT	C	Y	01	T	2	DBH	1.7	13.2				18	0.91
283	ALRU	T	PFT	C	Y	02	T	2	DBA	2.5	16.0				18	0.96
286	ALRU	T	VST	C	Y	01	T	2	DBH	1.7	13.2				18	0.96
290	ALRU	T	VST	C	Y	02	T	2	DBA	2.5	16.0				18	0.98
423	ALRU	T	VSW	W	G	01	T	2	DBH	2.54	63.5				53	0.98
262	ALSI	T	BFT	C	M	01	S	2	DBH	2.0	7.0				14	0.88
263	ALSI	T	BST	C	M	01	S	2	DBH	2.0	7.0				14	0.97
431	ARME	T	BBD	W	G	01	T	2	DBH	2.54	63.5				31	0.88
430	ARME	T	BCL	W	G	01	T	2	DBH	2.54	63.5				31	0.89
673	ARME	T	VAE	C	G	01	T	17	DBH	10.	70.	HT	60	300.	60	0.967
674	ARME	T	VSW	C	G	01	T	17	DBH	10.	70.	HT	60	300.	58	0.959
432	ARME	T	VSW	W	G	01	T	2	DBH	2.54	63.5				31	0.97
952	BEPA	T	BAT	G	G	01	T	9	DBH	4.5	30.6	HT	530.	2270.	40	0.96
950	BEPA	T	BBL	G	G	01	T	9	DBH	4.5	30.6	HT	530.	2270.	40	0.65
949	BEPA	T	BBS	G	G	01	T	9	DBH	4.5	30.6	HT	530.	2270.	40	0.65
951	BEPA	T	BFT	G	G	01	T	9	DBH	4.5	30.6	HT	530.	2270.	40	0.61
948	BEPA	T	BSB	G	G	01	T	9	DBH	4.5	30.6	HT	530.	2270.	40	0.93
947	BEPA	T	BSW	G	G	01	T	9	DBH	4.5	30.6	HT	530.	2270.	40	0.97

425	CACH	T	BBD	W	G	01	T	2	DBH	2.54	61.				30	0.88
42	CACH	T	BBD	W	O	01	T	2	DBH	5.8	36.0				19	0.81
41	CACH	T	BBL	W	O	01	T	2	DBH	5.8	36.0				19	0.89
424	CACH	T	BCL	W	G	01	T	2	DBH	2.54	61.				30	0.94
45	CACH	T	BFN	W	O	01	T	2	DBH	5.8	36.0				19	0.56
40	CACH	T	BFT	W	O	01	T	2	DBH	5.8	36.0				19	0.81
44	CACH	T	BSB	W	O	01	T	2	DBH	5.8	36.0				19	0.97
43	CACH	T	BSW	W	O	01	T	2	DBH	5.8	36.0				19	0.98
663	CACH	T	VAE	C	G	01	T	17	DBH	10.	80.	HT	60.	300.	60	0.96
664	CACH	T	VSW	C	G	01	T	17	DBH	10.	80.	HT	60.	300.	60	0.95
426	CACH	T	VSW	W	G	01	T	2	DBH	2.54	61.				30	0.99
385	CADE	T	BSB	S	O	01	T	2	DBH	25.0	143.9				25	0.94
386	CADE	T	BST	S	O	01	T	2	DBH	25.0	143.9				25	0.97
384	CADE	T	BSW	S	O	01	T	2	DBH	25.0	143.9				25	0.96
47	CEDAR	T	BBL	W	G	01	T	2	DBH	15.5	60.2				6	0.94
46	CEDAR	T	BFT	C	O	01	T	2	DBH	15.5	60.2				6	0.91
49	CEDAR	T	BSB	W	G	01	T	2	DBH	15.5	60.2				6	0.95
48	CEDAR	T	BSW	W	G	01	T	2	DBH	15.5	60.2				6	0.96
927	CHNO	T	BAT	G	G	01	T	9	DBH	8.2	42.4	HT	520.	3020.	41	0.99
925	CHNO	T	BBL	G	G	01	T	9	DBH	8.2	42.4	HT	520.	3020.	41	0.63
924	CHNO	T	BBS	G	G	01	T	9	DBH	8.2	42.4	HT	520.	3020.	41	0.50
926	CHNO	T	BFT	G	G	01	T	9	DBH	8.2	42.4	HT	520.	3020.	41	0.59
923	CHNO	T	BSB	G	G	01	T	9	DBH	8.2	42.4	HT	520.	3020.	41	0.91
325	CHNO	T	BSB	W	O	01	T	2	DBH	18.9	109.1				26	0.83
326	CHNO	T	BST	W	O	01	T	2	DBH	18.9	109.1				26	0.96
929	CHNO	T	BSW	G	G	01	T	9	DBH	8.2	42.4	HT	520.	3020.	41	0.91
324	CHNO	T	BSW	W	O	01	T	2	DBH	18.9	109.1				26	0.96
55	JUOC	T	AFT	E	G	01	T	2	CIR	14.5	273.0				10	0.99
52	JUOC	T	BBD	E	G	01	T	2	CIR	14.5	273.0				10	0.91
51	JUOC	T	BBL	E	G	01	T	2	CIR	14.5	273.0				10	0.99
50	JUOC	T	BFT	E	G	01	T	2	CIR	14.5	273.0				10	0.99
54	JUOC	T	BSB	E	G	01	T	2	CIR	14.5	273.0				10	0.99
53	JUOC	T	BSW	E	G	01	T	2	CIR	14.5	273.0				10	0.99
711	JUOC	T	VAE	R	G	01	T	38	DBA	10.16	127.0	HT	182.9	1524.	137	0.76
712	JUOC	T	VAE	R	G	02	T	38	DBA	10.16	101.6	HT	182.9	1067.	45	0.76
57	JUOC	T	VSB	E	G	01	T	2	CIR	14.5	273.0				10	0.98
56	JUOC	T	VSW	E	G	01	T	2	CIR	14.5	273.0				10	0.99
713	JUOC	T	VSW	E	G	02	T	39	DBH	12.7	77.22	HT	609.6	1829.	73	
710	JUSC	T	VAE	R	G	01	T	38	DBA	10.16	88.9	HT	121.9	914.4	197	0.70
897	LAOC	T	BAT	G	G	01	T	9	DBH	3.1	57.5	HT	290.	3850.	41	0.88
895	LAOC	T	BBL	G	G	01	T	9	DBH	3.1	57.5	HT	290.	3850.	41	0.14
894	LAOC	T	BBS	G	G	01	T	9	DBH	3.1	57.5	HT	290.	3850.	41	0.18
503	LAOC	T	BCL	R	G	01	T	2	DBH	2.54	88.9				45	0.96
576	LAOC	T	BCL	R	Y	01	T	32	HT	85.3	548.6				12	0.80
896	LAOC	T	BFT	G	G	01	T	9	DBH	3.1	57.5	HT	290.	3850.	41	0.19
893	LAOC	T	BSB	G	G	01	T	9	DBH	3.1	57.5	HT	290.	3850.	41	0.97
603	LAOC	T	BST	R	Y	01	T	9	DBH	0.	10.16	HT			12	0.99
604	LAOC	T	BST	R	Y	02	T	28	DBH	0.	10.16				12	0.99
892	LAOC	T	BSW	G	G	01	T	9	DBH	3.1	57.5	HT	290.	3850.	41	0.91
488	LAOC	T	VQW	R	M	01	T	21	DBH	7.62	45.72	HT	609.6	3353.	238	
489	LAOC	T	VQW	R	M	02	T	21	DBH	10.16	53.34	HT	914.4	3353.	220	
490	LAOC	T	VQW	R	M	03	T	21	DBH	12.7	53.34	HT	1219.	3353.	196	
491	LAOC	T	VQW	R	M	04	T	21	DBH	15.24	53.34	HT	1219.	3353.	168	
492	LAOC	T	VQW	R	M	05	T	21	DBH	17.78	53.34	HT	1524.	3353.	149	
493	LAOC	T	VQW	R	M	06	T	21	DBH	20.32	53.34	HT	1829.	3353.	133	
494	LAOC	T	VQW	R	M	07	T	21	DBH	22.86	53.34	HT	1829.	3353.	115	
441	LAOC	T	VSB	R	M	01	T	23	DBH	5.08	53.34	HT	609.6	3353.	259	
440	LAOC	T	VSW	R	M	01	T	22	DBH	5.08	53.34	HT	609.6	3353.	259	
434	LIDE	T	BBD	W	G	01	T	2	DBH	2.54	66.0				31	0.71
433	LIDE	T	BCL	W	G	01	T	2	DBH	2.54	66.0				31	0.94
677	LIDE	T	VAE	C	G	01	T	17	DBH	10.	100.	HT	60.	330.	60	0.9;
678	LIDE	T	VSW	C	G	01	T	17	DBH	10.	100.	HT	60.	330.	59	0.96
435	LIDE	T	VSW	W	G	01	T	2	DBH	2.54	.66.0				31	0.98
616	PIAB	T	BAT	R	Y	01	T	2	HT	0.	457.2				42	0.90
533	PIAL	T	BCD	R	G	01	T	9	DBH	2.54	27.94	LEN			13	0.86
534	PIAL	T	BCD	R	G	02	T	9	DBH	2.54	27.94	HT			13	0.85
535	PIAL	T	BCD	R	G	03	T	4	DBH	2.54	27.94				13	0.82
512	PIAL	T	BCL	R	G	01	T	24	DBH	2.54	20.32	CR			10	0.99
513	PIAL	T	BCL	R	G	02	T	4	DBH	2.54	20.32				10	0.91
574	PIAL	T	BCL	R	Y	01	T	4	HT	76.2	304.8				10	0.9:

607	PIAL	T	BST	R	M	01	T	9	DBH	0.	10.16	HT			8	0.95
608	PIAL	T	BST	R	M	02	T	4	DBH	0.	10.16				8	0.91
697	PICO	T	AFT	R	M	01	T	1	SPA						80	0.929
698	PICO	T	AFT	R	M	02	T	1	SPA						80	0.775
699	PICO	T	AFT	R	M	03	T	1	SPA						80	0.953
700	PICO	T	AFT	R	M	04	T	1	SPA						80	0.633
642	PICO	T	BAT	E	E	01	T	2	DBA	1.4	7.9				15	0.992
650	PICO	T	BAT	E	E	02	T	2	HT	38.	347.				15	0.977
646	PICO	T	BAT	E	E	03	T	36	DBA	1.4	7.9	HT	38.	347.	15	0.990
909	PICO	T	BAT	G	G	01	T	9	DBH	3.3	48.9	HT	230.	3960.	98	0.93
907	PICO	T	BBL	G	G	01	T	9	DBH	3.3	48.9	HT	230.	3960.	98	0.42
685	PICO	T	BBL	R	M	01	T	4	DBH	0.	10.				80	0.829
684	PICO	T	BBL	R	M	02	T	4	DBH	10.	60.				80	0.873
64	PICO	T	BBL	R	M	03	T	2	DBH	2.5	28.7				19	0.89
906	PICO	T	BBS	G	G	01	T	9	DBH	3.3	48.9	HT	230.	3960.	98	0.35
530	PICO	T	BCD	R	G	01	T	30	DBH	2.54	25.4	BIO				
531	PICO	T	BCD	R	G	02	T	1	BIO							
507	PICO	T	BCL	R	G	01	T	24	DBH	2.54	40.64	CR			45	0.88
508	PICO	T	BCL	R	G	02	T	2	DBH	2.54	40.64				45	0.88
573	PICO	T	BCL	R	Y	01	T	4	HT	48.8	399.3				12	0.96
908	PICO	T	BFT	G	G	01	T	9	DBH	3.3	48.9	HT	230.	3960.	98	0.24
63	PICO	T	BFT	R	M	01	T	2	DBH	2.5	28.7				19	0.84
686	PICO	T	BFT	R	M	02	T	4	DBH	20.	60.				80	0.906
687	PICO	T	BFT	R	M	03	T	4	DBH	10.	30.				80	0.828
688	PICO	T	BFT	R	M	04	T	4	DBH	10.	30.				80	0.841
689	PICO	T	BFT	R	M	05	T	4	DBH	0.	30.				80	0.839
690	PICO	T	BFT	R	M	06	T	1	SPA						80	0.929
691	PICO	T	BFT	R	M	07	T	1	SPA						80	0.775
692	PICO	T	BFT	R	M	08	T	1	SPA						80	0.953
693	PICO	T	BFT	R	M	09	T	1	SPA						80	0.633
695	PICO	T	BKL	R	M	01	T	4	DBH	10.	60.				70	0.813
696	PICO	T	BKL	R	M	02	T	4	DBH	0.	10.				70	0.913
904	PICO	T	BSB	G	G	01	T	9	DBH	3.3	48.9	HT	230.	3960.	98	0.90
412	PICO	T	BSB	R	O	01	T	2	DBH	12.2	48.5				30	0.386
643	PICO	T	BST	E	E	01	T	2	DBA	1.4	7.9				15	0.996
647	PICO	T	BST	E	E	02	T	36	DBA	1.4	7.9	HT	38.	347.	15	0.998
651	PICO	T	BST	E	E	03	T	2	HT	38.	347.				15	0.990
65	PICO	T	BST	R	M	01	T	2	DBH	2.5	28.7				19	0.98
682	PICO	T	BST	R	M	02	T	4	DBH	10.	60.				80	0.961
683	PICO	T	BST	R	M	03	T	4	DBH	0.	10.				80	0.970
413	PICO	T	BST	R	O	01	T	2	DBH	12.2	48.5				30	0.946
597	PICO	T	BST	R	Y	01	T	32	DBH	0.	10.16				8	0.97
905	PICO	T	BSW	G	G	01	T	9	DBH	3.3	48.9	HT	230.	3960.	98	0.95
411	PICO	T	BSW	R	O	01	T	2	DBH	12.2	48.5				30	0.957
481	PICO	T	VQW	R	M	01	T	21	DBH	7.62	45.72	HT	609.6	3048.	213	
482	PICO	T	VQW	R	M	02	T	21	DBH	10.16	45.72	HT	914.4	3048.	193	
483	PICO	T	VQW	R	M	03	T	21	DBH	12.7	45.72	HT	914.4	3048.	169	
484	PICO	T	VQW	R	M	04	T	21	DBH	15.24	45.72	HT	1219.	3048.	151	
485	PICO	T	VQW	R	M	05	T	21	DBH	17.78	45.72	HT	1524.	3048.	143	
486	PICO	T	VQW	R	M	06	T	21	DBH	20.32	45.72	HT	1524.	3048.	133	
487	PICO	T	VQW	R	M	07	T	21	DBH	22.86	45.72	HT	1524.	3048.	116	
439	PICO	T	VSB	R	M	01	T	21	DBH	5.08	45.72	HT	609.6	3048.	227	
438	PICO	T	VSW	R	M	01	T	22	DBH	5.08	45.72	HT	609.6	3048.	227	
879	PIEN	T	BAT	G	G	01	T	9	DBH	4.9	57.6	HT	320.	4080.	43	0.98
877	PIEN	T	BBL	G	G	01	T	9	DBH	4.9	57.6	HT	320.	4080.	43	0.57
876	PIEN	T	BBS	G	G	01	T	9	DBH	4.9	57.6	HT	320.	4080.	43	0.24
526	PIEN	T	BCD	R	G	01	T	2	DBH	2.54	58.42				14	0.87
504	PIEN	T	BCL	R	G	01	T	2	DBH	2.54	73.66				29	0.96
567	PIEN	T	BCL	R	Y	01	T	2	HT	57.9	317.0				12	0.94
878	PIEN	T	BFT	G	G	01	T	9	DBH	4.9	57.6	HT	320.	4080.	43	0.37
875	PIEN	T	BSB	G	G	01	T	9	DBH	4.9	57.6	HT	320.	4080.	43	0.95
415	PIEN	T	BSB	R	O	01	T	2	DBH	17.0	66.8				16	0.900
416	PIEN	T	BST	R	O	01	T	2	DBH	17.0	66.8				16	0.971
594	PIEN	T	BST	R	Y	01	T	2	DBH	0.	10.16				10	0.96
874	PIEN	T	BSW	G	G	01	T	9	DBH	4.9	57.6	HT	320.	4080.	43	0.99
414	PIEN	T	BSW	R	O	01	T	2	DBH	17.0	66.8				16	0.9138
388	PIJE	T	BSB	S	O	01	T	2	DBH	22.4	133.1				21	0.9131
389	PIJE	T	BST	S	O	01	T	2	DBH	22.4	133.1				21	0.978
387	PIJE	T	BSW	S	O	01	T	2	DBH	22.4	133.1				21	0.975
67	PILA	T	BBL	W	O	01	T	2	DBH	20.6	43.3				5	0.81

