Version 4.0 beta version

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Beta Documentation

This documentation is currently under construction, therefore, we cannot guarantee the accuracy of the information described herein. A much more user-friendly manual is in progress. Revisions will be made available to registered users over the World Wide Web at http://www.lms.si.edu/PAUP. A list of frequently asked questions is also available at this website. Many of the commands and options described in this document are hyper-linked to facilitate and promote on-line use until a final draft is complete. Comments regarding this document should be addressed to paup-support@onyx.si.edu.
PAUP* 4.0 beta version disclaimer and user agreement

The version of PAUP* 4.0 currently available is a beta version. We are not aware of bugs that would cause the program to obtain incorrect results, but they could certainly exist. Other bugs could cause the program to terminate abnormally or misbehave in other ways. Your use of this software implies your acceptance of its unfinished status. We would greatly appreciate receiving reports of any problems you encounter. Send them by email to: paup-support@onyx.si.edu. Please include all details necessary to reproduce the problem, including: (1) type of machine and operating system version; (2) specific version number of PAUP* (e.g., PAUP*4.0b1); (3) a specific sequence of operations that will cause the problem to occur, beginning with start-up of the program; and (4) a sample data file and any other associated files that will enable the problem to be reproduced.

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Suggested Citation

PAUP* 4.0 is in many ways comparable to a monographic article. In its approximately 180,000 lines of code, PAUP* implements numerous original concepts and ideas and contains many new algorithms. For these reasons, citation of the program in a book format is recommended:


# Table of Contents

Table of Contents ................................................................................. 1
Command Reference ............................................................................... 5
Command Format .................................................................................. 5
  Identifiers ............................................................................................. 6
  Common Command Elements ................................................................. 8
Commands used in the TAXA Block .................................................... 9
  Dimensions ............................................................................................ 10
  TaxLabels ............................................................................................. 10
Commands used in the CHARACTERS Block ...................................... 10
  Dimensions ............................................................................................ 11
  Format .................................................................................................... 11
  Eliminate ............................................................................................... 15
  TaxLabels ............................................................................................. 15
  CharStateLabels .................................................................................. 16
  CharLabels ........................................................................................... 16
  StateLabels .......................................................................................... 16
  Matrix .................................................................................................... 17
Commands used in the DATA Block ................................................... 18
Commands used in the ASSUMPTIONS Block ..................................... 19
  Options ................................................................................................. 19
  UserType ............................................................................................... 20
  TypeSet ................................................................................................. 21
  WtSet .................................................................................................... 21
  ExSet ..................................................................................................... 21
  AncStates .............................................................................................. 22
Commands used in the SETS Block .................................................... 22
  CharSet ................................................................................................. 22
  TaxSet ................................................................................................. 23
  CharPartition, TaxPartition ................................................................. 23
Commands used in the TREES Block ................................................... 24
  Translate ............................................................................................... 24
  TREE ..................................................................................................... 24
Commands used in the CODONS Block ............................................. 26
  CodonPosSet ........................................................................................ 26
Commands used in the DISTANCES Block...............................................26

   Dimensions ............................................................................................27
   Format ........................................................................................................27
   TaxLabels ....................................................................................................29
   Matrix .........................................................................................................29

Commands used in the PAUP Block............................................................29