66	PILA	T	BFT	W	O	01	T	2	DBH	20.6	43.3				5	0.52
391	PILA	T	BSB	S	O	01	T	2	DBH	15.7	179.6				60	0.93
69	PILA	T	BSB	W	O	01	T	2	DBH	20.6	43.3				5	0.91
392	PILA	T	BST	S	O	01	T	2	DBH	15.7	179.6				60	0.98
390	PILA	T	BSW	S	O	01	T	2	DBH	15.7	179.6				60	0.97
68	PILA	T	BSW	W	O	01	T	2	DBH	20.6	43.3				5	0.96
903	PIMO	T	BAT	G	G	01	T	9	DBH	3.7	52.4	HT	250.	3780.	40	0.96
901	PIMO	T	BBL	G	G	01	T	9	DBH	3.7	52.4	HT	250.	3780.	40	0.44
900	PIMO	T	BBS	G	G	01	T	9	DBH	3.7	52.4	HT	250.	3780.	40	0.80
532	PIMO	T	BCD	R	G	01	T	2	DBH	2.54	63.5				18	0.80
509	PIMO	T	BCL	R	G	01	T	9	DBH	2.54	109.2	CR			44	0.97
510	PIMO	T	BCL	R	G	02	T	24	DBH	2.54	109.2	HT			44	0.95
511	PIMO	T	BCL	R	G	03	T	2	DBH	2.54	109.2				44	0.95
572	PIMO	T	BCL	R	Y	01	T	1	HT	85.3	350.5				13	0.97
902	PIMO	T	BFT	G	G	01	T	9	DBH	3.7	52.4	HT	250.	3780.	40	0.37
899	PIMO	T	BSB	G	G	01	T	9	DBH	3.7	52.4	HT	250.	3780.	40	0.96
898	PIMO	T	BSW	G	G	01	T	9	DBH	3.7	52.4	HT	250.	3780.	40	0.99
60	PINUS	T	BBD	G	M	01	T	2	DBH	15.5	79.5				14	0.53
59	PINUS	T	BBL	G	M	01	T	2	DBH	2.5	79.5				33	0.95
58	PINUS	T	BFT	G	M	01	T	2	DBH	2.5	79.5				33	0.89
62	PINUS	T	BSB	G	M	01	T	2	DBH	15.5	79.5				14	0.95
61	PINUS	T	BSW	G	M	01	T	2	DBH	15.5	79.5				14	0.98
640	PIPO	T	BAT	E	E	01	T	2	DBA	0.9	10.5				60	0.97
644	PIPO	T	BAT	E	E	02	T	36	DBA	0.9	10.5	HT	29.	303.	60	0.98
648	PIPO	T	BAT	E	E	03	T	2	HT	29.	303,				60	0.98
706	PIPO	T	BAT	E	Y	04	T	17	DBH	5.3	38.7	HT	311.	2063.	23	0.99
867	PIPO	T	BAT	G	Y	01	T	9	DBH	3.4	62.5	HT	210.	4080.	42	0.98
72	PIPO	T	BBD	R	G	01	T	2	DBH	15.5	79.5				9	0.64
702	PIPO	T	BBL	E	Y	01	T	17	DBH	5.3	38.7	HT	311.	2063.	23	0.95
703	PIPO	T	BBL	E	Y	02	T	2	DBH	5.3	38.7				23	0.94
865	PIPO	T	BBL	G	Y	01	T	9	DBH	3.4	62.5	HT	210.	4080.	42	0.46
71	PIPO	T	BBL	R	G	01	T	2	DBH	15.5	79.5				9	0.99
864	PIPO	T	BBS	G	Y	01	T	9	DBH	3.4	62.5	HT	210.	4080.	42	0.0
537	PIPO	T	BCD	R	G	01	T	2	DBH	2.54	86.36				26	0.87
582	PIPO	T	BCD	R	M	01	T	2	DBH	2.54	30.48				15	0.81
516	PIPO	T	BCL	R	G	01	T	17	DBH	2.54	86.36	CR			40	0.97
517	PIPO	T	BCL	R	G	02	T	2	DBH	2.54	86.36				40	0.95
580	PIPO	T	BCL	R	M	01	T	2	HT	116.9	445.0				10	0.35
581	PIPO	T	BCL	R	M	02	T	2	DBH	2.54	30.48				15	0.90
571	PIPO	T	BCL	R	Y	01	T	1	HT	70.1	304.8				12	0.81
583	PIPO	T	BCT	R	M	01	T	2	DBH	2.54	30.48				15	0.95
75	PIPO	T	BFN	R	G	01	T	2	DBH	15.5	79.5				9	0.86
701	PIPO	T	BFT	E	Y	01	T	2	DBH	5.3	38.7				23	0.97
866	PIPO	T	BFT	G	Y	01	T	9	DBH	3.4	62.5	HT	210.	4080.	42	0.40
70	PIPO	T	BFT	R	G	01	T	2	DBH	15.5	79.5				9	0.84
316	PIPO	T	BSB	E	O	01	T	2	DBH	24.1	117.7				42	0.96
705	PIPO	T	BSB	E	Y	01	T	17	DBH	5.3	38.7	HT	311.	2063.	23	0.99
863	PIPO	T	BSB	G	Y	01	T	9	DBH	3.4	62.5	HT	210.	4080.	42	0.93
74	PIPO	T	BSB	R	G	01	T	2	DBH	15.5	79.5				9	0.97
641	PIPO	T	BST	E	E	01	T	2	DBA	0.9	10.5				60	0.97
645	PIPO	T	BST	E	E	02	T	36	DBA	0.9	10.5	HT	29.	303.	60	0.99
649	PIPO	T	BST	E	E	03	T	2	HT	29.	303.				60	0.98
317	PIPO	T	BST	E	O	01	T	2	DBH	24.1	117.7				42	0.98
610	PIPO	T	BST	R	M	01	T	9	DBH	0.	10.16	HT			11	0.92
611	PIPO	T	BST	R	M	02	T	28	DBH	0.	10.16				11	0.79
596	PIPO	T	BST	R	Y	01	T	4	DBH	0.	10.16				11	0.96
315	PIPO	T	BSW	E	O	01	T	2	DBH	24.1	117.7				42	0.98
862	PIPO	T	BSW	G	Y	01	T	9	DBH	3.4	62.5	HT	210.	4080.	42	0.92
73	PIPO	T	BSW	R	G	01	T	2	DBH	15.5	79.5				9	0.99
474	PIPO	T	VQW	R	M	01	T	21	DBH	7.62	58.42	HT	609.6	3353.	338	
475	PIPO	T	VQW	R	M	02	T	21	DBH	10.16	58.42	HT	609.6	3353.	308	
476	PIPO	T	VQW	R	M	03	T	21	DBH	12.7	58.42	HT	914.4	3353.	269	
477	PIPO	T	VQW	R	M	04	T	21	DBH	15.24	58.42	HT	914.4	3353.	247	
478	PIPO	T	VQW	R	M	05	T	21	DBH	17.78	58.42	HT	1219.	3353.	229	
479	PIPO	T	VQW	R	M	06	T	21	DBH	22.86	58.42	HT	1219.	3353.	212	
480	PIPO	T	VQW	R	M	07	T	21	DBH	22.86	58.42	HT	1524.	3353.	197	
704	PIPO	T	VSB	E	Y	01	T	17	DBH	5.3	38.7	HT	311.	2063.	23	0.99
437	PIPO	T	VSB	R	M	01	T	21	DBH	5.08	58.42	HT	304.8	3353.	362	
436	PIPO	T	VSW	R	M	01	T	20	DBH	5.08	58.42	HT	304.8	3353.	362	
849	PISI	T	BAT	G	Y	01	T	9	DBH	5.3	45.1	HT	460.	2250.	40	0.96

466	PISI	T	BBL	A	M	01	T	2	DBH	3.0	77.7				28	0.80
471	PISI	T	BBL	A	M	02	T	17	DBH	3.0	77.7	SAP	0.6	3.8	28	0.92
847	PISI	T	BBL	G	Y	01	T	9	DBH	5.3	45.1	HT	460.	2250.	40	0.42
846	PISI	T	BBS	G	Y	01	T	9	DBH	5.3	45.1	HT	460.	2250.	40	0.41
467	PISI	T	BCL	A	M	01	T	2	DBH	3.0	77.7				28	0.81
472	PISI	T	BCL	A	M	02	T	17	DBH	3.0	77.7	SAP	0.6	3.8	28	0.94
463	PISI	T	BFN	A	M	01	T	2	DBH	3.0	77.7				28	0.71
469	PISI	T	BFN	A	M	02	T	18	DBH	3.0	77.7	SAP	0.6	3.8	28	0.90
465	PISI	T	BFT	A	M	01	T	2	DBH	3.0	77.7				28	0.81
470	PISI	T	BFT	A	M	02	T	19	DBH	3.0	77.7	SAP	0.6	3.8	28	0.95
848	PISI	T	BFT	G	Y	01	T	9	DBH	5.3	45.1	HT	460.	2250.	40	0.46
370	PISI	T	BSB	C	M	01	T	2	DBH	20.7	176.0				27	0.90
310	PISI	T	BSB	C	O	01	T	2	DBH	35.4	283.0				41	0.81
403	PISI	T	BSB	C	Y	01	T	2	DBH	24.3	41.5				14	0.66
845	PISI	T	BSB	G	Y	01	T	9	DBH	5.3	45.1	HT	460.	2250.	40	0.93
464	PISI	T	BST	A	M	01	T	2	DBH	3.0	77.7				21	0.97
371	PISI	T	BST	C	M	01	T	2	DBH	20.7	176.0				27	0.93
311	PISI	T	BST	C	O	01	T	2	DBH	35.4	283.0				41	0.95
404	PISI	T	BST	C	Y	01	T	2	DBH	24.3	41.5				14	0.87
369	PISI	T	BSW	C	M	01	T	2	DBH	20.7	176.0				27	0.93
309	PISI	T	BSW	C	O	01	T	2	DBH	35.4	283.0				41	0.95
402	PISI	T	BSW	C	Y	01	T	2	DBH	24.3	41.5				14	0.87
844	PISI	T	BSW	G	Y	01	T	9	DBH	5.3	45.1	HT	460.	2250.	40	0.98
468	PISI	T	PFT	A	M	01	T	2	DBH	3.0	77.7				28	0.79
473	PISI	T	PFT	A	M	02	T	31	DBH	3.0	77.7	SAP	0.6	3.8	28	0.95
716	POTR	T	BAE	R	Y	01	T	36	DBH	2.0	31.5	HT	124.9	2774.	279	0.98
946	POTR	T	BAT	G	G	01	T	9	DBH	6.0	34.8	HT	540.	2560.	40	0.94
718	POTR	T	BAT	R	Y	01	T	36	DBH	2.0	31.5	HT	124.9	2774.	279	0.98
944	POTR	T	BBL	G	G	01	T	9	DBH	6.0	34.8	HT	540.	2560.	40	0.26
943	POTR	T	BBS	G	G	01	T	9	DBH	6.0	34.8	HT	540.	2560.	40	0.49
717	POTR	T	BCL	R	Y	01	T	36	DBH	2.0	31.5	HT	124.9	2774.	279	0.82
945	POTR	T	BFT	G	G	01	T	9	DBH	6.0	34.8	HT	540.	2560.	40	0.37
942	POTR	T	BSB	G	G	01	T	9	DBH	6.0	34.8	HT	540.	2560.	40	0.94
719	POTR	T	BSB	R	Y	01	T	40	DBH	2.0	31.5	HT	124.9	2774.	279	
715	POTR	T	BST	R	Y	01	T	36	DBH	2.0	31.5	HT	124.9	2774.	279	0.99
941	POTR	T	BSW	G	G	01	T	9	DBH	6.0	34.8	HT	540.	2560.	40	0.98
714	POTR	T	BSW	R	Y	01	T	36	DBH	2.0	31.5	HT	124.9	2774.	279	0.99
934	POTR2	T	BAT	G	Y	01	T	9	DBH	5.6	31.5	HT	690.	2540.	40	0.95
932	POTR2	T	BBL	G	Y	01	T	9	DBH	5.6	31.5	HT	690.	2540.	40	0.66
931	POTR2	T	BBS	G	Y	01	T	9	DBH	5.6	31.5	HT	690.	2540.	40	0.83
933	POTR2	T	BFT	G	Y	01	T	9	DBH	5.6	31.5	HT	690.	2540.	40	0.55
930	POTR2	T	BSB	G	Y	01	T	9	DBH	5.6	31.5	HT	690.	2540.	40	0.83
922	POTR2	T	BSW	G	Y	01	T	9	DBH	5.6	31.5	HT	690.	2540.	40	0.92
615	PPPA	T	BAT	R	Y	01	T	2	HT	0.	457.2				58	0.93
625	PREM	T	BAT	E	E	01	T	35	LEN			WID			11	0.97
635	PREM	T	BAT	E	E	02	T	2	VOL	11.76	6551.				11	0.98
189	PSME	T	BAP	W	Y	01	T	2	DBA	0.29	6.1				23	0.93
301	PSME	T	BAT	C	Y	01	T	2	DBH	1.4	13.4				18	0.97
307	PSME	T	BAT	C	Y	02	T	2	DBA	2.1	21.9				18	0.97
750	PSME	T	BAT	C	Y	03	T	2	DBH	8.9	26.1				240	0.93
759	PSME	T	BAT	C	Y	04	T	17	DBH	8.9	26.1	HT	990.	1840.	240	0.95
830	PSME	T	BAT	C	Y	05	T	2	DBH						40	0.93
838	PSME	T	BAT	C	Y	06	T	9	DBH	4.5	66.0	HT	410.	4400.	49	0.99
861	PSME	T	BAT	G	G	01	T	9	DBH	3.1	63.2	HT	260.	3450.	41	0.84
1093	PSME	T	BAT	W	E	02	T	11	DBA	0.1	0.7				11	0.97
1094	PSME	T	BAT	W	E	03	T	17	DBA	0.1	0.7	HT	3.0	24.0	11	0.98
1095	PSME	T	BAT	W	E	04	T	2	HT	3.0	24.0				11	0.94
444	PSME	T	BAT	W	G	01	T	9	DBH	2.5	162.0	HT			144	0.69
190	PSME	T	BAT	W	Y	01	T	2	DBA	0.29	6.1				23	0.94
3	PSME	T	BBD	W	G	01	T	2	DBH	1.8	162.0				85	0.84
298	PSME	T	BBL	C	Y	01	T	2	DBH	1.4	13.4				18	0.94
304	PSME	T	BBL	C	Y	02	T	2	DBA	2.1	21.9				18	0.94
755	PSME	T	BBL	C	Y	03	T	2	DBH	8.9	26.1				240	0.74
764	PSME	T	BBL	C	Y	04	T	17	DBH	8.9	26.1	HT	990.	1840.	240	0.73
842	PSME	T	BBL	C	Y	05	T	9	DBH	4.5	66.0	HT	410.	4400.	49	0.56
825	PSME	T	BBL	C	Y	06	T	2	DBH						40	0.92
859	PSME	T	BBL	G	G	01	T	9	DBH	3.1	63.2	HT	260.	3450.	41	0.45
2	PSME	T	BBL	W	G	01	T	2	DBH	1.8	162.0				123	0.92
446	PSME	T	BBL	W	G	02	T	9	DBH	1.0	220.7	HT			171	0.77
824	PSME	T	BBS	C	Y	01	T	2	DBH						40	0.93

841	PSME	T	BBS	C	Y	04	T	9	DBH	4.5	66.0	HT	410.	4400.	49	0.64
858	PSME	T	BBS	G	G	01	T	9	DBH	3.1	63.2	HT	260.	3450.	41	0.45
538	PSME	T	BCD	R	G	01	T	24	DBH	2.54	86.36	LEN			21	0.98
539	PSME	T	BCD	R	G	02	T	28	DBH	2.54	86.36				21	0.91
586	PSME	T	BCD	R	M	01	T	2	DBH	2.54	27.94				15	0.89
419	PSME	T	BCD	W	O	01	T	2	DBH	60.	160.				32	0.79
752	PSME	T	BCL	C	Y	01	T	2	DBH	8.9	26.1				240	0.78
761	PSME	T	BCL	C	Y	02	T	17	DBH	8.9	26.1	HT	990.	1840.	240	0.77
826	PSME	T	BCL	C	Y	04	T	2	DBH						40	0.93
518	PSME	T	BCL	R	G	01	T	2	DBH	2.54	43.18				41	0.93
519	PSME	T	BCL	R	G	02	T	4	DBH	2.54	86.36				41	0.85
579	PSME	T	BCL	R	M	01	T	2	HT	109.7	475.5				10	0.66
584	PSME	T	BCL	R	M	02	T	33	DBH	2.54	27.94	HT			15	0.96
585	PSME	T	BCL	R	M	03	T	2	DBH	2.54	27.94				15	0.90
566	PSME	T	BCL	R	Y	01	T	2	HT	112.8	347.5				11	0.83
417	PSME	T	BCL	W	O	01	T	13	DBH	60.	160.				32	0.73
587	PSME	T	BCT	R	M	01	T	2	DBH	2.54	27.94				15	0.94
7	PSME	T	BFN	W	O	01	T	2	DBH	25.9	162.0				29	0.93
297	PSME	T	BFT	C	Y	01	T	2	DBH	1.4	13.4				18	0.94
303	PSME	T	BFT	C	Y	02	T	2	DBA	2.1	21.9				18	0.94
756	PSME	T	BFT	C	Y	03	T	2	DBH	8.9	26.1				240	0.76
765	PSME	T	BFT	C	Y	04	T	17	DBH	8.9	26.1	HT	990.	1840.	240	0.76
823	PSME	T	BFT	C	Y	05	T	2	DBH						40	0.93
843	PSME	T	BFT	C	Y	06	T	9	DBH	4.5	66.0	HT	410.	4400.	49	0.56
860	PSME	T	BFT	G	G	01	T	9	DBH	3.1	63.2	HT	260.	3450.	41	0.40
1	PSME	T	BFT	W	G	01	T	2	DBH	1.8	162.0				123	0.86
247	PSME	T	BFT	W	O	01	T	2	DBH	110.	190.				7	0.599
445	PSME	T	BFT	W	O	02	T	9	DBH	1.0	220.7	HT			171	0.80
188	PSME	T	BFT	W	Y	01	T	2	DBA	0.29	6.1				23	0.906
6	PSME	T	BRL	W	G	01	T	2	DBH	2.3	135.0				26	0.96
450	PSME	T	BRT	W	G	02	T	9	DBH	2.5	60.0	HT			13	0.99
754	PSME	T	BSB	C	Y	01	T	2	DBH	8.9	26.1				240	0.87
763	PSME	T	BSB	C	Y	02	T	17	DBH	8.9	26.1	HT	990.	1840.	240	0.88
828	PSME	T	BSB	C	Y	04	T	2	DBH						40	0.85
840	PSME	T	BSB	C	Y	05	T	9	DBH	4.5	66.0	HT	410.	4400.	49	0.98
857	PSME	T	BSB	G	G	01	T	9	DBH	3.1	63.2	HT	260.	3450.	41	0.80
5	PSME	T	BSB	W	G	01	T	2	DBH	1.8	162.0				99	0.99
448	PSME	T	BSB	W	G	02	T	9	DBH	2.5	162.0	HT			120	0.68
254	PSME	T	BSB	W	M	01	T	2	DBH	17.0	212.7				215	0.915
364	PSME	T	BSB	W	M	02	T	2	DBH	24.6	206.5				34	0.958
328	PSME	T	BSB	W	O	01	T	2	DBH	31.5	215.0				45	0.835
343	PSME	T	BSB	W	O	02	T	2	DBH	17.2	177.4				116	0.933
352	PSME	T	BSB	W	O	03	T	2	DBH	38.6	161.0				20	0.802
300	PSME	T	BST	C	Y	01	T	2	DBH	1.4	13.4				18	0.97
306	PSME	T	BST	C	Y	02	T	2	DBA	2.1	21.9				18	0.97
751	PSME	T	BST	C	Y	03	T	2	DBH	8.9	26.1				240	0.93
760	PSME	T	BST	C	Y	04	T	17	DBH	8.9	26.1	HT	990	1840.	240	0.96
829	PSME	T	BST	C	Y	05	T	2	DBH						40	0.89
609	PSME	T	BST	R	M	01	T	4	DBH	0.	10.16				8	0.97
595	PSME	T	BST	R	Y	01	T	4	DBH	0.	10.16				12	0.99
449	PSME	T	BST	W	G	01	T	9	DBH	2.5	162.0	HT			144	0.74
256	PSME	T	BST	W	M	01	T	2	DBH	17.0	212.7				215	0.973
365	PSME	T	BST	W	M	02	T	2	DBH	24.6	206.5				34	0.990
329	PSME	T	BST	W	O	01	T	2	DBH	31.5	215.0				45	0.957
344	PSME	T	BST	W	O	02	T	2	DBH	17.2	177.4				116	0.972
353	PSME	T	BST	W	O	03	T	2	DBH	38.6	161.0				20	0.937
753	PSME	T	BSW	C	Y	02	T	2	DBH	8.9	26.1				240	0.92
762	PSME	T	BSW	C	Y	03	T	17	DBH	8.9	26.1	HT	990	1840.	240	0.93
827	PSME	T	BSW	C	Y	04	T	2	DBH						40	0.89
839	PSME	T	BSW	C	Y	05	T	9	DBH	4.5	66.0	HT	410.	4400.	49	0.99
856	PSME	T	BSW	G	G	01	T	9	DBH	3.1	63.2	HT	260.	3450.	41	0.80
4	PSME	T	BSW	W	G	01	T	2	DBH	1.8	162.0				99	0.99
447	PSME	T	BSW	W	G	02	T	9	DBH	2.5	162.0	HT			120	0.88
255	PSME	T	BSW	W	M	01	T	2	DBH	17.0	212.7				215	0.970
363	PSME	T	BSW	W	M	02	T	2	DBH	24.6	206.5				34	0.987
327	PSME	T	BSW	W	O	01	T	2	DBH	31.5	215.0				45	0.953
342	PSME	T	BSW	W	O	02	T	2	DBH	17.2	177.4				116	0.970
351	PSME	T	BSW	W	O	03	T	2	DBH	38.6	161.0				20	0.926
302	PSME	T	HST	C	Y	01	T	2	DBH	1.4	13.4				18	0.83
308	PSME	T	HST	C	Y	02	T	2	DBA	2.1	21.9				18	0.78

758	PSME	T	PFT	C	Y	01	T	2	SPA	43.2	309.7				240	0.69
766	PSME	T	PFT	C	Y	02	T	17	DBH	8.9	26.1	HT	990.	1840.	240	0.73
757	PSME	T	PFT	C	Y	03	T	2	DBH	8.9	26.1				240	0.73
817	PSME	T	PFT	C	Y	04	T	2	DBH						16	0.94
818	PSME	T	PFT	C	Y	05	T	2	DBH						16	0.94
819	PSME	T	PFT	C	Y	06	T	2	DBH						8	0.85
820	PSME	T	PFT	C	Y	07	T	2	SPA						16	0.95
821	PSME	T	PFT	C	Y	08	T	2	SPA						16	0.95
822	PSME	T	PFT	C	Y	09	T	2	SPA						8	0.85
495	PSME	T	VQW	R	M	01	T	21	DBH	7.62	55.88	HT	609.6	3048.	332	
496	PSME	T	VQW	R	M	02	T	21	DBH	10.16	66.04	HT	914.4	3353.	300	
497	PSME	T	VQW	R	M	03	T	21	DBH	12.7	66.04	HT	914.4	3353.	273	
498	PSME	T	VQW	R	M	04	T	21	DBH	15.24	66.04	HT	1219.	3353.	248	
499	PSME	T	VQW	R	M	05	T	21	DBH	17.78	55.88	HT	1219.	3048.	221	
500	PSME	T	VQW	R	M	06	T	21	DBH	20.32	55.88	HT	1524.	3048.	197	
501	PSME	T	VQW	R	M	07	T	21	DBH	22.86	66.04	HT	1524.	3353.	184	
443	PSME	T	VSB	R	M	01	T	21	DBH	5.08	55.88	HT	304.8	3048.	361	
299	PSME	T	VST	C	Y	01	T	2	DBH	1.4	13.4				18	0.97
305	PSME	T	VST	C	Y	02	T	2	DBA	2.1	21.9				18	0.97
442	PSME	T	VSW	R	M	01	T	20	DBH	5.08	55.88	HT	304.8	3048.	361	
665	QUAG	T	VAE	C	G	01	T	17	DBH	10.	100.	HT	60.	300.	60	0.96
666	QUAG	T	VSW	C	G	01	T	17	DBH	10.	100.	HT	60.	300.	59	0.97
661	QUCH	T	VAE	G	G	01	T	17	DBH	10.	80.	HT	60.	300.	58	0.97
662	QUCH	T	VSW	G	G	01	T	17	DBH	10.	80.	HT	60.	300.	58	0.98
659	QUDO	T	VAE	G	G	01	T	17	DBH	10.	70.	HT	60.	240.	60	0.97
660	QUDO	T	VSW	G	G	01	T	17	DBH	10.	70.	HT	60.	240.	60	0.97
667	QUEN	T	VAE	C	G	01	T	17	DBH	10.	80.	HT	60.	150.	61	0.96
668	QUEN	T	VSW	C	G	01	T	17	DBH	10.	80.	HT	60.	150.	61	0.96
675	QUGA	T	VAE	G	G	01	T	17	DBH	10.	90.	HT	60.	270.	60	0.96
676	QUGA	T	VSW	G	G	01	T	17	DBH	10.	90.	HT	60.	270.	60	0.95
656	QUKE	T	VAE	G	G	01	T	17	DBH	10.	110.	HT	90.	420.	59	0.97
657	QUKE	T	VSW	G	G	01	T	17	DBH	10.	110.	HT	90.	420.	60	0.96
679	QULO	T	VAE	G	G	01	T	17	DBH	10.	100.	HT	60.	300.	59	0.95
680	QULO	T	VSW	G	G	01	T	17	DBH	10.	100.	HT	60.	300.	59	0.99
669	QUWI	T	VAE	G	G	01	T	17	DBH	10.	100.	HT	60.	270.	58	0.97
670	QUWI	T	VSW	G	G	01	T	17	DBH	10.	100.	HT	60.	270.	58	0.96
394	SEGI	T	BSB	S	O	01	T	2	DBH	96.8	614.3				45	0.72
395	SEGI	T	BST	S	O	01	T	2	DBH	96.8	614.3				45	0.95
393	SEGI	T	BSW	S	O	01	T	2	DBH	96.8	614.3				45	0.95
617	THLAPI	T	BAT	R	Y	01	T	2	HT	0.	457.2				37	0.87
192	THPL	T	BAP	W	Y	01	T	2	DBA	0.18	2.23				5	0.98
855	THPL	T	BAT	G	G	01	T	9	DBH	3.8	68.9	HT	340.	4000.	70	0.97
457	THPL	T	BAT	W	G	01	T	9	DBH	2.5	119.6	HT			26	0.90
1126	THPL	T	BAT	W	O	01	T	1	DBA	4.2	7.0				4	0.9:
193	THPL	T	BAT	W	Y	01	T	2	DBA	0.18	2.23				5	0.99
853	THPL	T	BBL	G	G	01	T	9	DBH	3.8	68.9	HT	340.	4000.	70	0.66
459	THPL	T	BBL	W	G	01	T	9	DBH	0.2	119.6	HT			50	0.91
1127	THPL	T	BBL	W	O	01	T	1	DBA	4.2	7.0				4	0.55
852	THPL	T	BBS	G	G	01	T	9	DBH	3.8	68.9	HT	340.	4000.	70	0.2(
536	THPL	T	BCD	R	G	01	T	28	DBH	2.54	68.58				20	0.91
592	THPL	T	BCD	R	M	01	T	2	DBH	2.54	27.94				13	0.9(
514	THPL	T	BCL	R	G	01	T	25	DBH	2.54	93.98	CR			34	0.9;
515	THPL	T	BCL	R	G	02	T	2	DBH	2.54	93.98				34	0.9(
578	THPL	T	BCL	R	M	01	T	4	HT	112.8	317.0				11	0.9(
591	THPL	T	BCL	R	M	02	T	2	DBH	2.54	27.94				13	0.9
569	THPL	T	BCL	R	Y	01	T	4	HT	54.9	307.8				12	0.9(
593	THPL	T	BCT	R	M	01	T	2	DBH	2.54	27.94				13	0.9!
854	THPL	T	BFT	G	G	01	T	9	DBH	3.8	68.9	HT	340.	4000.	70	0.6:
458	THPL	T	BFT	W	G	01	T	9	DBH	0.2	119.6	HT			47	0.9!
1128	THPL	T	BFT	W	O	01	T	1	DBA	4.2	7.0				4	0.9:
191	THPL	T	BFT	W	Y	01	T	2	DBA	0.18	2.23				5	0.9!
851	THPL	T	BSB	G	G	01	T	9	DBH	3.8	68.9	HT	340.	4000.	70	0.8:
461	THPL	T	BSB	W	G	01	T	9	DBH	2.5	119.6	HT			26	0.6(
331	THPL	T	BSB	W	O	01	T	2	DBH	11.8	168.5				17	0.9.
346	THPL	T	BSB	W	O	02	T	2	DBH	17.1	123.7				22	0.86
355	THPL	T	BSB	W	O	03	T	2	DBH	31.2	95.5				12	0.65
400	THPL	T	BSB	W	O	04	T	2	DBH	11.8	168.5				52	0.81
612	THPL	T	BST	R	M	01	T	4	DBH	0.	10.16				10	0.97
599	THPL	T	BST	R	Y	01	T	29	DBH	0.	10.16				13	0.99
462	THPL	T	BST	W	G	01	T	9	DBH	2.5	119.6	HT			26	0.9:

332	THPL	T	BST	W	O	01	T	2	DBH	11.8	168.5				17	0.991
347	THPL	T	BST	W	O	02	T	2	DBH	17.1	123.7				22	0.986
356	THPL	T	BST	W	O	03	T	2	DBH	31.2	95.5				12	0.918
401	THPL	T	BST	W	O	04	T	2	DBH	11.8	168.5				52	0.979
1129	THPL	T	BST	W	O	05	T	1	DBA	4.2	7.0				4	0.759
850	THPL	T	BSW	G	G	01	T	9	DBH	3.8	68.9	HT	340.	4000.	70	0.95
460	THPL	T	BSW	W	G	01	T	9	DBH	2.5	119.6	HT			26	0.95
330	THPL	T	BSW	W	O	01	T	2	DBH	11.8	168.5				17	0.989
345	THPL	T	BSW	W	O	02	T	2	DBH	17.1	123.7				22	0.985
354	THPL	T	BSW	W	O	03	T	2	DBH	31.2	95.5				12	0.916
399	THPL	T	BSW	W	O	04	T	2	DBH	11.8	168.5				52	0.978
619	THPSPI	T	BAT	R	Y	01	T	2	HT	0.	457.2				31	0.79
195	TSHE	T	BAP	W	Y	01	T	2	DBA	0.12	4.29				18	0.970
873	TSHE	T	BAT	G	G	01	T	9	DBH	3.1	70.5	HT	350.	4370.	70	0.98
618	TSHE	T	BAT	R	Y	01	T	2	HT	0.	457.2				11	0.71
451	TSHE	T	BAT	W	G	01	T	9	DBH	2.5	92.4	HT			47	0.88
1130	TSHE	T	BAT	W	O	01	T	1	DBA	4.2	7.9				4	0.935
196	TSHE	T	BAT	W	Y	01	T	2	DBA	0.12	4.29				18	0.969
544	TSHE	T	BBD	C	M	01	T	2	DBH	9.9	47.8				21	0.93
545	TSHE	T	BBD	C	M	02	T	2	DBH	9.9	47.8				21	0.93
10	TSHE	T	BBD	W	O	01	T	2	DBH	15.3	78.0				18	0.62
129	TSHE	T	BBL	C	M	01	T	2	DBH	2.1	13.4				9	0.97
542	TSHE	T	BBL	C	M	02	T	2	DBH	9.9	47.8				21	0.89
543	TSHE	T	BBL	C	M	03	T	2	DBH	9.9	47.8				21	0.89
871	TSHE	T	BBL	G	G	01	T	9	DBH	3.1	70.5	HT	350.	4370.	70	0.55
453	TSHE	T	BBL	W	G	01	T	9	DBH	0.2	118.0	HT			74	0.98
9	TSHE	T	BBL	W	O	01	T	2	DBH	15.3	78.0				18	0.98
1131	TSHE	T	BBL	W	O	02	T	1	DBA	4.2	7.9				4	0.875
176	TSHE	T	BBS	C	M	01	T	2	DBH	9.9	47.8				21	0.91
872	TSHE	T	BBS	G	G	01	T	9	DBH	3.1	70.5	HT	350.	4370.	70	0.52
540	TSHE	T	BCD	R	G	01	T	17	DBH	2.54	53.34	HT			20	0.92
541	TSHE	T	BCD	R	G	02	T	2	DBH	2.54	53.34				20	0.84
420	TSHE	T	BCD	W	O	01	T	2	DBH	30.	110.				29	0.73
520	TSHE	T	BCL	R	G	01	T	26	DBH	2.54	81.28	LEN			27	0.98
521	TSHE	T	BCL	R	G	02	T	27	DBH	2.54	81.28	HT			27	0.98
522	TSHE	T	BCL	R	G	03	T	2	DBH	2.54	81.28				27	0.98
575	TSHE	T	BCL	R	Y	01	T	2	HT	109.7	414.5				12	0.91
418	TSHE	T	BCL	W	O	01	T	13	DBH	30.	110.				29	0.82
13	TSHE	T	BFN	W	O	01	T	2	DBH	15.3	78.0				10	0.81
128	TSHE	T	BFT	C	M	01	T	2	DBH	2.1	13.4				9	0.96
175	TSHE	T	BFT	C	M	02	T	2	DBH	9.9	47.8				21	0.91
870	TSHE	T	BFT	G	G	01	T	9	DBH	3.1	70.5	HT	350.	4370.	70	0.55
452	TSHE	T	BFT	W	G	01	T	9	DBH	0.2	118.0	HT			66	0.99
8	TSHE	T	BFT	W	O	01	T	2	DBH	15.3	78.0				18	0.96
1133	TSHE	T	BFT	W	O	02	T	1	DBA	4.2	7.9				4	0.817
194	TSHE	T	BFT	W	Y	01	T	2	DBA	0.12	4.29				18	0.952
174	TSHE	T	BSB	C	M	01	T	2	DBH	9.9	47.8				19	0.97
373	TSHE	T	BSB	C	M	02	T	2	DBH	19.3	121.6				41	0.939
376	TSHE	T	BSB	C	M	03	T	2	DBH	27.5	73.4				31	0.589
313	TSHE	T	BSB	C	O	01	T	2	DBH	19.6	172.3				47	0.895
406	TSHE	T	BSB	C	Y	01	T	2	DBH	25.6	45.7				25	0.287
869	TSHE	T	BSB	G	G	01	T	9	DBH	3.1	70.5	HT	350.	4370.	70	0.92
455	TSHE	T	BSB	W	G	01	T	9	DBH	2.5	92.4	HT			37	0.73
367	TSHE	T	BSB	W	M	01	T	2	DBH	15.3	134.7				21	0.963
12	TSHE	T	BSB	W	O	01	T	2	DBH	15.3	78.0				18	0.99
257	TSHE	T	BSB	W	O	02	T	2	DBH	8.9	134.7				207	0.842
334	TSHE	T	BSB	W	O	03	T	2	DBH	8.9	113.3				80	0.873
349	TSHE	T	BSB	W	O	04	T	2	DBH	14.4	114.8				91	0.780
358	TSHE	T	BSB	W	O	05	T	2	DBH	24.7	56.0				15	0.861
130	TSHE	T	BST	C	M	01	T	2	DBH	2.1	13.4				9	0.99
374	TSHE	T	BST	C	M	02	T	2	DBH	19.3	121.6				41	0.981
377	TSHE	T	BST	C	M	03	T	2	DBH	27.5	73.4				31	0.878
314	TSHE	T	BST	C	O	01	T	2	DBH	19.6	172.3				47	0.961
407	TSHE	T	BST	C	Y	01	T	2	DBH	25.6	45.7				25	0.840
598	TSHE	T	BST	R	Y	01	T	28	DBH	0.	10.16				13	0.98
601	TSHE	T	BST	R	Y	02	T	33	DBH	0.	10.16	HT			12	0.98
602	TSHE	T	BST	R	Y	03	T	4	DBH	0.	10.16				12	0.97
456	TSHE	T	BST	W	G	01	T	9	DBH	2.5	92.4	HT			47	0.97
368	TSHE	T	BST	W	M	01	T	2	DBH	15.3	134.7				21	0.978
259	TSHE	T	BST	W	O	01	T	2	DBH	8.9	134.7				207	0.943

335	TSHE	T	BST	W	O	02	T	2	DBH	8.9	113.3				80	0.97
350	TSHE	T	BST	W	O	03	T	2	DBH	14.4	114.8				91	0.91
359	TSHE	T	BST	W	O	04	T	2	DBH	24.7	56.0				15	0.91
1132	TSHE	T	BST	W	O	05	T	1	DBA	4.2	7.9				4	0.94
173	TSHE	T	BSW	C	M	01	T	2	DBH	9.9	47.8				19	0.98
372	TSHE	T	BSW	C	M	02	T	2	DBH	19.3	121.6				41	0.98
375	TSHE	T	BSW	C	M	03	T	2	DBH	27.5	73.4				31	0.88
312	TSHE	T	BSW	C	O	01	T	2	DBH	19.6	172.3				47	0.95
405	TSHE	T	BSW	C	Y	01	T	2	DBH	25.6	45.7				25	0.84
868	TSHE	T	BSW	G	G	01	T	9	DBH	3.1	70.5	HT	350.	4370.	70	0.99
454	TSHE	T	BSW	W	G	01	T	9	DBH	2.5	92.4	HT			37	0.98
366	TSHE	T	BSW	W	M	01	T	2	DBH	15.3	134.7				21	0.97
11	TSHE	T	BSW	W	O	01	T	2	DBH	15.3	78.0				18	0.99
258	TSHE	T	BSW	W	O	02	T	2	DBH	8.9	134.7				207	0.94
333	TSHE	T	BSW	W	O	03	T	2	DBH	8.9	113.3				80	0.87
348	TSHE	T	BSW	W	O	04	T	2	DBH	14.4	114.8				91	0.92
357	TSHE	T	BSW	W	O	05	T	2	DBH	24.7	56.0				15	0.90
915	TSME	T	BAT	G	G	01	T	9	DBH	8.9	44.0	HT	400.	2530.	39	0.99
16	TSME	T	BBD	W	O	01	T	2	DBH	17.0	54.6				6	0.98
913	TSME	T	BBL	G	G	01	T	9	DBH	8.9	44.0	HT	400.	2530.	39	0.70
15	TSME	T	BBL	W	O	01	T	2	DBH	17.0	76.2				11	0.99
912	TSME	T	BBS	G	G	01	T	9	DBH	8.9	44.0	HT	400.	2530.	39	0.69
914	TSME	T	BFT	G	G	01	T	9	DBH	8.9	44.0	HT	400.	2530.	39	0.63
14	TSME	T	BFT	W	O	01	T	2	DBH	17.0	76.2				11	0.97
911	TSME	T	BSB	G	G	01	T	9	DBH	8.9	44.0	HT	400.	2530.	39	0.95
340	TSME	T	BSB	G	M	01	T	2	DBH	11.5	125.7				399	0.91
18	TSME	T	BSB	W	O	01	T	2	DBH	17.0	76.2				14	0.97
337	TSME	T	BSB	W	O	02	T	2	DBH	22.3	88.8				15	0.95
341	TSME	T	BST	G	M	01	T	2	DBH	11.5	125.7				399	0.95
338	TSME	T	BST	W	O	01	T	2	DBH	22.3	88.8				15	0.98
916	TSME	T	BSW	G	G	01	T	9	DBH	8.9	44.0	HT	400.	2530.	39	0.99
339	TSME	T	BSW	G	M	01	T	2	DBH	11.5	125.7				399	0.95
17	TSME	T	BSW	W	O	01	T	2	DBH	17.0	76.2				14	0.98
336	TSME	T	BSW	W	O	02	T	2	DBH	22.3	88.8				15	0.97
671	UMCA	T	VAE	C	G	01	T	17	DBH	10.	80.	HT	60.	330.	60	0.96
672	UMCA	T	VSW	C	G	01	T	17	DBH	10.	80.	HT	60.	330.	60	0.95

, Equation Selection Penalties (ESP)

Section

In many instances, the plants used to construct the equations in the Library will closely match the plants in the Input Data File. There also will be instances, however, when the plant sizes, geographic areas, seral stages, or other factors will not match. With each mismatch, there is an associated Equation Selection Penalty.