   Options And Subcommands Affecting Multiple Commands ..................29
   ? ..............................................................................................................32
   ! ..............................................................................................................32
   Agree .......................................................................................................32
   AllTrees ...................................................................................................33
   Ancstates .................................................................................................35
   Assume ....................................................................................................35
   BandB .......................................................................................................36
   BaseFreqs ...............................................................................................38
   BootStrap .................................................................................................38
   CharPartition ..........................................................................................41
   CharSet .....................................................................................................41
   ClearTrees .................................................................................................41
   Condense .................................................................................................41
   Constraints ..............................................................................................42
   ConTree ....................................................................................................42
   CStatus .....................................................................................................45
   CType .......................................................................................................46
   Defaults .................................................................................................46
   Delete .......................................................................................................46
   DerootTrees ..............................................................................................47
   DescribeTrees ..........................................................................................48
   DOS .........................................................................................................50
   DScores ....................................................................................................50
   DSet .........................................................................................................52
   Edit ..........................................................................................................56
   Exclude ....................................................................................................57
   Execute .....................................................................................................57
   ExSet .......................................................................................................57
   Filter ........................................................................................................57
   Factory ....................................................................................................59
   FStatus ....................................................................................................60
   GammaPlot ...............................................................................................60
   GenerateTrees ..........................................................................................60
   GetTrees ..................................................................................................61
   Help .........................................................................................................61
   HomPart ...................................................................................................64
   HSearch .................................................................................................65
   Include .....................................................................................................69
   InGroup ....................................................................................................70
   JackKnife .................................................................................................70
<table>
<thead>
<tr>
<th>Command</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lake</td>
<td>73</td>
</tr>
<tr>
<td>Leave</td>
<td>74</td>
</tr>
<tr>
<td>LoadConstr</td>
<td>74</td>
</tr>
<tr>
<td>Log</td>
<td>75</td>
</tr>
<tr>
<td>LScores</td>
<td>77</td>
</tr>
<tr>
<td>LSet</td>
<td>79</td>
</tr>
<tr>
<td>MPRSets</td>
<td>84</td>
</tr>
<tr>
<td>NJ</td>
<td>85</td>
</tr>
<tr>
<td>Outgroup</td>
<td>86</td>
</tr>
<tr>
<td>PairDiff</td>
<td>87</td>
</tr>
<tr>
<td>Permute</td>
<td>87</td>
</tr>
<tr>
<td>Pscores</td>
<td>89</td>
</tr>
<tr>
<td>PSet</td>
<td>91</td>
</tr>
<tr>
<td>Puzzle</td>
<td>93</td>
</tr>
<tr>
<td>Quit</td>
<td>94</td>
</tr>
<tr>
<td>RandTrees</td>
<td>95</td>
</tr>
<tr>
<td>RateSet</td>
<td>96</td>
</tr>
<tr>
<td>Reconstruct</td>
<td>96</td>
</tr>
<tr>
<td>Restore</td>
<td>97</td>
</tr>
<tr>
<td>RevFilter</td>
<td>97</td>
</tr>
<tr>
<td>Reweight</td>
<td>97</td>
</tr>
<tr>
<td>RootTrees</td>
<td>99</td>
</tr>
<tr>
<td>SaveAssum</td>
<td>99</td>
</tr>
<tr>
<td>SaveDist</td>
<td>100</td>
</tr>
<tr>
<td>SaveTrees</td>
<td>101</td>
</tr>
<tr>
<td>Set</td>
<td>103</td>
</tr>
<tr>
<td>ShowAnc</td>
<td>110</td>
</tr>
<tr>
<td>ShowCharParts</td>
<td>111</td>
</tr>
<tr>
<td>ShowConstr</td>
<td>111</td>
</tr>
<tr>
<td>ShowDist</td>
<td>111</td>
</tr>
<tr>
<td>ShowMatrix</td>
<td>111</td>
</tr>
<tr>
<td>ShowRateSets</td>
<td>112</td>
</tr>
<tr>
<td>ShowTaxParts</td>
<td>112</td>
</tr>
<tr>
<td>ShowTrees</td>
<td>112</td>
</tr>
<tr>
<td>ShowUserType</td>
<td>113</td>
</tr>
<tr>
<td>StarDecomp</td>
<td>113</td>
</tr>
<tr>
<td>SurfCheck</td>
<td>114</td>
</tr>
<tr>
<td>TaxPartition</td>
<td>115</td>
</tr>
<tr>
<td>TaxSet</td>
<td>115</td>
</tr>
<tr>
<td>TIME</td>
<td>115</td>
</tr>
<tr>
<td>ToNEXUS</td>
<td>116</td>
</tr>
<tr>
<td>TreeDist</td>
<td>117</td>
</tr>
<tr>
<td>TreeInfo</td>
<td>119</td>
</tr>
<tr>
<td>TreeWts</td>
<td>119</td>
</tr>
<tr>
<td>TStatus</td>
<td>119</td>
</tr>
<tr>
<td>TypeSet</td>
<td>119</td>
</tr>
<tr>
<td>Undelete</td>
<td>119</td>
</tr>
<tr>
<td>UPGMA</td>
<td>120</td>
</tr>
<tr>
<td>UserTree</td>
<td>121</td>
</tr>
</tbody>
</table>
This document describes the PAUP* command format. Unless stated otherwise, these commands may be included in the PAUP block of a NEXUS file, or typed from the command line. The EDIT command may only be issued from the command line. All users will need to be familiar with the commands available in the TAXA, CHARACTERS, ASSUMPTIONS, SET, TREES, CODON, and DISTANCE blocks, which are normally placed in PAUP input files. In versions of PAUP* that provide a menu-based interface, only knowledge of these "block" commands is required, as other instructions to PAUP* can be accomplished through the menu system. Some users, however, may prefer a command-driven interface. Consequently, except for certain machine-specific features, PAUP* may be controlled entirely by a command-line system. Commands may also be placed into input files for convenience (i.e., to avoid repeated typing of complicated commands) and to provide a simple "batch" facility.