The severity of the mismatch will depend on the particular situation. For example, if your Input Data File is from coastal Washington, but an equation is used from southeast Alaska, a slight geographic mismatch will occur. If the equation were from the **Rocky Mountains, however, the mismatch would be more severe.**

This section describes how BIOPAK chooses the "best" equation(s) for calculating the value of a component. These procedures are always used unless (1) all elements of a Request to Library were replaced by the Substitution Key of a reassignment statement (that is, all elements of the Original Equation Request were replaced), or (2) a Local Equation Number is specified in a Request to Library. In the former instance, BIOPAK uses the first library equation it encounters that exactly matches the Request to Library (see *Appendix: Selecting Equations and Summations: table* **5). An error results if such an equation is not found.**

Equation Selection Penalty (ESP) calcula

It is assumed for purposes of the following discussion that no reassignments were made, so that the Requests to Library are the same as Original Equation Requests. When a Request to Library is made, BIOPAK will try to choose the "best" equation by selecting the equation with the lowest ESP within the constraints discussed in *Appendix: Equation Selection Penalties:* **Maximum,** *Threshold and Summation ESP Levels.*

The ESP is greater than zero when one or more characteristics of the Candidate Equation in the Equation List do not exactly match the Request to Library (see *Appendix: Selecting Equations and Summations:* table 5). Six sources that can contribute to the ESP of a Candidate Equation are described in the next six sections: *Geographic area, Serall stage, Extrapolation, Coppice lifeform substitution, Substitution of BAT for BFT,* and *Equation list search failure.* The ESP for a Candidate Equation is the sum of the ESP values from these six sources. The values assigned to each of the sources contributing to the total ESP can be modified by you as described in *Appendix: Customizing BIOPAK.*

Geographic Area--

The ESP increases as the difference in climate between the geographic area in the Request to Library and the geographic area for the Candidate Equation increases. This method assumes a direct relations between geographic area, climate, and plant growth form.

Seral Stage--

Greater differences in seral stage between the Request to Library and the equation have greater ESPs. Seral stages are based primarily on the form of trees in the sampled community.

Extrapolation--

The range(s) of the independent or prediction variable(s) (for example, DBH) of the plants measured to build an equation can be found in the Library for most equations. An overextrapolation occurs when one or more of the parameters in the Request is greater than the largest value of the plants used to build the equation. An underextrapolation occurs when one or more of the parameters in the request is less than the smallest value of the plants used to build the equation. Overextrapolation has a greater ESP because it can potentially lead to greater errors than underextrapolation. If the range of the dependent variable is not stored in the Library, a different ESP penalty is assigned (PARAMETER RANGE UNKNOWN). When any of these three conditions occurs, a warning message appears in the individual plant report.

Coppice lifeform substitution--

A plant has a coppice lifeform if it is a stump sprout; such plants can be only trees or shrubs. The coppice lifeform is recognized because stump sprouts often have a different growth form than plants grown from seed. When coppice lifeform is in the Request, BIOPAK also considers Candidate Equations with the taxonomic lifeform for that species in the Equation Library.

Substituting BAT for EFT--

For lifeforms other than trees, shrubs, and coppice, total biomass of foliage (BFT) may be identical to, or a reasonable estimate of, total aboveground biomass (BAT). BIOPAK will consider this alternative: For herbs, grasses, and sedges, an ESP of 5,000 is imposed when a BAT equation is used to calculate BFT. For bryophytes and lichens, no penalty is added under these circumstances.

Equation list search failure--

The No Value Calculated ESP occurs when no value can be calculated because no equation exists for that species in the Equation List File, or because a parameter needed for the equation is not included in the input record. For the files shipped with BIOPAK, this ESP value has been set at 80,000.

ESP calculation for summations-

In general, the ESP assigned to summations of several equations is set equal to the greatest ESP among the individual equations. Note, however, that the ESPs of certain components are reduced by prescribed weighting factors because they are less critical to the accuracy of the sum (weighted ESP = ESP*weight). These components and their weighting factors are given in figures 2-4. The ESP weighting occurs whether the summation is specified by equation reassignment or is chosen by BIOPAK.

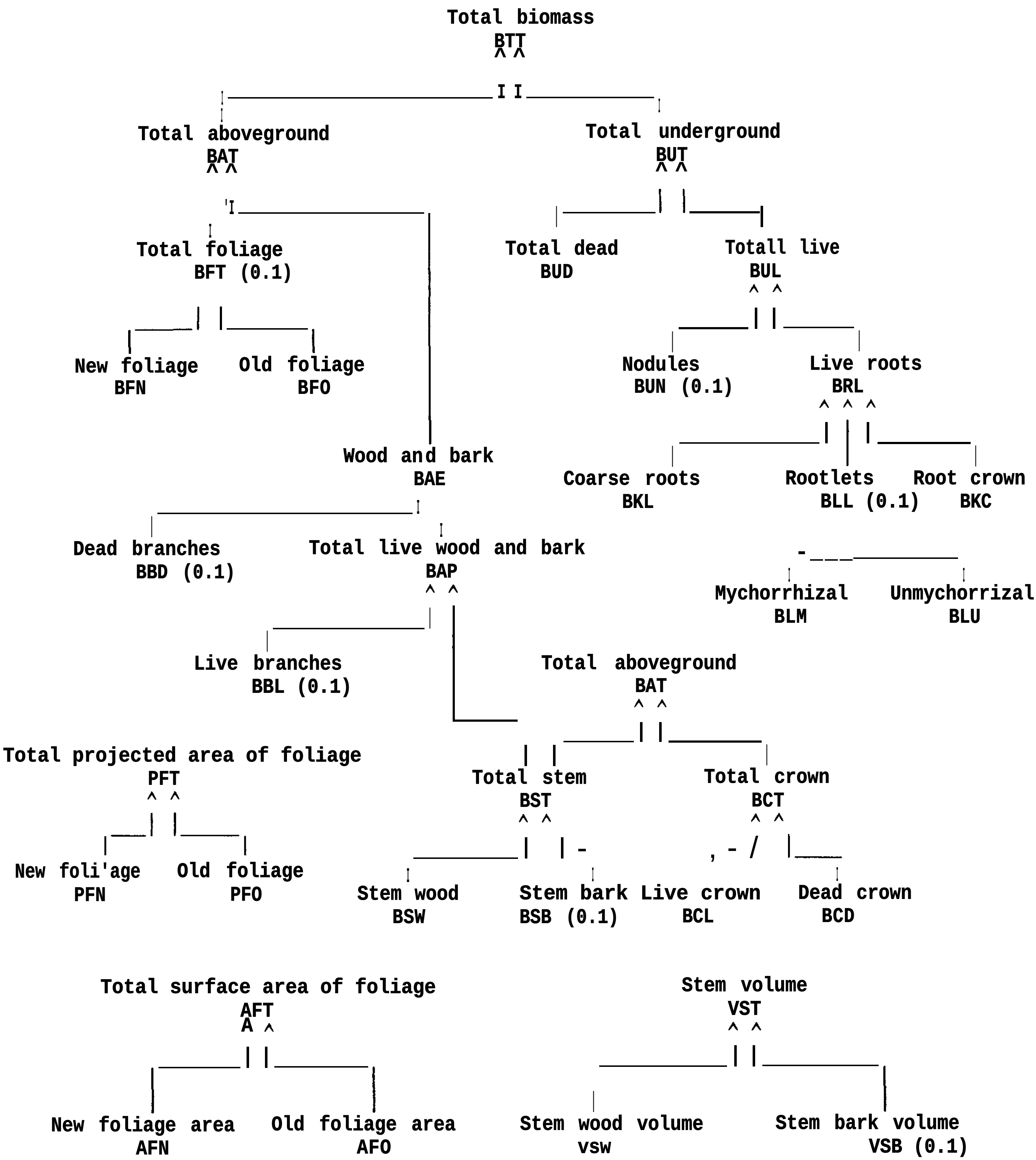


Figure 2--Default summations for tree, shrub, and coppice lifeforms.

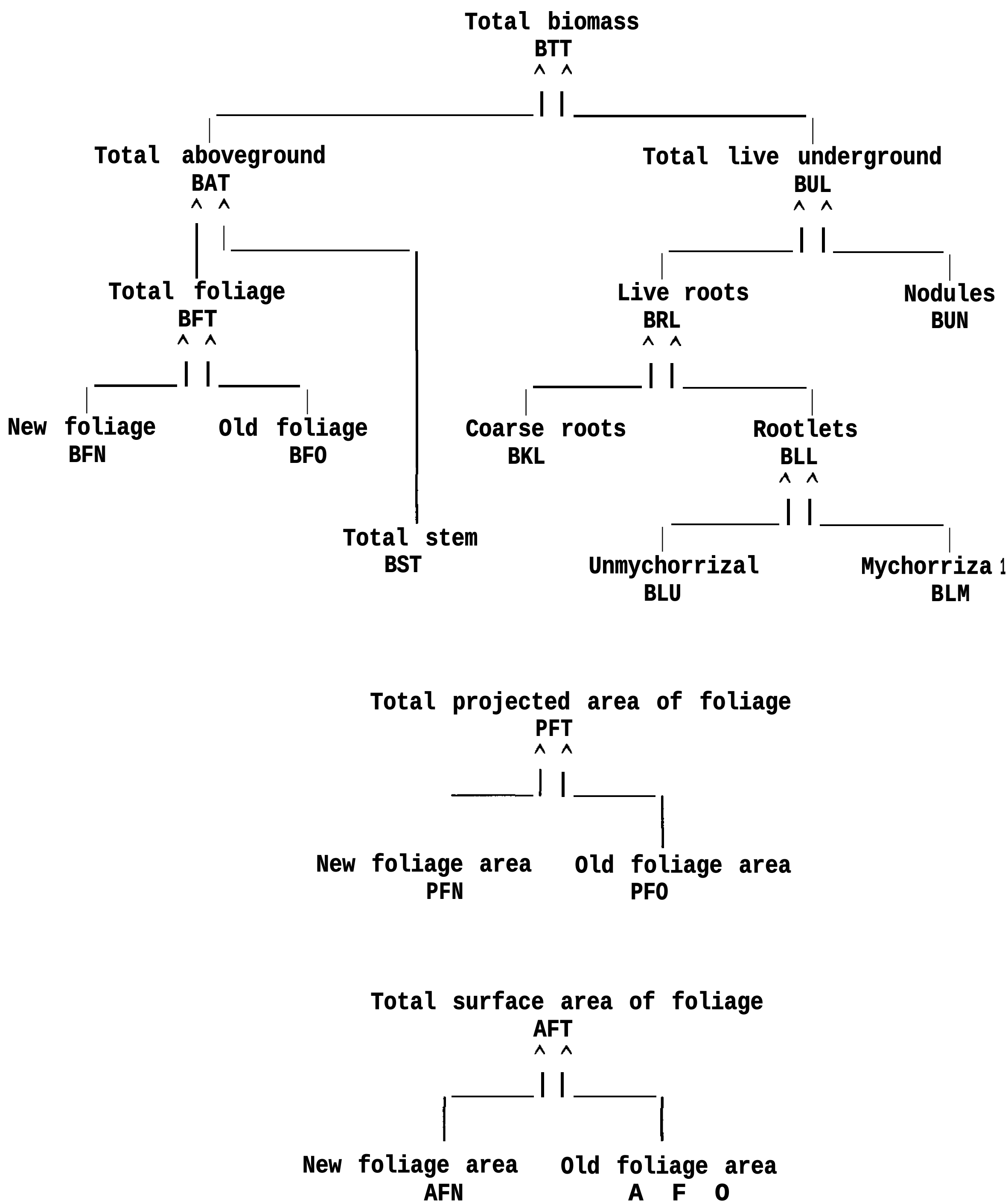


Figure 3--Default summations for herb, grass, and sedge lifeforms.

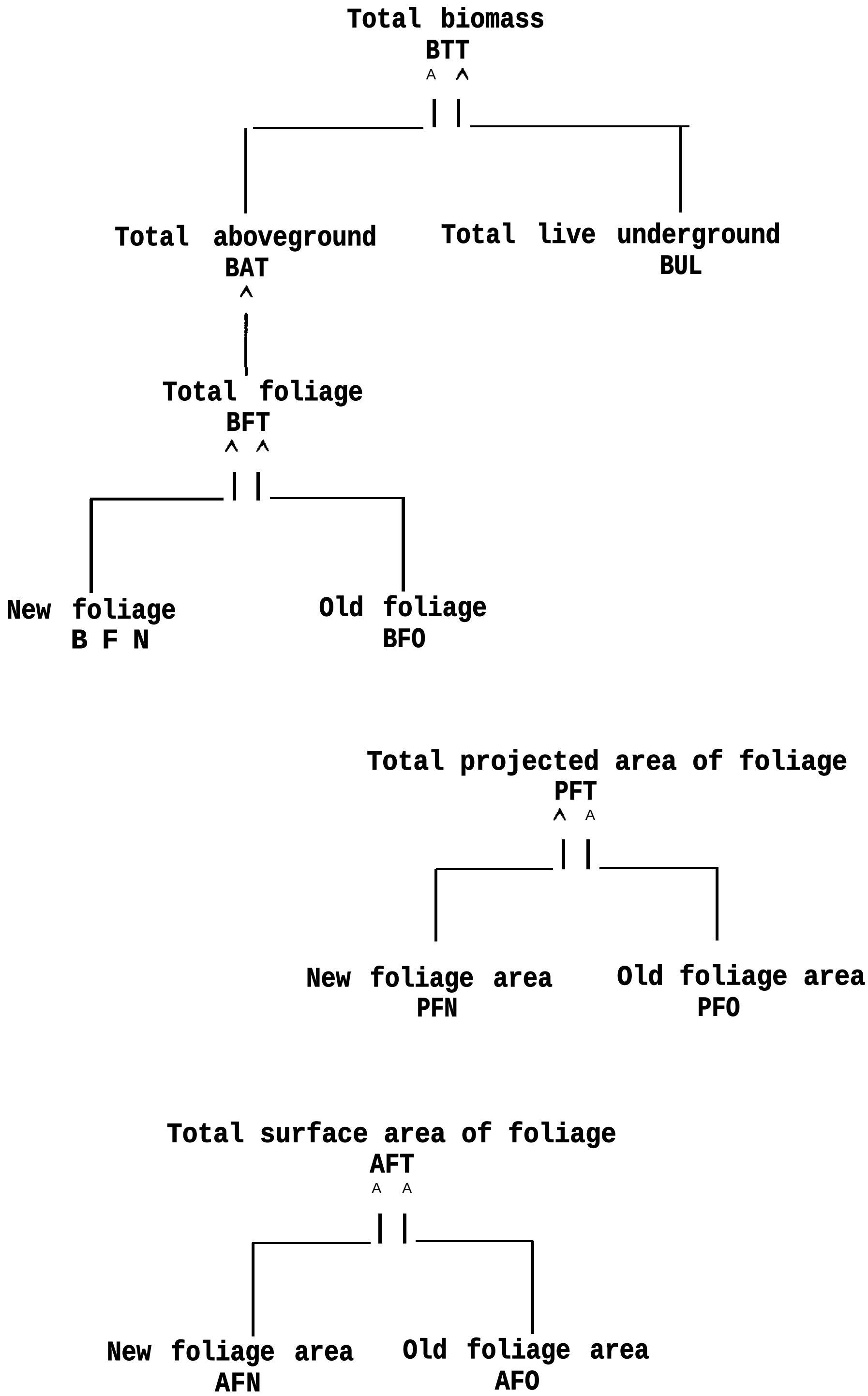


Figure 4--Default summations for bryophyte (moss) and lichen lifeforms.

Maximum, Threshold and Summation ESP Levels

These levels control the maximum acceptable ESP level (Maximum ESP), the ESP level below which the search for a lower ESP is discontinued (Threshold ESP), and the ESP level at which summation will be attempted (Summation ESP). You set these levels when Designing a Run. These values influence execution time and affect equation selection. The maximum allowable values for the three ESPs, can be modified by the user as described in *Appendix: Customizing BIOPAK.*

Maximum ESP Level--

It determines the poorest acceptable equation match allowed by the user. More specifically, it determines the poorest acceptable match between the Request to Library and the equation used to calculate a component value. BIOPAK does not allow this level to be set higher than the No Value Calculated ESP (80,000 as supplied with BIOPAK). A component value will not be calculated if the best ESP of the Candidate Equations (or summations) exceeds the Maximum ESP Level.

The Maximum ESP Level can range in value from 1 to 79,999. For example, if you assign a Maximum ESP Level of 70,000, then any equation with an ESP value greater than 70,000 will not be considered for calculation. If the chosen Maximum ESP Level is low, BIOPAK will be more selective in choosing Candidate Equations than if a higher ESP is given. If the Maximum ESP Level is not specified, the program will not be able to select any equations.

Threshold ESP Level--

This level determines when the ESP of a Candidate Equation is low enough that the search for an equation with a lower ESP can be discontinued. The Threshold ESP Level can range in value from 0 to 79,999. BIOPAK will end its equation search when it finds the first equation that is lower than, or meets, the Threshold ESP value.

A high Threshold ESP Level results in faster execution but can cause selection of less appropriate equations. A low Threshold ESP Level lengthens execution time, but may allow more appropriate equations to be selected.

The following diagram shows how BIOPAK selects equations based on user-assigned Maximum ESP and Threshold ESP Levels. For example, if a value of 70,000 were assigned to the Maximum ESP Level and a value of 5,000 to the Threshold ESP Level, BIOPAK would continue to search for equations until it found the first equation with an ESP less than 5,000. No equation with an ESP greater than 70,000 would be considered. In this example, BIOPAK began by finding.five Candidate Equations (El-E5 in succession) with an ESP value less than 70,000. Equations El-E5 also had higher ESP values than the assigned Threshold ESP, so BIOPAK continued its search. When BIOPAK found the next Candidate Equation (E6) with an ESP value below 5,000, it stopped searching.

Had BIOPAK been allowed to continue searching, an equation with an even better ESP value (equation E7) might have been found. This is the possible consequence of selecting a Threshold ESP Level greater than zero (that is, the best equation may not be selected). On the other hand, if equations E6 and E7 did not exist, thereby making it impossible for BIOPAK to find an equation with an ESP value less than 5,000, equation E3, the Candidate Equation with the best (lowest) ESP value, would have been selected.

```
    79,999 - |
             |
             |------------------ 70,000 Maximum ESP Level
             |
             |<----- E6
             |
Equation     |
Selection    |<----- E2
Penalty      |<----- E1
             |
             |<---- E4
             |
             |<---- E3
             |
             |------------------ 5,000 Threshold ESP Level
           * |<----- E6
             |
             |<----m E7
       0 -   |
```

An assigned Threshold ESP Level of zero will allow for selection of the best equations, and it is strongly recommended that a value of zero be assigned whenever possible. Those users with large Input Data Files or slower computers, however, may want to raise the Threshold ESP Level above zero to speed calculations.

Summation ESP Level--

The Summation ESP Level does not apply to summations specified by an equation reassignment statement. The steps BIOPAK uses to select summations are described in *Appendix: Selecting Equations and Summations: Biopak Selects.* The summation or single equation with the lowest ESP is used to estimate the plant component.

The Summation ESP value can be best explained by referring to the following diagram. Suppose BIOPAK is performing the routine task of searching for the most appropriate equation for a given plant component based on Maximum, Threshold, and Summation ESP Levels. If it finds no single equation in the Equation Library (in this case, equations El-E3) with a lower ESP value than the Summation ESP Level, then BIOPAK will begin to consider Default Summations to sum for the desired plant component. (See figures 2-4)

```
                     79,999 - |
                              |
                              | ----------------- 70,000 Maximum ESP Level
                              |
                              | <----- S1
                              |
   Equation                   |
   Selection                  | <----- E2
   Penalty                    | <----- E1
                              | <----- E3
                              | ----------------- 15,000 Summation ESP Level
                              | <----- S2
                              |
                              | <----- S4
                              |
                              | -----------------   5,000 Threshold ESP Level
                         *    | <-----S3
                              |
                              |
                              |
                         0 -  |
```

When the first summation of equations is found that has an ESP value less than the Threshold ESP Level (in this example, summation S3), then BIOPAK will immediately end its search and accept this summation as the best method of calculating a particular plant component. If no equation summation is found that has an ESP value less than the Threshold ESP Level (that is, S3 does not exist), then the summation with the lowest ESP is selected (in this example, summation S4).

Summation ESP values are calculated by multiplying the ESP of individual equations used in a summation by their weighted value (see figures 2-4). The highest resulting ESP value will be used as the ESP for the entire summation. For example, summation for the component BAT for trees, shrubs, and coppice lifeforms (see fig. 2) might be calculated by summing the equation results for BFT, BBD, BBL, and BST. So, calculation of the ESP value of the summation would look like this:

Plant component	Weight	ESP	(Weight) X (ESP)
BFT	0.10	4000	400
BBD	0.01	200	2
BBL	0.10	400	40
BST	1.00	500	500

Thus, the summation ESP would be 500.

Setting levels

In the Default Settinqs Window of Design a Run, enter ESP levels based on the contributions of individual sources to the total Equation Selection Penalty that you will accept. *Getting Started: Suggestions for Using BIOPAK* **discusses setting these levels. As discussed above, ESP for a Candidate Equation is the sum of the contributions to ESP from the individual sources. A Maximum ESP Level of 212, for example, would allow relatively minor mismatches between Seral Stage codes in conjunction with relatively minor mismatches between Geographic Area codes. It would not allow extrapolation. A Maximum ESP Level of 21000, in contrast, would allow any mismatch between Geographic Area codes, Seral Stage codes, or overextrapolation and underextrapolation. It would not, however, allow some combinations of mismatches; for example, no mismatch could occur in combination with overextrapolation.**

Changing contributions to the Equation Selection Penalty

The contributions to ESP given in *Appendix: Customizing BIOPAK: BIOCODES File* **were chosen so that normally less significant mismatches between the equation used and the request are assigned a lower ESP than mismatches considered to be generally more serious. They are specific to the Pacific Northwest region and may not be appropriate for data obtained from other locales. These values can be changed as described in** *Appendix: Customizing BIOPAK: BIOCODES File.*

Files

You need to keep track of many files. One is provided by you, some are used by BIOPAK and can be modified by you, and others are produced during a run. This appendix describes only files the user needs to keep track of. See also *Installation: Files shipped with BIOPAK* **and** *Installation: Files in the BIOPAK directory* **for lists of files corresponding to these titles.**

User files

Input Data File--

The file containing the data used for executing the component calculations. This file must be in ASCII format. *See Reference: Input Data File* **for a more detailed description.**

Run Design files

Run Design File (.RD)--*

This file is a product of Design a Run. The Run Design File is given the extension .RD. The file contains default settings, the format of the input data records, the plant components to be calculated, and any equation reassignments.

Run Design Report (.RDR)--*

This report is a flat ASCII file that documents the Run Design File contents. It can be produced by selecting "run Design report" from the File Menu of Design a Run. The report will be given an .RDR extension.

Equation Library files

The Equation Library consists of the database file and its associated memo file. The database file supplied with BIOPAK (BIOLIB.DBF) may be retrieved and then, along with the memo file (BIOLIB.FPT), browsed and edited. The two other files listed below can be produced from the Library. A new Library also may be created by the user.

Equation Database fife (.DBF)--*

This is the Equation Library. This file (*.DBF) can be created, browsed, searched, sorted, and modified.

Equation Database memo file (.FPT)--*

This contains the text in the Sources of Data Window for each equation. Each record is linked directly with the coresponding record in the Equation Database file and can be modified whenever that file is modified.

Equation List file (/EQN)--*

This is created by the Library Editor and used in calculations. This file can be created by saving the Equation Library as an Equation list file--under the File Menu of the Equation Library Editor (the Library must first be saved as a Database file).

Equation documentation text fife (.TXT)--*

A text file containing all the documentation (from the editing windows) for the equations in the Library. It can be very long.

Program files

There are several files read by the program that you can also modify or produce.

Intermediate Binary File (.IBF)--*

A binary file used for generating reports. It is produced when Calculate Plant Components is executed, during which time the file can be named.

BIOCODES File--

BIOCODES is a flat ASCII file containing all the valid codes for components, geographic area, and seral stage, the component units, as well as the Equation Selection Penalty values. The file can be modified by you. *See Appendix: Customizing BIOPAK: BIOCODES File* for more details about this file.

BIOSUMM File--

BIOSUMM is a flat ASCII file containing the default summation trees to be used by BIOPAK. This file can be modified. *See Appendix: Customizing BIOPAK: BIOSUMM File* for more details about this file.

Reports

Reports can be produced during a run, if requested. The reports are described in more detail in *Reference: Reports and Other Output.*

Reports for People (.RPT)--*

This report, which may include an Individual Plant Report, Plot Summary Report, and Stand Summary Report, can be requested when Generate Reports is selected from the Main Menu.

Machine Readable Reports--

individual Plant Report (.lND)--*

This report lists all input parameters (predictor variables) and calculated components for each individual plant (input record).

*Plot Summarv Report (*PLT) --*

This report gives all input parameters and the per-hectare values (or per acre) for components by species and by vegetation strata for each plot within each stand.

Stand Summarv Report (.STA)--*

This report gives averages and standard errors of all input parameters and the values per-hectare (or per acre) for each component by spec ies and vegetat ion strata over all plots within each stand.

Diagnostic Reports--

Summarized Eaua tion Use RePort (.USE)--*

This report presents a summary of the equations used for calculations. It lists all combinations of Original Equation Request, Request(s) to Library, Equation(s) Actually Used and the number of times each combination was used during calculations.

Detailed Eauation Use Report (.DET)--*

This report lists individually, for every component of every plant (input record) within the specified strata, the Original Equation Request, the Request(s) to Library, the Equation(s) Actually Used, and the Equation Selection Penalty for the equation (or summation) used.

Error Report (.ERR)--*

This report lists codes for the two most serious errors and warnings detected by BIOPAK during selection of an equation or group of summed equations and computation of a component value.

Lifeform

Section

BIOPAK must associate a Lifeform code with each input record. Without a Lifeform code, calculations cannot be executed. Lifeform codes affect the matching of Equation Reassignments to input records, equation selection, the plant components calculated, and the community stratum within which output is listed in reports. *See Appendix: Codes* for valid Lifeform codes.

substitutions

Ideally, Lifeform comes in from the Input Data File. If the lifeform is not included in the Input Data File, or is missing from a given record, BIOPAK will try to substitute a lifeform. The desired lifeform will be used in the Original Equation Request if these guidelines are followed:

1. If possible, include Lifeform codes for each record in your Input Data File. A list of valid Lifeform codes can be found in *Appendix: Codes.*

2. If lifeform is a variable in your dataset, but is missing in some cases, do this for each species with missing lifeform data:
   a. Include the species code (but no lifeform code) in the Criteria and Substitution sections of the Reassignments Add/Modify Window, and
   b. Add the desired lifeform as the Primary Lifeform Default.
   For each record with missing lifeform data, BIOPAK will substitute the Primary Lifeform Default.

3. If lifeform is not included in your dataset for each species:
   a. Include the Species code in the Criteria and Substitution sections of the Reassignments Add/Modify Window, and
   b. Add the desired lifeform in the Substitution section.

For each species, BIOPAK will consider only equations with the requested lifeform.

BIOPAK Life form substitution procedures

In most cases, users will not need to be concerned with these procedures. They are included here to make the documentation complete.

These procedures are followed only if Lifeform is not included in the Data

Input Format or if Lifeform for the plant in the Input Data File is missing. They are followed sequentially until a suitable Lifeform code is found.

No Reassignment: Taxonomic Life form from Library--

If there is no Equation Reassignment for the combined Species-Geographic Area-Seral Stage key of the input record, one of two things occurs: (1) BIOPAK wi 11 substitute the Taxonomic Lifeform code assigned to this species in the Equataion Library (.EQN file); or (2) if the species is not in the library, the input record cannot be processed, and an error code is reported.

Reassignment without Criteria Life form: Primary Life form Default, Taxonomic Life form, or from Substituted Species--

If there is a set of (one or more) Equation Reassignment criteria that matches the Original Equation Request, BIOPAK will look for one of these reassignment criteria with a blank lifeform. If found, and if a primary lifeform default is included in this reassignment, this primary lifeform default is used for the lifeform in the Original Equation Request. If the primary lifeform default is blank, BIOPAK will try to substitute the Taxonomic ifeform code assigned to this species in the equation library. If the species is not included in the library, then the Lifeform code specified in the Substitution Key of the reassignment will be used. If this code is blank, then the Taxonomic Lifeform code present in the library for the species of the Substitution Key is used. If the latter species is not in the library, the input record cannot be processed, and an error code is reported.

Reassignment with Specified Life form: Taxonomic Life form, Criterion Lifeform--

If all of the Equation Reassignment criteria in the set of those matching the Species-Geographic Area-Seral Stage key of the input record have Lifeform codes, then all reassignments of the set are lifeform dependent. In this case, BIOPAK will try to substitute the Taxonomic Lifeform code assigned to the input species in the equation library. If the input species is not included in the library, and if there is only one matching Reassignment in the set, the lifeform of the criterion for that matching Reassignment is substituted. If the set includes more than one matching Reassignment, no presumption regarding lifeform can be made, the input record is not processed, and an error is reported.

Note: If the lifeform is specified in the input record, but an equation reassignment matching the input record is present in the Run Design File and the reassignment includes a primary lifeform default, the latter controls the Community Stratum assignment of the report output. It does not, however, substitute for the Lifeform code. This obscure condition allows you to force report values to be assigned to a stratum that does not match the Lifeform code used in equation selection.

Selecting Equations and Summations

Section

BIOPAK uses built-in rules when selecting an equation from the Equation List File as described in *Appendix: Selecting Equations and Summations: BIOPAK Selects.* **This is the default method for BIOPAK to use. Alternatively, you may control selection of the equation with an Equation Reassignment as described in** *Appendix: Selecting Equations and Summations: User Selects.*

One must understand the basic steps BIOPAK uses to process input data to understand how equations are selected. It may be helpful to refer to figure 1. BIOPAK processes the Input Data File one plant at a time. In the Components to Output Window of Design a Run, you specify the components to be calculated, and the community strata for each component. If the Lifeform of a given plant in your Input Data File falls within the community strata you specified (see *Appendix: Codes* **for a list of** *Lifeform* **codes and strata designation), that plant component will be calculated for that plant. The calculations are processed as follows (see fig. 5):**

1. **An Original Equation Request is constructed by using data from the Input Data File and the Run Design File.**
2. **The Original Equation Request is compared with the Reassignment Criteria you listed (in the equation <u>Reassignments Add/Modify Window</u> of Design a Run). If the Criteria match the Original Equation Request, the information listed in the Substitution Key is substituted. A Request to Library is produced, which includes the substituted information. In this instance, the Request to Library differs from the Original Equation Request.**
3. **The Equation List File is searched and the "best" equation (if any can be found) is used to compute the user-specified plant component.**

The Original Equation Request is constructed with the elements shown in table 3. Species code and the values(s) of the parameter(s) must come from the Input Data File. Usually, BIOPAK supplies the Lifeform code for the particular species from the Equation List File (from the "TL" column--Taxonomic Lifeform) or an Equation Reassignment, as described in *Appendix: Lifeform,* **and you need not be concerned about this. Alternatively, the Lifeform code may come from the Input Data File. The Geographic Area code and Seral Stage code may be read from the data, or the Default Settings in the Run Design File may be used. The Plant Component code comes from the Run Design File (Components to Output). This process is shown diagramatically in figure 5.**

Table 3--Elements in the Original Equation Request, that is, before Equation Reassignment, if any

Element	Possible sources"
Species code	I
Lifeform code	R, L, I
Plant Component code	C
Geographic Area code	I, D
Seral Stage code	I, D
Parameter 1 code[b]	F
Parameter 1 value[b]	I
Parameter 2 code[b]	F
Parameter 2 value[b]	I
Parameter 3 code[b]	F
Parameter 3 value[b]	I

[a] I = Input Data File, R = Reassignment, L = Library, C = Components to Output Window, D = Default Settinos Window, F = Data Input Format Window. The windows rentioned are described in Design a Run.
One to 3 parameters may be present.

If no Equation Reassignments are specified, or if no match between the Original Equation Request and a Reassignment is found, BIOPAK produces a Request to Library that is identical to the Original Equation Request and processes it as described in *BIOPAK Selects Equations and Summations.* Otherwise BIOPAK modifies the codes in the Original Equation Request, according to the Substitution Keys in Equation Reassignments, to produce a Request to Library, and processes it as described in *User Selects Equations and Summations.*

```
Input Data File             )
   Species Code             )
   Parameter values         )
   (Geographic Area code)   )----------------------------------+
   (Seral Stage code)                                          |
   (Lifeform code)          )                                  |
                                                               |
Run Design File          )                                     |
 Plant Component code )                                        |
 Default settings:    )-----------------------------+          |
   Geographic Area code )                           |          |
   Seral Stage code    )                            |          |
                                                    |          |
Lifeform Substitution )--------------------------   |          |
   Lifeform Code       |                       |    |          |
                                               |    |          |
                                        ORIGINAL EQUATION REQUEST
Matching Reassignment Criteria?                          |
   |            |                                        |
   No           Yes                                      |
   |            |                                        |
   |            Substitutions in  )                      |
   |            the Reassignment  )---------------       |
   |            change the Original )                    |
   |            Equation Request. )               |      |
   |                                        REQUEST TO LIBRARY
   No change made in
   Original Equation Request.                     |
                                                  |
                                             Choose from
                                          EQUATION LIST FILE
```

Figure 5--Flow of information in the Equation Reassignment process and selection of an equation from the Equation List File. Elements in the Original Equation Request are shown under their common sources.

BIOPAK selects Equations and Summations

To satisfy a Request to Library, BIOPAK may:

Select a single equation from the Equation List File,

2 Select a group of equations and sum the calculated components from each equation in the group to produce the needed plant component estimate,

3. Or determine that no suitable equation can be found and give an error code in reports.

BIOPAK will scan the Equation List File looking for Candidate Equations. To be considered for selection by BIOPAK, a Candidate Equation must be of the same species and lifeform, and the equations must use the same parameters, which are found in the Input Data File record. BIOPAK will consider using equations with different Geographic Area codes and Seral Stage codes than those in the Request to Library. For each input record, the Request to Library will be compared to the Candidate Equations, and the best equation will be selected.

Often, there will not be an equation available for a requested plant component, yet equations may exist for several other components whose results can be

summed to give an acceptable estimate. The summations that BIOPAK may select on its own are called Default Summations and are displayed as Summation Trees in figures 2 through 4. These are different for different lifeforms. The value of each 'parent' component can be calculated by summing values of the components immediately below. Any component needed for this summation, but for which an equation is not available, can in turn be calculated by summing the components below it. In this way, BIOPAK may consider summing two, three, or more components. For example, for a tree, BAT (total aboveground biomass) could be calculated as BFT t BAE, BFT t BBD t BAP, BFT t BBD t BBL t BST, or BFN t BFO t BBD t BBL t BSW t BSB.

Choosing the equation used--

As described above, several single equations and several summations may be Candidate Equation(s) to calculate the plant component. BIOPAK uses the Candidate Equation(s) with the lowest (best) Equation Selection Penalty (ESP). An ESP is calculated for each Candidate Equation. The ESP is lower when the Candidate Equation matches the Request to Library closely and is higher when the match is poor. Mismatches in Geographic Area code and Seral Stage code, overextrapolation and underextrapolation and other factors are considered in calculating the ESP, as described in *Appendix: Equation Selection Penalties.* **In fisures 2 throush 4, the numbers in parentheses next to the components are used to weight the ESPs associated wi th'individual components of a'summation. The ESP for the overall summation is the largest, weighted ESP among the components that are summed, as descri bed in** *Appendix: Equation Selection Penalties.*

Three ESP levels limit the Candidate Equation(s) BIOPAK will consider. These are described fully in *Appendix: Equation Selection Penalties: Maximum, Threshold, and Summation ESP Levels* **and briefly here. BIOPAK will not consider a Candidate Equation with an ESP greater than the Maximum ESP Level. BIOPAK will stop searching for other Candidate Equations when it has found one with an ESP less than the Threshold ESP Level. BIOPAK will not search for Candidate Equations that are Default Summations if it finds a single Candidate Equation with an ESP less than the Summation ESP Level. The Maximum ESP Level allows you to limit the extent of mismatches. The Threshold ESP Level and Summation ESP Level allow you to manage the tradeoff between less execution time and better Candidate Equations.**

BIOPAK selects equations for each requested component independently. Therefore, values for different components of the same plant or of the Candidate Equations in a summation, for example, may be calculated by using equations with different Geographic Area codes or Seral Stage codes.

EXAMPLE: This example illustrates the equation selection process when BIOPAK selects the equations to be used in calculations. The illustration considers one line of data from the Input Data File. In this example, the user selected total aboveground biomass (BAT) as a component to be calculated. In the Data Input Format Window of Design a Run, the user defined two variables in the data file: tree diameter at breast height (DBH) and height of the tree (HT). From the Input Data File, BIOPAK read the Species code and the values for the variables DBH and.HT. The Input Data File did not include codes for Lifeform, Geographic Area, or Seral Stage; the user selected the default Geographic Area and Seral Stage codes in the Default Settings Window, and BIOPAK included the Taxonomic Lifeform code found in the Equation Library for the equation it selected.

Line of Input Data File:	Information from Run Design File:	
NFGYBLNF 1 9 ABAM 116 6320	Default Settings:	W, 0
Used: ABAM 116 6320	Data Input Format:	DBH, HT
	Components to Output:	BAT

Original Equation Request: ABAM _ BAT W 0 _ DBH 116.0 HT 6320

Request to Library: ABAM _ BAT W 0 _ DBH 116.0 HT 6320

Equations Used: ABAM T BFT G M 1
ABAM T BSB W G 1
ABAM T BSW W 0 2
ABAM T BBL G 0 1

In this example, BIOPAK did not find an equation for the BAT of Pacific silver fir (ABAM) in old-growth forests (0), on the west side of the Cascades (W). Instead, it summed four components for ABAM: total foliar biomass (BFT), biomass of stem bark (BSB), biomass of stem wood (BSW), and biomass of live branches (BBL). The components, which were summed to estimate BAT, were not complete; for example, there was no equation in .the Library for dead branch biomass (BBD) of ABAM. There may have been an equation for BBD of a related species, but BIOPAK will not substitute a different species. The numbers following the Geographic Area and Seral Stage codes are the local equation numbers for the equations selected.

Notice that BIOPAK selected some equations with different Geographic Areas and Seral Stages; for example, an equation for the BFT of a general Geographic Area (G) and a mature stand (M) was selected rather than the specified defaults (W and 0). This sort of substitution is usually acceptable. BIOPAK substitutions can be controlled by the user in two ways, however: (1) by setting the ESP levels so substitution would not occur *(see Appendix: Maximum, Threshold and Summation ESP Levels),* or (2) by specifying the Substitution(s) in an Equation Reassignment.