Command Format

The command descriptions below use some conventions that will be more fully described in subsequent editions of this reference document. Remember that upper-case items are to be entered as shown. Italicized items—e.g., user-item—represent variable items to be substituted by the user. Items inside of square brackets—e.g., [OPTIONAL_ITEM]—are optional. Items inside of curly braces and separated by vertical bars—e.g., { X | Y | Z }—are mutually exclusive options; only one of the choices indicated may be used. The default item (if any) is underlined, as in { ABC | DEF }. Options in commands are generally specified as "KEYWORD = VALUE" for options that have two or more potential values. For options that represent simple "on-off" ("Boolean") switches, KEYWORD = YES and KEYWORD = NO can be used to select or deselect options, respectively. Also, options may be selected by simply specifying KEYWORD.

Each command begins with a command-name and ends with a semicolon. Otherwise, the commands are completely free-form. A command may span any number of lines and whitespace (tabs and blanks) may be inserted at will. Input of PAUP* commands is case-insensitive, so you may enter command names, option keywords, etc., in any combination of upper- and lower-case characters (the only exception pertains to the MATRIX command). In addition, PAUP* allows abbreviation of command names and keywords to the shortest unambiguous truncation. Note that other NEXUS-conforming programs may not accept these abbreviations. MacClade 3.0, in particular, does not allow abbreviations, so if you want your data file to be MacClade-compatible, then commands visible to MacClade (i.e., those not contained within a PAUP block) should not be abbreviated.
**IDENTIFIERS**

"Identifiers" are simply names given to taxa, characters, and other PAUP input elements such as character-sets, taxon-sets, and exclusion-sets. They may include any combination of upper- and lower-case alphabetic characters, digits, and punctuation. If the identifier contains any of the following characters:

\( ( ) [ ] \{ \} / \ , \ ; \ : \ = \ \ast \ '' \ ` \ + \ - \ < \ > \)

or a blank, the entire identifier must be enclosed in single quotes. Underscores (_ ) are translated to blanks, unless the identifier is enclosed in single quotes. For example, the identifiers `Homo_sapiens` and `Homo sapiens'` are equivalent, but distinct from `Homo_sapiens'`. To include a single-quote in the identifier, you must use two consecutive single quotes. Any trailing blanks are stripped before the identifier is stored; leading blanks are preserved.

Examples of valid identifiers:

- subterraneous
- Mus_musculus
- H._sapiens
- 'H. sapiens #429'
- 'Fred''s new sp.'
- 'rusticus (1)'
- ''shoal bass''
- AMNION
- _23
- x21.02
- myType

PAUP* imposes limits on the lengths of identifiers as defined below. If you use identifiers that exceed these limits, PAUP* simply truncates them to the maximum acceptable length. If you use names that are longer than the maximum lengths (e.g., for other NEXUS programs that allow longer identifiers), you should make sure that identifiers in the same class will be unique after truncation by PAUP*.

MacClade will not accept all-digit character or taxon names. PAUP* allows them, with a warning that taxon/character names have precedence over numbers (e.g., if the tenth character is named "5", the command `EXSET *no_5=5` causes character number five to be excluded by MacClade and character number ten to be excluded by PAUP*). It is not advisable to use all-digit names in PAUP*, especially if you intend to also use the data file in MacClade. (See `ALLDIGLAB` on page 109 for a description of digit label handling.)

**Taxon identifiers**

For input, taxa may be referenced either by name or by number. The numbers are simply the row number of the taxon in the input data matrix. Note that if you delete taxa, the original taxon numbers are still used to refer to taxa.
Taxon names may be up to 32 characters in length, however for most output they are truncated to 16 characters. Thus, you should choose names that are unique up to at least the first 16 characters. The full 32-character names are used only when drawing trees.

Taxon names have priority over taxon numbers in input commands. This only becomes an issue if you use all-digit taxon names. For example, if five taxa in a data file are, for whatever reason, given the names

```
One
34
three
3
673
```

then the command `delete 3;` would cause deletion of the fourth taxon. Because of the potential confusion, you are strongly urged not to use all-digit taxon names.

The name "ALL" is reserved for a taxon list containing all of the taxa in the data matrix (see below). You may not name a taxon "ALL".

**Character identifiers**

Ordinarily, PAUP* refers to characters by consecutive integers starting with 1. These integers are used both for input commands and in the output. You may also assign alphanumeric character names if you wish. The maximum length of a character name is 32, but PAUP* truncates character names to 10 characters in its output. Thus, you should choose names that are unique up to at least the first 10 characters. If you assign alphanumeric character names, these will also be used to identify characters in PAUP* output.