BIOPAK will make substitutions for plant components (through summation), Geographic Area and Seral Stage to carry out calculations. It will never select equations for a different species or lifeform (unless specified by the user in Equation Reassignments).

User selects Equations and Summations

Reassigning Equations--

One of the most useful features of BIOPAK is that it allows you to control selection of the equation used for calculating a plant component. This is done with an Equation Reassignment. In this section, we describe how BIOPAK processes data when the Original Equation Request is changed by an Equation Reassignment. The windows used for making Equation Reassignments are described in *Reference: Design a Run.*

Now we describe the steps BIOPAK uses to process data from the Input Data File when you have created one or more Equation Reassignment(s). Later we use examples to illustrate the process. This explanation picks up after the Original Equation Request has been produced. Figure 5 illustrates the flow of information in the Equation Reassignment process.

There are two parts to every Equation Reassignment: the Reassignment Criteria and the Substitution Keys(s) (table 4). The user requests a summation by including all the components to be summed in the Substitution section (bottom half of the Reassignment Add/Modify Window) of Reassignments. In other words, specify a Substitution Key for each component to be included in the summation.

Table 4--Information that may be in an Equation Reassignment[a]

Elements in Reassignment Criteria	Elements in Substitution Key (may be repeated 9 times)
Species code (not optional)	Species code (not optional)
Lifeform code	Lifeform code
Component code	Component code
Geographic Area code	Geographic Area code
Seral Stage code	Seral Stage code
	Local Equation number
Parameter 1 code[b]	
Parameter 1 lower bound[b]	
Parameter 1 upper bound[b]	
Parameter 2 code[b]	
Parameter 2 lower bound[b]	
Parameter 2 upper bound[b]	
Parameter 3 code[b]	
Parameter 3 lower bound[b]	
Parameter 3 upper bound[b]	

[a] There are two parts to every Equation Reassignment: the reassignment Criteria and the Substitution Keys(s). The user requests a summation by specifying Substitution Keys for each component to be summed.
[b] One to 3 parameters may be present. They may be in any order.

For each Original Equation Request, a binary search is made of the Equation Reassignments for a match between the Original Equation Request and Reassignment Criteria. The first match found, if any, is used. A match occurs when each element in the Original Equation Request (see table 3) matches the corresponding element in the Reassignment Criteria. Most elements match if their values are the same or the Reassignment Criteria element is blank. Parameters, a special case, match if the Parameter codes are the same and the parameter values from the Original Equation Request are within the ranges in the Reassignment Criteria List. If the Original Equation Request and the Reassignment Criteria do not match, then the Equation Reassignment is not used, and processing occurs as described in *BIOPAK Selects Equations and Summations.*

When the Reassignment Criteria match the Original Equation Request, the Request to Library is made from the Original Equation Request and the Substitution Key(s). If an element in a Substitution Key is blank, the corresponding value from the Original Equation Request is used. If an element in a Substitution

Key is included, it is used. If there is more than one Substitution Key per Criteria, this process is done for each. Thus the Request to Library may be for a single equation or for a summation of several equations that will serve as an estimate of the requested plant component.

If the Request to Library is for a single equation, BIOPAK may consider Candidate Equations that are Default Summations. If you have specified a summation with more than one Substitution Key (more than one line of information in the Substitutions section of the Reassignments Add/Modify Window), then no Default Summation will be considered.

At this point, the Request to Library is processed as described in *BIOPAK Selects Equations and Summations,* with the following exception. Elements in the Request to Library that are set by the Substitution Key must exactly match those of a Candidate Equation for it to be considered. An Equation Selection Penalty (ESP) is determined for each Candidate Equation as described in *Appendix: Equation Selection Penalties.* The equation used for component calculations is the one with the lowest (best) ESP.

Occasionally, more than one equation in the Equation List can exactly match a Request to Library (table 5). Such equations are distinguished in the library by having different Local Equation Numbers. Including the Local Equation Number, along with a complete Substitution Key in an Equation Reassignment, assures the use of that specific equation--no other equation will be considered. A complete Substitution Key would have values assigned to every variable of the list.

If you do not take care in specifying the equation to be used, and more than one equation in the Equation List matches the Request to Library, then the equation with the lowest ESP will be selected. If the total ESPs are equal, then BIOPAK will select the first one it encounters with the lowest ESP.

Table 5--Information in the Request to Library[a]

Elements in Request to Library
Species code
Lifeform code
Component code
Geographic Area code
Seral Stage code
Local Equation number
Parameter 1 code[b]
Parameter 1 value[b]
Parameter 2 code[b]
Parameter 2 value[b]
Parameter 3 code[b]
Parameter 3 value[b]

[a] The first 6 variables (that is, the Substitution Key) will be repeated in a request for a summation. The local equation number can be used to distinguish Equations that have the same values for all 5 codes in the Substitution Key.
[b] One to 3 parameters may be present.

EXAMPLE 1: This example illustrates the equation selection process when the user selects the equations to be used in calculations. The illustration considers one line of data from the Input Data File. In this example, the user selected total aboveground biomass (BAT) as a component to be calculated. In the Data Input Format Window of Design a Run, the user defined two variables in the data file: tree diameter at breast height (DBH) and height of the tree (HT). From the Input Data File, BIOPAK read the Species code and the values for the variables DBH and HT. The Input Data File did not include codes for Lifeform, Geographic Area, or Seral Stage; the user selected the default Geographic Area and Seral Stage codes in Default Settings; and the Lifeform codes were specified by the user in Equation Reassignments.

For the purposes of this example, we will assume that there is not an equation for the BAT of Pacific silver fir (ABAM, *Abies amabilis*) in old-growth forests (0), in the west side of the Cascades (W). Instead, the user chose to sum five components: total foliar biomass (BFT), biomass of stem bark (BSB), biomass of stem wood (BSW), biomass of live branches (BBL), and the biomass of dead branches (BBD). Because there was not an equation in the Library for the BBD of ABAM, the user specified that an equation for the BBD of western hemlock (TSHE) be substituted. Notice that BIOPAK selected some equations with different geographic areas and seral stages; for example, an equation for the BFT of a general Geographic Area (G) and a mature stand (M) was selected rather than the specified defaults (W and 0). The numbers following the Geographic Area and Seral Stage codes are the local equation numbers of the equations selected.

```
Line of Input Data File:    Information from Run Design File:
NFGYBLNF 1 9 ABAM 116 6320 Default Settings:       W, O
Used:        ABAM 116 6320 Data Input Format:      DBH, HT
                           Components to Output:   BAT
____________________________________________________________________
                           ↓
Original Equation Request: ABAM _ BAT W 0 _ DBH 116.0 HT 6320

Reassignment Criteria:     ABAM _ BAT _ _ _ DBH 20-999

Substitution Keys:         ABAM T BFT _ _ _
                           ABAM T BSB _ _ _
                           ABAM T BSW _ _ _
                           ABAM T BBL _ _ _
                           TSHE T BBD _ _ _

Request to Library:        ABAM T BFT W 0 _ DBH 116.0 HT 6320
                           ABAM T BSB W 0 _ DBH 116.0 HT 6320
                           ABAM T BSW W 0 _ DBH 116.0 HT 6320
                           ABAM T BBL W 0 _ DBH 116.0 HT 6320
                           TSHE T BBD W 0 _ DBH 116.0 HT 6320

Equations Used:            ABAM T BFT G M 1
                           ABAM T BSB W G 1
                           ABAM T BSW W 0 2
                           ABAM T BBL G 0 1
                           TSHE T BBD W 0 1
```

EXAMPLE 2: This example illustrates the equation selection process when the

user selects a specific equation to be used in calculations. The following illustration considers one line of data from the Input Data File. In this example, the user selected total aboveground biomass (BAT) as a component to be calculated. In the Data Input Format Window of Design a Run, the user defined two variables in the data file: tree diameter at breast height (DBH) and height of the tree (HT). The Input Data File did not include codes for Lifeform, Geographic Area, or Seral Stage; the user selected the default Geographic Area and Seral Stage codes in Default Settings.

Line of Input Data File:		Information from Run Design File:	
NFGYBLNF 1 9	ABAM 13.2 820	Default Settings:	W, O
Used:	ABAM 13.2 820	Data Input Format:	DBH, HT
		Components to Output:	BAT

1

Original Equation Request: ABAM _ BAT W 0 _ DBH 13.2 HT 820

Reassignment Criteria: ABAM _ BAT _ _ _ DBH O-19.9

Substitution Key: ABPR T BAT _ M 2

Request to Librarv: ABPR T BAT W M 2 DBH 13.2 HT 820

Equation Used: ABPR T BAT W M 2

For this example, we will assume that there is not an equation for the BAT of Pacific silver fir (ABAM) in old-growth forests (0) in the west side of the Cascades (W). Instead, the user decided to substitute an equation for BAT of noble fir (ABPR, Abies procera), but only for trees with a DBH less than 19.9. There is a specific equation in the librarv for the BAT of noble fir mature stands (M) in the west side of the Cascades (W) with local equation number 2. Therefore, the user included the relevant Seral Stage code (M), and the local equation number (2), in the Substitution Key. In this case, the user has decided that substituting an equation for a mature stand instead of an old-growth stand would be acceptable for their research purposes.

Selecting Species--

By setting the "Select Only Reassigned Species" flag when you Design a Run (in the Default Settings Window), you can specify that only those input records whose species occur in at least one equation Reassignment Criteria be processed. All other species in the data file are ignored.

This allows you to specify, for example, that data for only one or a few tree species be processed. To do this you would create Reassignment(s) with the same species code in the criteria and substitution sections. No Equation Reassignments would occur, but only the particular species, would be flagged for processing.

Situations when Reassignments are recommended

1. Lifeform: When the Lifeform of the plant sampled is different from the Taxonomic Lifeform, as recorded in the Equation Library; AND Lifeform was not a variable in your Input Data File.

For example, when Lifeform is not specified in the dataset, if a plant sampled had a coppice Lifeform, and the Taxonomic Lifeform of the species is shrub, BIOPAK will use only shrub equations.

2. **Species:** When you want BIOPAK to use equations for a species other than the species you sampled.

For example, if there are no equations in the Library for a particular species in your Input Data File, BIOPAK can be instructed to substitute equations for a similar species. To do this, add the new species to the Substitution Key in Reassignments.

3. Geographic Area, Seral Stage: By default, BIOPAK will use equations from different geographic areas and seral stages, within the specified ESP constraints. To avoid this, specify the desired Geographic Area and Seral Stage in the Substitution Key of Reassignments. Only equations with the specified Geographic Area and Seral Stage will be used.

For example, assume there are many equations in the Library for a particular species in your Input Data File. After the first run, you notice that equations were used from a region and seral stage much different from those in your dataset The run can be repeated after specifying the geographic areas and seral stages which BIOPAK should use, by adding these to the Substitution Key in Reassignments.

4. Selects a specific equation: You may want BIOPAK to select a specific equation in the Library and may have identified an equation in the Library for BIOPAK to use for a particular calculation. By including the Substitution Key, and the Local Equation number, of the desired equation, BIOPAK will select the specific equation.

5. Reassign species by size: You may want the smaller plants of a particular species sampled to be reassigned in one way, and the larger ones in another way. There are several reasons you may want to do this; for example, there may be no equations for a tree species you sampled. You may decide to reassign the smaller diameter trees to a related shrub species, and the larger diameter trees to a related tree species. In another instance, there may be no equations for a specific herb species. You may want to reassign the less dense occurrences to one seral stage, and the denser occurrences to another seral stage.

6. To specify a summation: As described earlier in *User Selects Equations and Summations,* you can specify a summation. You can either do the minimum, and specify the components to be used, or be more precise and specify the exact equations to be used.

7. Cover as input parameter: For component calculations based on cover data, you should, when possible, select library equations based on a plot size equal to the plot size of the Input Data File to be used. See *Reference: Library Editor: Parameters* for more information on Cover as a parameter in the Library.

Troubleshooting

Section

Despite the best of intentions and preparation, you may have problems using BIOPAK. The problems may come in the form of warning or error messages, or you may have trouble just getting BIOPAK started. This section is intended to ease your troubles as much as possible.

Error messages

Because an error message can come from several sources (FoxPro, Fortran, Batch Files, and BIOPAK), the error messages have been listed alphabetically by location in BIOPAK.

Ins errors

Error: BIOPAK installation files not on current drive.
Reason: One or more files expected on the BIOPAK disk was not found.
Suggestion: Insert a complete BIOPAK installation disk and try again.

Error: Bad input drive. Only drives A:, B:, C:,D: are allowed.
Reason: The install program attempted to determine the drive with the instalation files but was unsuccessful because it was not one of these.
Suggestion: Install BIOPAK from the root directory of one of these drives.

??? Invalid drive letter for the BIOPAK directory. Try again.
Reason: Drives C: D: E: F: G: are the only drives allowed by the installation

batch programs for the location of the BIOPAK directory.
Suggestion: Type one of these letters. The colon is not needed.

??? Above file is not on this disk. This is not a complete Biopak Disk 1. Press Ctrl-Break to stop installation, or insert BIOPAK Disk and press any key to continue.
Reason: A critical BIOPAK file is missing from this diskette.
Suggestion: Insert a good BIOPAK diskette and press any key to continue.

??? Unable to decompress this file. If due to insufficient hard disk space in X:\Biopak, make more space on this disk, or find a disk with more space, then repeat installation. Be sure all files are erased from X:\BIOPAK before repeating installation.
Reason: Probably due to insufficient hard disk space. Possibly due to corrupted BIOPAK files.
Suggestion: Delete files to create more space or find a drive with more space, then reinstall BIOPAK *(See Installation* for the amount of space needed). If this does not work, then a BIOPAK file may be corrupted so try installing from the backup copy you made of the BIOPAK disk when it first arrived.

??? Invalid drive letter for temporary files. Try again.
Reason: Drives C: D: E: F: G: H: I: J: K: L: M: N: 0: P: Q: R: are the only drives allowed by the installation batch programs for the location of BIOPAK temporary files.
Suggestion: Type one of these letters. The colon is not needed.

Errors when starting BIOPAK

??? Not enough free space (2 Mbytes) on %Biotmp% to load Biopak. Delete some files, reinstall BIOPAK, or change the Biotmp environment variable in this BIOPAK.BAT file to point to a drive with sufficient space.
More free space will be required to do some tasks, for example, to work with large equation libraries like the one shipped with BIOPAK.

??? The BIOPAK directory %biodir% does not exist. It must be changed to specify the path on which the BIOPAK files reside before this batch file is run.
Suggestion: Reinstall BIOPAK or change the Biodir environment variable in BIOPAK.BAT to specify the path on which the BIOPAK files reside.

??? A critical file is missing from the BIOPAK directory (X:\biopak). Reinstall BIOPAK.
Suggestion: Follow the installation instructions to reinstall BIOPAK.

*** ERROR in SYSINFO.BIO. Delete SYSINFO.BIO in this directory and restart BIOPAK.

Design a Run warnings and error messages

In general, a warning will allow continuation of the program. An error message indicates more serious problems and will not allow saving of the Run Design File, or subsection, without further action by the user. If messages in red boxes are encountered *see Appendix: Troubleshooting, Strange and unusual behavior and red error boxes.*

Default Settings section--

Error: Blank ESP values are not allowed.
Reason: Values for one or more ESP Levels are blank in the Default Settings Window.
Suggestion: Go back and fill in values for all three ESP Levels

Error: Invalid Seral Stage. Use FlO for list.
Reason: Seral Stage code was entered that does not conform to the valid BIOPAK seral stage codes specified in the BIOCODES File.
Suggestion: Enter a valid code. Press <F10> and select from list. To add new seral stage codes to the list of valid codes, refer to *Appendix: Customizing BIOPAK.*

Error: Invalid Geographic Area. Use F10 for list.
Reason: Geographic Area code was entered that does not conform to the valid Geographic Area codes as specified in the BIOCODES file.
Suggestion: Enter a valid code. Press <F10> and select from list. To add new Geographic Area codes to the list of valid codes, refer to *Appendix: Customizing BIOPAK.*

Error: Invalid units. Use F10 for list.
Reason: Units were entered that do not conform to the valid BIOPAK units.
Suggestion: Enter valid units. Press <FlO> and select from list, or refer to *Appendix: Units* **for a list of valid units.**

Error: No Units entered for Plot Area. Exit canceled.
Suggestion: Enter units. Press <FlO> and select from list, or refer to *Appendix: Units* **for a list of valid units.**

Error: No Units entered for Plot Slope. Exit canceled.
Suggestion: Enter units. Press <F10> and select from list, or refer to *Appendix: Units* **for a list of valid units.**

Error: Units entered without Plot/Prism Area default. Exit canceled.
Reason: Units were entered without entering values for plot size.
Suggestion: Go back and enter values, or delete units.

Error: Use either Plot or Prism Area, not both. Exit canceled.
Reason: BIOPAK cannot accept both Fixed Plot Area AND Prism Basal Area Factor defaults. Because these defaults are used, if the plot area is not present in the Input Data File, there would be no way of determining which plot size default to use.
Suggestion: Go back and delete one of the plot size specifications, or add plot size to the dataset.

Valid range ? to ?????.
Reason: Value entered is notwithin the valid range noted.
Suggestion: Enter a value that falls within the allowable range noted.

Data Input Format section--

Error: Number of decimals places exceeds. Len.
Reason: Number of decimal places cannot exceed the total length of the data field.

Suggestion: Correct the specification so that number of decimal places is equal to or less than the length of the data field.

Error: Use length l-?? for variable ???.
Reason: There is a maximum length allowed for each of the data fields specified in the Data Input Format Window.
Suggestion: Reduce the length of this data field.

Error: At least one parameter (BIO thru WID) must be included.
Reason: Input parameters are necessary for selecting equations and executing calculations. BIOPAK cannot function without at least one parameter in your Input Data File.
Suggestion: Specify at least one of the parameters present in the Input Data File. Make sure that all the parameters to be used in the equations for the species in your dataset are included. If uncertain as to which parameters will be necessary, browse the Equation Library and note the parameters listed for the equations for your particular species-.

Error: Species must be included in Data Input Format.
Reason: Species code is necessary for selecting equations and executing calculations.
Suggestion: Specify the location of Species code in the Input Data File. If Species code is not in your dataset, add it before proceeding.

Warning: Data in Pos and Len field exactly overlap with another record.
Reason: You have specified that two, or more, different variables, for example, DBH and DBA, are occupying the same location in the Input Data File.
Suggestion: If you do not wish to intentionally specify different variables as occupying the same location in the Input Data File, then go back and change the specifications for the variables in question.

Warning: Data in Pos or Len field overlap with data in another record.
Reason: Input variable specifications indicate partial overlap of data fields in the Input Data File. For example, part of one data field (columns 12-18) overlaps with part of another (columns 16-23).
Suggestion: Look for incorrect specifications. Correct the position or length specification causing the overlap.

Components to Output section--

Error:
Component code must be associated with at least one strata.
Reason: BIOPAK will calculate the specified component only for the lifeforms within the specified stratum. For example, if BAT is specified as a component to be calculated, and "S" is selected as the only stratum, BAT will be calculated only for species within the shrub stratum (all with S and K lifeforms).
Suggestion: Go back and toggle the "N" to "Y" for at least one stratum.

Reassignments section--

Error:
Invalid ??????. Use F10 for list.
Reason: Code you have entered for either Lifeform, Plant Component, Geographic Area, or Seral Stage is invalid. Press <F10> for list of valid codes.

Suggestion: Enter valid codes only. If you want to modify valid codes for all except Lifeform, *see Appendix: Customizing BIOPAK.*

Error:
Species.not specified in Criteria section. Exit canceled.
Reason: You tried to save a reassignment without species specified as a reassignment criterion. Species is a required criterion for a reassignment.
Suggestion: Go back and specify the species to be reassigned. Or use <Ctrl-Q> instead of <Ctrl-S> to exit.

Warning:
Species MUST be specified when using Reassignments.
Reason: When the cursor moves beyond the Species field in the Criteria section, BIOPAK warns that this is a required criterion.
Suggestion: Speci.fy the species to be reassigned. Or use <Ctrl-Q> to quit without saving changes.

Saving Run Design Fife section--

Changes have not been saved to the Run Design File.
Quit without saving? N
Reason: You may have modified (entered the section and used <Ctrl-S> to exit) one or more sections of Design a Run without saving the Run Design File.
Suggestion: If you made any changes you want to save, go back and select File from the Main Menu, and then Save the Run Design File.

Error: At least one Component to Output must, be specified.
Run Design File was not saved.
Reason: No components were specified in Components to Output. Without component specification, BIOPAK would not be able to select equations for calculations.
Suggestion: Go back to the Default Settinqs Window and specify at least one component and stratum.

Error: Geographic Area and/or Seral Stage were not specified.
Run Design File was not saved.
Reason: Both Geographic Area and Seral Stage must be specified. Each can be specified in Default Settings or in Data Input Format. Geographic Area and Seral Stage codes are necessary for BIOPAK to select equations.
Suggestion: Go back to Default Settings and specify the Geographic Area and Seral Stage codes that best represents your data.

Warning: Plot Area and/or Slope were not specified.
Area1 calculations are not possible.
Reason: Plot Area and Slope must both be specified in order to make area1 calculations. Each can be specified in Default Settings or in Data Input Format.
Suggestion: If Plot Size or Slope is present in Input Data File, go back to Data Input Format and specify their locations in the file. If Plot Size or Slope is not in Input Data File, and all plots were of the same size and slope, go to Default Settings and specify the size, slope, and units for both. If plots sizes differ, add plot size to your Input Data File, or split your dataset by plot size and do a separate run for each.

Library Editor errors and warnings

Most errors and warnings in the Library Editor are self-explanatory. A few may need further explanation, however. If messages in red boxes are encountered, *see Appendix: Troubleshooting, Strange and unusual behavior and red error* **boxes.**

All nine equation substitutions are full.
No equation can be selected - selection aborted.
Reason: There are already nine equation substitutions in the Reassignment Add/Modify Window. Nine is the maximum.
Suggestion: Check the equations you have already entered in the Reassignment Add/Modify Window. Delete any you do not want.

Equation not found.
Reason: No equation matches the specified equation key or equation number.
Suggestion: Use the wild card character (?) 'to be less specific in your search.

Invalid range - deletion aborted.
Reason: The ending equation number is smaller than the starting equation number.
Suggestion: Use an ending number greater than the starting number.

No equations are marked - selection aborted.
Reason: Marking equations is necessary for this procedure.
Suggestion: Use the mark function in the Edit Library Menu to mark the desired equations.

No more than 9 equations can be selected!
Selection aborted.
Reason: Nine is the maximum number that can be selected for a given reassignment.
Suggestion: Unmark equations until there are a total of nine or fewer.

Errors when calculating plant components

IBF file not specified.
Reason: An Intermediate Binary File must be specified for BIOPAK output before components can be calculated.
Suggestion: Specify an Intermediate Binary File. For more information see Reference: Calculate Plant *Components.*

ERROR IN BIOCODES:
DUPLICATE IN XXX CODES.
Reason: The code XXX is used more than once.
Suggestion: Double check the information in this section of BIOCODES to match the specifications in *Appendix: Customizing BIOPAK: BIOCODES File.*

ERROR IN BIOCODES:
SECTION FOR XXX IS MISSING.
Reason: The specified section is missing or invalid in BIOCODES file.
Suggestion: If you have not modified the BIOCODES File in the BIOPAK directory then reinstall BIOPAK to get a correct copy. If you have modified it, double check the section information and title to match the required formats (see *Appendix: Customizing BIOPAK: BIOCODES File).*

MORE THAN 200 EQUATION REASSIGNMENT LINES
Reason: Only 200 equation reassignments are allowed in a given run.
Suggestion: Reduce reassignments to 200, or split them into several runs.

MORE THAN 400 EQUATION REASSIGNMENTS AND SUMMATION LINES
Reason: Total number of equations specified as reassignments and summations in Reassignment Summary Window of Design a Run exceed maximum of 400.
Suggestion: Reduce number of reassignments so there are no more than 400 equations specified as substitutions.

"SELECT SPECIES" OPTION REQUESTED WITHOUT EQUATION REASSIGNMENT
Reason: The "Select Only Reassigned Species?" option was toggled to "Yes" in the Default Settings Window of Design a Run; however, no reassignments were specified.
Suggestion: Go back to Default Settings Window and change selection to "No," or specify at least one reassignment, see the section *Reference: Design a Run: Equation Reassignments.*

Errors when generating reports

These errors would occur when attempting to generate reports from the Generate Reports Window.

IBF file not specified
Reason: An Intermediate Binary File is needed because reports are generated from it.
Suggestion: Select the Intermediate Binary File from which you want to generate reports. *See Reference: Generate Reports* for more information.

No reports specified
Reason: You tried to generate report(s) but did not specify any report to generate.
Suggestion: Specify the reports you want to generate, then select Go.

COMPONENT CODE SECTION NOT FOUND IN BIOCODES
Reason: The section of Component Codes in the BIOCODES file is missing or invalid.
Suggestion: Check the information and title in the Component Codes section against the required formats in *Appendix: Customizing BIOPAK: BIOCODES File.*

REPORT 1 SUMMARY TABLE OVERFLOW, RECORD #
Reason: Number of different species in one plot exceeds the maximum allowed (600) for the purpose of generating the Plot Summary Report.
Suggestion: The data may be divided so subgroups of plots or lifeforms (trees, shrubs) may be run separately. Process only those species for which you create reassignments by setting the Select Species flag in the Default Settings Window to Y, and making Equation Reassignments for a subset of the species in the Input Data File.

REPORT 2 SUMMARY TABLE OVERFLOW, RECORD #
Reason: Number of different species in one stand exceeds the maximum allowed (600) for the purpose of generating the Stand Summary Report.
Suggestion: The data may be divided so subgroups of plots or lifeforms (trees, shrubs) may be run separately. Process only those species for which you create reassignments by setting the Select Species flag in the Default

Settinss Window to Y, and making Equation Reassignments for a subset of the species in the Input Data File.

UNIT OF ???? NOT RECOGNIZED IN BIOCODES
Reason: Unit specified in BIOCODES file is not a valid output unit. The BIOCODES File has been modified.
Suggestion: Either reinstall BIOPAK to get a valid BIOCODES File, or search for incorrect units and correct them (see *Appendix: Units* for acceptable BIOPAK units).

Errors when viewing reports

No file selected to view
Reason: You tried to view a file when none was selected.
Suggestion: First select the file to view, then select the menu item to view that file.

Errors in reports

These errors describe problems BIOPAK encountered in selecting an equation (or suitable summation), calculating a component, or making area1 calculations. When these are generated, codes for the two rated most serious are placed in the Error Report (most error codes), Reports for People, and Machine-readable Reports. Codes for these errors are ordered alphabetically in approximate order from more serious to less serious.

- This component not requested for this lifeform.
Reason: This component was not requested for the community stratum assigned to this species.
Suggestion: To have components calculated for this plant, go back to the Components to Output Window of Design a Run and put a Y under the strata that would include the lifeform for this species.

A NO EST: No species code for this case.
Reason: Species code not in the Input Data File.
Suggestion: Add Species code(s) to your Input Data File and make sure their location is given correctly in the Data Input Format Window.

B NO EST: No parameter measurements for this case.
Reason: There are no parameter measurements for this case in the data.
Suggestion: Add parameter measurements and make sure their field(s) are given correctly in the Data Input Format Window.

C NO EST: No LF in data. No Reass w/ match spp, GA & SS. Spp not in .EQN file.
Reason: No Lifeform was found in the data and BIOPAK could not associate one with this species code. BIOPAK searched for a lifeform code but found no Equation Reassignment with Criteria with matching Species, Geographic Area, and Seral Stage codes, and did not find this species in the Equation Library. No Lifeform could be associated with this plant, so no calcualtions were made.
Suggestion: Have Lifeform come in from the data, or make a Reassignment with matching Species, Geographic Area, and Seral Stage codes and a lifeform code in the Primary Lifeform Default.

D NO EST: No LF in data. OK Reass match & No Criter w/ blank LF. LF not found.

Reason: No Lifeform was found in the data, BIOPAK found one or more Equation Reassignments with Criteria with matching Species, Geographic Area, and Seral Stage codes, and none of these Criteria had a blank lifeform, however, no Lifeform could be associated with this plant.
Suggestion: Have Lifeform come in from the data, or make a Reassignment with matching Species, Geographic Area, and Seral Stage codes and a Lifeform code in the Primary Lifeform Default.

E NO EST: No LF in data. OK Reass match & Criteria w/ blank LF. LF not found.
Reason: No Lifeform found in the data, BIOPAK found one or more Equation Reassignments with Criteria with matching Species, Geographic Area and Seral Stage codes, and one or more of these Criteria had a blank LF, but no Lifeform could be associated with this plant.
Suggestion: Get Lifeform from the data, or make a Reassignment with matching Species, Geographic Area and Seral Stage codes and a Lifeform code in the Primary Lifeform Default.

F NO EST: LF in data is invalid.
Suggestion: Correct the lifeform code in the data, or make a Reassignment with matching Species, Geographic Area and Seral Stage codes and a lifeform code in the Primary Lifeform Default.

G NO EST: Reass match. Spp/LF/Comp not satisfied in .EQN file.
Reason: A matching Reassignment was found but the resulting Species/Lifeform/Plant Component combination in the Request to Library was not satisfied in the library.
Suggestion: Change the Substitution in the Reassignment to point to a valid equation in the Library.

H . . . . ..This error code is currently undefined.

I NO EST: Reass match. Geog Area &/or Seral Stg substit but GA/SS not satis in .EQN
Reason: When the Geographic Area or Seral Stage code(s) is substituted by a Reassignment they must be matched exactly by any candidate equation.
Suggestion: Change the Substitution to use an existing equation or add a new equation to the Library.

J . . . . ..This error code is currently undefined.

K NO EST: Reass match: Local Eqn Num substit but LEN not satisfied in .EQN file.
Reason: When the Local Equation Number is substituted in an Equation Reassignment every element of the Request to the Library must be matched exactly by a candidate equation.
Suggestion: Change the Substitution to use an existing equation or add a new equation to the Library.

L NO EST: Reass match: Maximum ESP (Equation Selection Penalty) exceeded.
Suggestion: Specify a higher value for the Maximum ESP in the Default Settings Window or change the Substitution of the Reassignment to specify an equation(s) with an ESP lower that the Maximum ESP.

J . . . . ..This error code is currently undefined.

M NO EST: One or more parameters are missing for all candidate equations.
Reason: All candidate equations require parameters not available for this case.
Suggestion: Use an Equation Reassignment to substitute an equation that uses only available parameters.

N NO EST: No match for Request to Lib in .EQN since Spp/LF/Comp not found at any ESP.
Reason: A suitable equation could not be found because none in the Equation List File has matching Species/Lifeform/Plant component code combinations.
Suggestion: Use an equation Reassignment to substitute a suitable equation.

0 . . . . ..This error code is not used because it looks a lot like zero.

P NO EST: No match for Request to Lib in .EQN since Spp/LF/Comp not satisfied at any ESP.
Reason: A suitable equation could not be found because none in the Equation List File have suitable Geographic Area/Seral Stage code combinations.
Suggestion: Use an equation Reassignment to substitute a suitable equation.

Q NO EST: Matching Candidate Eqn found; Overextrapolation and Max ESP exceeded.
Reason: One or more candidate equations exist in the .EQN file that would be suitable except their Equation Selection Penalty (ESP) exceeds the Maximum ESP and overextrapolation contributed to their ESP.
Suggestion: Decide if this is a serious problem. If so, make an Equation Reassignment to use an equation that you believe will give reasonable estimates for plants as this large; If not, iterativeiy increase the Maximum ESP in the Default Settinss Window until a suitable equation is se1ected.

R NO EST: Matching Candidate Eqn found; Max ESP exceeded (no overextrapolation).
Reason: One or more candidate equations exist in the .EQN file that would be suitable except their Equation Selection Penalty (ESP) exceeds the Maximum ESP
Suggestion: Reassign this equation to one with a lower ESP; or Iteratively increase the Maximum ESP in the Default Settinqs Window until suitable equations are selected.

S ND AREAL EST: Both fixed area plot and variable radius plot are specified.
Reason: BIOPAK cannot determine which plot to use to calculate plant components on an area1 basis (kg/ha or lb/at).
Suggestion: Bring the .RD file into Design a Run, Default Settings and change the Area1 Defaults to specify one or the other.

T NO AREAL EST: Neither fixed area nor variable radius plot are available.
Reason: Components cannot be calculated on an area1 basis (for example, kg/ha) because neither plot area nor prism factor is given.
Suggestion: Either provide plot slope and one of plot area or prism factor in the Data Input Format Window or bring the .RD file into Design a Run, Default Settinss Window and change the Area1 Defaults to specify one or the other.

U NO AREAL EST: Variable radius plot specified but DBH missing for some tree(s).
Reason: When data are from a variable radius plot, all trees must have a DBH or the area1 values (for example, kg/ha) for all components will be underestimated.
Suggestion: Provide all DBH values in the Input Data File, or omit trees with

missing DBHs knowing area1 estimates of components will be underestimated.

V WARNING: Overextrapolation occurred.
Reason: The parameter(s) for this case in your Input Data File is greater than the largest of those for the plants used to construct the equation.
Suggestion: If you are concerned, make a Reassignment to use a better equation.

W WARNING: Invalid Lifeform encountered in .EQN file.
Suggestion: Bring this Library into the Equation Library Editor. Sort the Library by Lifeform. Correct invalid Lifeform codes between the groups of valid codes. Create a new .EQN File.

X WARNING: Invalid Lifeform encountered in an Equation Reassignment.
Suggestion: Examine all Equation Reassignments and correct invalid codes in Criteria, Primary Lifeform Default and Substitution sections.

Y WARNING: Invalid Lifeform encountered in Primary Lifeform Default in Reassignment.
Suggestion: Examine all Primary Lifeform Default codes in Equation Reassignments and correct invalid codes.

Z . . . ..This error code is currently undefined.

a INFORM: Reassignment match. Summation was specified in Reassignment Substitutions.
Reason: Reassignment was used that specified a summation.

b INFORM: Calculated component value is based on a default summation.
The Default Summations are shown in figs. 2, 3, and 4. Actual equations used are shown in the Summarized Equation Use Report and Detailed Equation Use Report.

c WARNING: Equation used lacks parameter range, so no extrapolation test was done.
Reason: The Equation Library does not contain the range for one or more parameters for this equation.
Suggestion: Determine if this is a problem. The source information included in the Equation Library documentation may include hopeful information. If you are concerned, make an Equation Reassignment to use a better equation.

d WARNING: Taxonomic Lifeform was substituted for Coppice LF in Request to Library.
Reason: A tree or shrub lifeform code was used instead of the original coppice code to use an equation with a lower Equation Selection Penalty (ESP).
Suggestion: If this is a problem, make a Reassignment to use a better equation.

e WARNING: BAT was substituted for BFT for Herb, Grass, or Shrub LF.
Reason: An equation for BAT was used instead of the requested BFT.
Suggestion: May not be a problem because foliar biomass often represents such a large proportion of the total biomass of these lifeforms.

f WARNING: One or more minor Plant Components of a Summation were omitted.
Reason: A summation was done to calculate the requested plant component; however, at least one subcomponent (element of this summation) was missing.
Suggestion: Determine if this is a problem. The Summarized Equation Use

Report and the Detailed Equation Use Report show all the components in a complete summation (under Request to Library) and those actually used. Figures 2-4 show the built in Default Summations and may be helpful as guidelines for building your own summations using Equation Reassignments.

g WARNING: Parameter(s) was/were missing for potential Candidate.Eqn(s) in .EQN file.
Reason: At least one equation was not considered because it required parameter(s) not available from your dataset. At least one equation with matching Species/lifeform/Component had all needed parameters.
Suggestion: May not be a problem, but if you want to use one of the ignored equations, the missing parameter(s) would need to be added to your dataset.

h WARNING: Underextrapolation occurred.
Reason: The parameter(s) for this case in your Input Data File is less than the smallest of those for the plants used to construct the equation.
Suggestion: If you are concerned, make an Equation Reassignment to use a better equation.

i INFORM: No LF in data, LF came from Reassign: Taxonomic LF of Substit section.
Reason: BIOPAK used the taxonomic lifeform (in the Library) for the species specified in the Reassignment Substitution.
Suggestion: May not be a problem. Check if an acceptable equation was used.

j INFORM: No LF in data, LF came from Reassign: LF of Criteria section.
Reason: BIOPAK used lifeform specified in the Reassignment Criteria.
Suggestion: May not be a problem. You can check the equation used.

k INFORM: No LF in data, LF came from Reassign: LF of a Substitution
Reason: BIOPAK used the lifeform specified in the Equation Key of a Reassignment Substitution.
Suggestion: May not be a problem. Check to be sure an acceptable equation was used.

l . ..This error code is not used because it looks a lot like one.

m INFORM: A plant component value c= 0.0 was calculated and set to zero.
Reason: The parameters and equation used gave a value less than or equal to zero. This usually happens with small plants. BIOPAK sets these values to zero.
Suggestion: You may add a new equation to the library that gives values approaching zero as plant size approaches zero. You may decide, for example, that a simple equation through the origin and intersecting the first equation where the latter's predictions begin to be unreliable is appropriate. In this case, setting the input parameter upper bound for the new equation and the lower bound for latter equation to this intersection will cause BIOPAK to use each over the intended range, provided the Local Equation Number is not specified in an Equation Reassignment.

n . . . . ..This error code is currently undefined.

o . . . . ..This error code is not used because it looks a lot like zero.

p, q, r . . . .This error code is currently undefined.

Reason: All these error codes are currently undefined.

Known bugs

There are some bugs in BIOPAK that, although annoying, allow continuance of the program.

Design a Run: Data Input Format: Sometimes need to press <Ctrl-S> several times to save and exit from the Data Input Format Window.

Design a Run: Data Input Format: After typing in a unit, if you delete it, and then decide to select from the <FlO> list, the units do not show up in the window.
Suggestion: Delete all characters in cell before pressing <Fl0>.

Design a Run: Components to Output: If you enter a Component code, <Tab> to the strata, and then decide to quit without saving, the error message, "At least one strata must be specified..", still will appear. It will disappear with the next keystroke.