The rules for including punctuation, underscores, and blank characters are the same for character names as for taxon names (see page 6).

As for taxa, character names have priority over character numbers. For example, if you used all-digit character names (e.g., sequence positions or restriction-map locations) such as

```
2
4
11
23
89
102
```

and issued the command `exclude 4-5;` then all but the first and last characters would be excluded (i.e., name "4" through number 5). Because of the potential confusion, it is suggested that you always include at least one non-digit in alphanumeric character names.

The name "ALL" is reserved for a character list containing all of the characters in the data matrix (see below). You may not name a character "ALL".

Other names
Identifiers are also used for TYPESET, WtSET, ExSET, CHARSET, TAXSET, and ANCSTATES definitions. These names follow the same rules as taxon and character names, and have a maximum length of 10 characters.

COMMON COMMAND ELEMENTS

The following elements are used in more than one command and are defined here to minimize redundancy.

Taxon lists
A taxon list is a sequence of one or more taxon identifiers (names and/or numbers. If two taxon identifiers are separated by a hyphen, this indicates that the range of taxa between the first taxon and the second taxon (inclusive) are to be included in the list. (The second taxon must have a higher number than the first taxon).

A taxon list composed of the reserved name "ALL" specifies all of the taxa in the data matrix.

Examples of valid taxon lists (assuming that corresponding taxon identifiers have been defined in the TAXA block) are as follows:

```
  heteroclitus
  M23-Q45 S1 T5;
  1 3 5-8
  all
```

Character lists
A character list is a sequence of one or more character identifiers (names and/or numbers). If two character identifiers are separated by a hyphen, this indicates that the range of characters between the first character and the second character (inclusive) are to be included in the list. (The second character must have a higher number than the first character). If the second specification in the range is followed by a backslash (\), then an integer value immediately following the backslash represents an increment. For example, the list 3-24\3 consists of the characters 3, 6, 9, …, 21, 24. If a range-plus-increment is used, only those characters contained within the range are included in the list (e.g., the list 2-5\2 includes only characters 2 and 4).

The special identifier consisting only of an unquoted period refers to the last character in the data matrix (=NCHAR).

A character list composed of the reserved name "ALL" specifies all of the characters in the data matrix.
Examples of valid character lists (assuming that corresponding character identifiers have been defined in the SETS block) are as follows:

```
8
amnion appendages gizzard teeth;
1 two 5 7
11-.
1 3-7 16 31 28
LLSCALES-CPDSCALES
3-.\3
all
```

**Character states**  
A character state is a single digit, alphabetic character, or other symbol that represents a valid character state as defined by the SYMBOLS list.

**Tree lists**  
A tree list is simply a list of tree numbers referring to one or more trees currently stored in memory. If two tree numbers are separated by a hyphen, this indicates that the range of trees between the first tree number and the second tree number (inclusive) are to be included in the list. To include all trees currently in memory, specify "ALL" as the tree list.

**Input/Output files**  
A number of PAUP* commands contain options to input or output data. Unless PAUP* is told otherwise, the default path-name for an input/output file is the path-name of the most recently accessed file. To override this default you must specify an explicit path-name. Path-names must follow operating system conventions. For example:

<table>
<thead>
<tr>
<th>OS</th>
<th>Syntax</th>
</tr>
</thead>
<tbody>
<tr>
<td>Macintosh</td>
<td>‘Harddrivename:Tree Folder:treefile.trees’</td>
</tr>
<tr>
<td>Dos</td>
<td>C:\Tree_Fol\treefile.tre</td>
</tr>
<tr>
<td>Window95/NT</td>
<td>‘C:\Tree Folder\treefile.trees’</td>
</tr>
<tr>
<td>UNIX</td>
<td>/home/users/Bob/tree_folder/treefile.trees</td>
</tr>
</tbody>
</table>

Unlike the PAUP* convention for identifiers, underscores (_) are not translated into blanks. File-names containing blanks must be enclosed within single-quotes for the Macintosh and Window95/NT releases and are not allowed under either the DOS or Unix releases. See your operating system documentation for other file naming conventions.

---

**Commands used in the TAXA Block**

The TAXA block specifies information about taxa. In previous versions of PAUP, both the taxa information and the character matrix were contained in the DATA block. However, in some instances the character matrix is not needed, making the option to input only taxa labels useful. While it is still permitted, we strongly recommend against use of a DATA block or
definition of taxa in a CHARACTERS or DISTANCES block because this will prevent some programs from extracting taxon information from the file.