Design a Run: Components to Output: If you type all or part of a Component code, delete it, and then select a code from the <Fl0> list, the component does not appear in the window.
Suggestion: Delete all characters in cell before pressing <FlO>.

Design a Run: Reassignments: Sometimes you will need to press <Ctrl-S> several times to save and exit from the Reassignments Summary Window.

Design a Run: Reassignments: <Esc> functions as <Ctrl-S>, that is, saves and exits.

Strange behavior and red error boxes

If BIOPAK is behaving in a strange, unusual, or inconsistent manner, a few things can be done. Examples of "strange and unusual behavior" include:

- BIOPAK will not start.
- BIOPAK crashes or hangs in the middle of your work.
- FoxPro error messages in red boxes appear. Messages in these include:
  - File access denied...
  - File does not exist...
  - Not enough (memory, space...)...

  Other messages may indicate BIOPAK cannot find, open or write to a file. Some messages give <<Cancel>> and <<Ignore>> options. These messages primarily in Design a Run and Edit Equation library which are written in FoxPro.

Reboot your PC--

Turn the power off at the main line switch, not the reset button, and wait 5 seconds before turning it on again. Some settings are not reset by just pushing the reset button. Some software will leave some PCs in a condition that causes BIOPAK trouble. Now try to run BIOPAK again.

Check contents of BIOENV File--

The purpose of the BIOENV file (always on C:\) is to help find problems in the environment within which BIOPAK runs. BIOENV reports a snapshot of the DOS and

FoxPro environments created by BIOPAK.BAT (or BIOPAKN.BAT if you are running BIOPAK over a network) just before the main program is invoked. Problems caused by incorrect setting of a variable or file in the DOS or FoxPro environments are the easiest type to fix.

Check the contents of the BIOENV file. It does not matter whether the text in this file is upper or lower case.

1. DOS Environment:
   a. BIODIR should be set to the path for the BIOPAK directory. This directory contains all the BIOPAK program files. Permission to write is not needed here. On a network, it is safest if users cannot do so. If this does not point to the BIOPAK directory, you must rerun SETUP to correct this. People familiar with DOS can (1) rename the BIOPAK directory, (2) put the BIOPAK files on a new drive or directory, or (3) change the DOS statement that sets it in the beginning of BIOPAK.BAT (or BIOPAKN.BAT on a network).
   b. BIOTMP should be set to the path for the directory you have chosen for temporary files, with a backslash (\) at the end. Be sure you have permission to write here and that it can hold at least four Mbytes (six to be safer) of files. BIOPAK will not run if you cannot, write the necessary temporary files here. If BIOTMP does not point to such a directory, rerun SETUP to correct this. People familiar with DOS can correct the DOS statement that sets it in the beginning of BIOPAK.BAT (or BIOPAKN.BAT on a network).
   c. OLDPATH should be your DOS path before starting BIOPAK. Problems with this are best corrected by turning the PC off and then on again.
   d. PATH should be your DOS path with a path to the BIOPAK directory added to the front end.
   e. FOXPROCFG should be set to <BIOTMP>bpconfig.fp.

   Problems with any of these may be caused by insufficient DOS environment space (see DOS Environment Space later in this section).

2. Contents of FOXPROCFG File (<BIOTMP>BPCONFIG.FP):
   This file should contain:

```
path     = <BIODIR>
resource =  <BIOTMP>foxuser.dbf
tmpfiles = <BIOTMP>
overlay  = <BIOTMP> overwrite
```

   <BIODIR> and <BIOTMP> are the values of the respective DOS environment variables. An error indicates an error in BIOPAK.BAT or BIOPAKN.BAT, and BIOPAK must be reinstalled to obtain a good copy of the .BAT file.

3. BIOTMP (<BIOTMP>) Directory List:
   The BIOTMP directory must contain the file BPCONFIG.FP. If it does not, there is an error in BIOPAK.BAT or BIOPAKN.BAT, and BIOPAK must be reinstalled to obtain a good copy of the .BAT file.

Increase BIOPAK temporary file storage space--

Check the free disk space available on the drive you specified for temporary BIOPAK files. This drive is shown briefly every time BIOPAK is started. You specified this drive when you installed BIOPAK and can specify another drive by reinstalling (or editing the BIOPAK.BAT file to change the "Set Biotmp=<path>"). *See Installation: System Requirements* for amount of space needed. If problems arise we suggest increasing this value by 1 or 2 Mbytes.

Increase free memory--

Check the free system memory, RAM, using MAPMEM.COM on the BIOPAK directory or CHKDSK, a DOS utility. *See Installation: System Requirements* for amount of space needed. If problems arise we suggest providing an extra free 10 or 20 Kbytes. *See Installation: Installation on a* PC for suggestions about freeing up RAM. Then reboot your PC by turning off the main line switch.

Increase DOS environment space--

There may be insufficient DOS environment space allocated. This can be remedied by editing your C:\CONFIG.SYS file.

If you added 512 bytes when installing BIOPAK, then a second 512 bytes needs to be added to eliminate this as a potential problem. The relevant line in the C:\CONFIG.SYS file should look similar to this: SHELL=C:\DOS\COMMAND.COM /P /E:1536. In this case, 1536 bytes are set for DOS environment space. Increase the number to 2048. The exact method for increasing environment space differs with different DOS versions, so consult the DOS manual. Then reboot your PC by turning off the main line switch.

Units

Section

There are many locations within BIOPAK where units come into play. There are input parameter units, output component units, and metric and English unit options. This appendix clarifies the use and validity of units in BIOPAK.

You have several options for both metric and English parameter units. There is only one option each, however, for the metric and English component output units.

Parameter units

Input Data File--

The parameter units allowed in the Input Data File are those recognized by BIOPAK (see Metric input and English input in the table 6). In the Data Input Format Window of Design a Run, the valid units can be selected from popups by pressing <FlO>. *See Reference: **Input** Data File* **and** *Reference: Design a Run: Data Input Format* **for a more detailed description.**

Table 6--Valid Parameter units

Parameter codes	Metric input	English input	Standard metric	Standard English
BIO	g, KG	lb	g	lb
CIR, DBA, DBH, HT, LEN, SAP, WID	cm, dm, m	in, ft	cm	in
COV, CR, FC	%, ratio	%, ratio	%	%
NP, NUM	NA	NA	NA	NA
SPA	cm^2, dm^2, m^2	in^2, ft^2	cm^2	in^2
VOL	dm^3, cm^3, m^3	in^3, ft^3	dm^3	in^3
PLOTAREA	m^2, ha	ft^2, ac	m^2	ft^2
PRISMFAC	m^2/ha	ft^2/ac	m^2/ha	ft^2/ac
PLTSLOPE	%, deg	%, deg	%	%

Reassignments--

When performing equation reassignments in the Reassignments Add/Modifv Window of Design a Run, the Reassignment Criteria may include up to three parameters and size ranges *(see Reference: Design a Run: Reassignments).* If these are included in the Equation Reassignment, the parameter units are assumed to be the same as those entered in the Data Input Format Window (see Metric input and Enqlish input in table 6).

Equation Library--

For equations in the Library, the specific units associated with parameters are crucial. When View/Modify is selected from the Edit Library Menu, the first screen to appear will be the Orisinal and Final Eauations Window. There are two places where units come into play: Equation as in Oriqinal Source and Equation as in BIOPAK. The units as in BIOPAK must be the standard metric units shown in table 6. This often requires transformations for an equation to be used by BIOPAK. See *Appendix: Equation* Library for more information on the equations, and *Reference:* Library Editor on how to add them.

Reports--

The units associated with the parameters listed in reports will be either the standard metric or standard English units. If you select Metric as the output units in Generate Reports, the standard metric units will be associated with the parameters ; and if English is selected as the output option, English standard will be the units associated with the parameters in reports (see *Reference: Generate Reports* for more information on the Metric/English output units).

Component units

Table 7--Valid Component units.

Ouput component	Metro	
AFN, AFO, AFT, CSB, CSD, CZB, CZD, PCH, PCS, PFN, PFO, PFT,	cm2	in2
VQW, VSB, VST, VSW, VSZ	cm3	in3
HST	m	ft
VAE, VCT	m3	ft3
VY1, VY2	bdft[a]	bdft[a]
BAE, BAP, BAT, BBD, BBL, BBS, BCD, BCL, BCT, BFF, BFN, BFO, BFT, BFV, BIT, BKC, BKL, BLL, BLM, BLU, BRT, BSB, BST, BSW, BTT, BUL, BUN	gm	lb

[a] bdft = board feet

Equation Library--

The units for plant components in the Equation Library must be one of the metric units listed in table 7.

BIOCODES File--

The units for plant components in the BIOCODES file must be one of the metric units listed in table 7.

GLOSSARY

Candidate Equation--**Any equation (or equations in a summation) found in the Equation Library that meets the minimum criteria for equation selection. The minimum criteria are (1) the equation(s) is for the same species and lifeform as the record in the Input Data File, and (2) the equation(s) uses parameters found in the Input Data File record.**

*Community **Strata*** **--BIOPAK recognizes four strata classifications: Tree, Shrub, Herb, and Moss. The Tree Stratum includes only the tree Lifeform (T). The Shrub Stratum includes shrub (S) and coppice (K) lifeforms. The Herb Stratum includes herb (H), grass (G), and sedge (C) lifeforms. The Moss Stratum includes moss (M), lichen (L), and bryophyte (B) lifeforms. The components output in reports are organized by stratum.**

Default Summation-- The **summation chosen by BIOPAK when you do not specify a summation. These are different for different lifeforms. Figures 2-4 illustrate the BIOPAK default summation trees. The default summation would occur when an equation does not exist for the specified component, yet equations for subcomponents are present in the Equation Library. BIOPAK will calculate these subcomponents and sum the results. The default summation trees may be modified as described in** *Appendix: Customizing BIOPAK: BIOSUMM File.*

*Diagnostic **Reports*** **--There are three diagnostic reports: Summarized Equation Use Report (*.USE), Detailed Equation Use Report (*.DET), and Error Report (*.ERR). They can be produced from the Calculate Plant Components Window of BIOPAK.**

*Equation **Key*** **--In general, the equation key includes species, lifeform, plant component, geographic area, seral stage, and local equation number. In the Equation Library, it is also a search function used to locate equations. (See also:** *Substitution Key)*

Equation **Library --BIOPAK comes with a library of about 1,000 equations for calculating plant biomass for species in the Pacific Northwest. An editor facilitates searching, sorting, adding, deleting, or modifying the existing equations. The library can be modified to meet your particular needs.**

Equation Number--A **number the user gives to an equation. Each equation in an equation library should have a unique equation number.**

Equation Reassignments--The **user creates an equation reassignment to control the selection of equations from the Library. An Equation Reassignment can help determine the Request to Library, thereby allowing the user to specify any or all of the elements (that is, the Substitution Key species, lifeform, plant component, geographic area, seral stage, and local equation number) that a Candidate Equation must match to be selected.** *(See* **also** *Match, Original Equation Request, Reassignment* **Criteria,** *Request to* **Library,** *Substitution Key(s))*

Equation Selection Penalties **(ESPs)--In many instances, the plants used to**

construct the equations in the Library, will closely match the plants in the Input Data File. There will also be instances, however, when the plant sizes, geographic areas, seral stages, or other factors will not match. With each mismatch, there is an associated ESP.

When a request is made for an equation from the Library, BIOPAK will attempt to choose the "best" equation. It does this by selecting the equation with the lowest ESP (within the constraints set by the Maximum, Threshold and Summation ESP Levels specified in Default Settings). An ESP is greater than zero when one or more characteristics in the Candidate Equation do not exactly match the Original Request. For a more detailed description of ESPs *see Appendix: Equation Selection Penalties.* **The individual contributions to the Equation Selection Penalties can be found in** *Appendix: Customizing BIOPAK.*

*Geographic Area--***One of the factors considered when BIOPAK searches the Library for a suitable equation match. Refers to the geographic region from which the data were collected (specified by you in Data Input Format or Default Settings), and the region from which the particular equations in the Library were constructed.**

Lifeform--One **of the factors considered when BIOPAK searches the Library for a suitable equation match. Refers to the form in which the plant is growing, for example, shrub, coppice, or tree. May differ from the** *taxonomic lifeform* **for a given species. For example, the plant may have a coppice lifeform, and the taxonomic lifeform may be a tree.** *(See* **also** *Taxonomic Lifeform)*

Lifeform Substitution--If **the Input Data File does not contain** *Lifeform* **codes, BIOPAK will substitute the taxonomic lifeform of the species from the Equation Library. If an equation reassignment is requested, the lifeform to be substituted may be specified in the Substitution Key. This would then override the taxonomic lifeform substitution.** *See Appendix:* **Lifeform for more details.**

Local Equation **Number--This number is used in the Equation Library to distinguish equations with identical equation keys.**

Machine-readable **Reports--There are three Machine-readable Reports: Individual Plant Report (*. IND), Plot Summary Report (*.PLT), and Stand Summary Report (*.STA). These reports can be generated for use by other software.**

Match--In a Request to Library, a "match" refers to a situation when the species, lifeform, geographic area, seral stage, and measured parameters of the plant which was sampled "match" those of an equation in the Library (that is, REQUEST TO LIBRARY = CANDIDATE EQUATION).

In an Equation Reassignment, a match refers to a situation when the selection criteria "match" a given Original Equation Request. When this match occurs, the reassignment is executed. (Note: BIOPAK will search for an equation in the Library with an Equation Key which exactly matches this Substitution Key. If the Substitution Key is missing any values, there may be more than one equation with matching keys (blanks are considered a match). If the Substitution Key is complete, there will be only one equation in the Library which it exactly matches.)

Maximum ESP **Level--It determines the poorest acceptable equation match you will allow. The higher the Maximum ESP Level, the more flexibility in selecting** equations.

Original Equation **Request--Includes the species, lifeform, geographic area, seral stage, and measured parameters from the Input Data File; and the component to be calculated from the Run Design module. Geographic area and seral stage may come from Run Design if they are not present in the Input Data File. Lifeform may come from the Equation Library, or Run Design File, if it is not included in the Input Data File. If no Equation Reassignment is specified, the Request to Library will be identical to the Original Equation Request.**

Parameters--Parameters refer to the plant measurements, for example, DBH, HT. The Input Data File contains parameters measured in the field. The Equation Library lists parameters used to construct the plant component equations. For a particular equation to be used, the Input Data File must contain the same parameters as those found in the equation.

Plant Components--The **components of plants to be calculated. User specifies the components in the <u>Components to Output Window</u> of Design a Run. The equations in the Library are used to calculate the components requested. A list of the possible components can be found in** *Appendix: Codes.* **These components include biomass, area, and volume for leaves and flowers, branches, stems, crown, and roots.**

Primary Lifeform **Default--Found in the <u>Reassisnments Add/Modify Window</u> of Design a Run. The user can assign a Primary Lifeform Default to a given species that will be used when lifeform is not present in the Input Data File. In this manner, BIOPAK will attach the Primary Lifeform Default to the species in the Original Equation Request. The Primary Lifeform Default will also be the lifeform associated with the species when designating community strata in reports (See also Lifeform** *Substitutions, Original Equation Request, Request to* **Library)**

Prism Basal Area **Factor--The number of square meters per hectare (or square feet per acre) represented by each tree tallied when a prism or angle gauge is used to select the trees measured in the field.**

Reassignment **Criteria--Found in the <u>Reassignments Add/Modify Window</u> of Design a Run. The list of Criteria sets the conditions by which a reassignment is to be executed. In other words, if these conditions exist, then proceed with a reassignment. The Criteria must include the species. The lifeform, plant component to be calculated, geographic area, seral stage, and measured parameters are optional.**

Request to **Library--Used to request an equation from the Library. This is initiated when Calculate Plant Components is executed. When there are no reassignments, the Request to Library is identical to the Original Equation Request. When you specify an Equation Reassignment, and the Reassignment Criteria match the Original Equation Request, the Original Request is modified by the Substitution Key(s). For example, the species of the plant which was sampled may be substituted by another, or the Geographic Area code may be changed. -The Request to Library reflects these changes. (that is, REQUEST TO LIBRARY = ORIGINAL EQUATION REQUEST t REASSIGNMENTS)**

Seral **Stage--One of the factors considered when BIOPAK searches the Library for** a suitable equation match. Refers to the seral stage of the community from which the plant was sampled. The seral stage is based primarily on the form of trees in the sampled community. If no seral stage is specified in the Input Data File, then the seral stage indicated in the Default Settings is used.

Substitution Key(s)--Found in the Reassignments Add/Modify Window of Design a Run. The key(s) lists the values to be substituted for given Reassignment Criteria. Each key must include the species. The lifeform, plant component to be calculated, geographic area, seral stage, and local equation number are optiona?. When an *Original* Request matches a Reassignment Criteria, the Substitution Key(s) modifies the Original Equation Request to create the Request to Library. *(See* also *Equation Key, Equation Reassignments, Match,* Original *Equation Request)*

Summation ESP **Level**--This level determines when a summation will be attempted. If set at zero, there are no restrictions on summations. If set higher, default summation will be attempted only if the ESPs for the Candidate Equations are higher than the Summation ESP Level. If BIOPAK cannot find an individual equation to calculate a specified plant component with a lower ESP value than the assigned Summation ESP, then BIOPAK will begin to consider default summations.

Taxonomic **Lifeform**--The "true" *lifeform* of the species. This may differ from the lifeform as observed in the field. For example, a coppice lifeform may have either a tree or shrub Taxonomic Lifeform, and a shrub lifeform may have a tree taxonomic lifeform, and vice versa. Corresponds with the taxonomic lifeform listed for each species in the Equation Library. If lifeform is not specified in the Input Data File, BIOPAK will assign the taxonomic lifeform from the Equation Library. *(See* also *Lifeform, Lifeform Substitutions, Primary Lifeform Default)*

Threshold *ESP* **Level**--This value determines the level at which a Candidate Equation is considered acceptable and BIOPAK stops its search for a better one. A user assigned Threshold ESP of zero will assure selection of the best equations.

Yariable Radius **Plot**--Plot on which trees are selected by a horizontal angle gauge, such as a prism. *(See* also *Prism Basal Area Factor)*

INDEX

The page numbers given are often the first pages of multipage sections. The main discussions of these topics can often be found in the detailed tables of contents for each section. See the Glossary for definitions of many terms.

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Means, Joseph E.; Hansen, Heather A.; Koerper, Greg J.; Alaback Paul B.; Klopsch, Mark W. Software for computing plant biomass--BIOPAK users guide. Gen. Tech. Rep. PNW-GTR-340. Portland, OR: U.S. Department of Agriculture, Forest Service, Pacific Northwest Research Station. 184 p.

BIOPAK is a menu-driven package of computer programs for IBM-compatible personal computers that calculates the biomass, area, height, length, or volume of plant components (levels, branches, stem, crown, and roots). The routines were written in FoxPro Fortran and C.

BIOPAK was created to facilitate linking of a diverse array of vegetation datasets with the appropriate subset of available equations for estimating plant components, such as biomass and leaf area. BIOPAK produces reports that are formatted for people and files that are compatible with other software. Other reports document the design of computation run and the equations used. BIOPAK includes a library of about 1,000 predictions equations and an editor for updating it. Most of the equations in the library were developed in the Pacific Northwest, including southeast Alaska.

Keywords: Dimension analysis, software, plant biomass, plant leaf area, plant volume, crown mass, crown volume, manual, microcomputer, users guide.

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