BEGIN TAXA;
  DIMENSIONS NTAX=number-of-taxa;
  TAXLABELS taxon-name taxon-name ...;
END;

DIMENSIONS must appear before TAXLABELS, and only one of each command is allowed per block.

DIMENSIONS

The DIMENSIONS command specifies the size of the data matrix. The syntax is:

DIMENSIONS NTAX = number-of-taxa

where number-of-taxa and are integer values.

TAXLABELS

The TAXLABELS command defines taxa, specifies their names, and determines their order. The syntax is:

TAXLABELS taxon-label1 taxon-label2 ... taxon-label NTAX ;

The length limit on these labels is 16 characters, although up to 31 characters may included in graphical tree output. This is due to line-length constraints on PAUP* output. Any TAXLABELS command issued from the command line overrides any labels provided in the matrix. MacClade ignores TAXLABELS unless the data matrix is transposed.

Taxa may also be defined in the CHARACTERS and DISTANCES blocks, if the NEWTAXA token is included in the DIMENSIONS command; see the descriptions of those blocks for details.

Commands used in the CHARACTERS Block

A CHARACTERS block contains the data matrix and other associated information. Taxa are usually not defined in a CHARACTERS block; if they are not defined here, this block must be preceded by a block which defines taxon labels and ordering (e.g., TAXA). The syntax is:
BEGIN CHARACTERS;
DIMENSIONS
   [ NEWTAXA NTAX=number-of-taxa ]
   NCHAR = number-of-characters;
[ FORMAT
   [ DATATYPE = { STANDARD | DNA | RNA | NUCLEOTIDE | PROTEIN } ]
   [ RESPECTCASE ]
   [ MISSING = symbol ]
   [ GAP = symbol ]
   [ SYMBOLS = "symbol symbol..."]
   [ EQUATE = "symbol=entry [ symbol=entry... ]"
   [ MATCHCHAR = symbol ]
   [ LABELS = { NO | LEFT | RIGHT } ]
   [ TRANSPOSE ]
   [ INTERLEAVE ]
   [ [NO]TOKENS ]; ]
[ ELIMINATE character-set; ]
[ TAXLABELS taxon-name taxon-name...; ]
[ CHARSTATELABELS
   character-number [ character-name ]
   [ /state-name [ state-name... ]],...; ]
[ CHARLABELS character-name [character-name... ]; ]
[ STATELABELS character-number [ state-name [ state-name... ]],...; ]
MATRIX data-matrix;
END;

DIMENSIONS, FORMAT, and ELIMINATE must all precede CHARLABELS,
STATELABELS, and MATRIX. DIMENSIONS must precede ELIMINATE. Only
one of each command is allowed per block.

DIMENSIONS

The DIMENSIONS command specifies the size of the data matrix. Ordinarily,
the CHARACTERS block is proceeded by a TAXA block which contains taxa
information. However, if new taxa are to be defined in the CHARACTERS
block, this must be indicated by the NEWTAXA subcommand. NEWTAXA, if
present, must appear before the NTAX subcommand. The number
following NCHAR is the number of characters in the data matrix.

FORMAT

The FORMAT command is used to specify information pertaining to the
format of the data file. The DATATYPE subcommand must appear first in the
command. The RESPECTCASE subcommand must appear before the
MISSING, GAP, SYMBOLS, and MATCHCHAR subcommands.

Any or all of the following option specifications may be given:
Commands used in the CHARACTERS Block

**DATATYPE** = { **STANDARD** | DNA | RNA | NUCLEOTIDE | PROTEIN }

This subcommand specifies the class of data. If present, it must be the first subcommand in the FORMAT command. If **DATATYPE** = **STANDARD**, the **SYMBOLS** list is taken from the **SYMBOLS** = "symbols-list" item, above (default = "01"). If **DATATYPE** is set to one of the molecular sequence types, a predefined **SYMBOLS** list is used ("ACGT" for DNA, "ACTU" for RNA, and the standard one-letter amino acid codes for **PROTEIN**). In addition, standard ambiguity codes are implemented by predefined **EQUATE** macros.

**RESPECTCASE**

By default, PAUP* does not distinguish between upper- and lower-case character-state symbols in the data matrix. If you want upper- and lower-case representations of the same alphabetic character to refer to different character states, specify **RESPECTCASE**. This subcommand must appear before the **SYMBOLS** subcommand and is not applicable to **DATATYPE**=DNA, RNA, NUCLEOTIDE, and PROTEIN.

**MISSING** = **symbol**

The **symbol** specifies a character used to represent missing data. Any alphabetic, numeric, or other character that may be used as a character-state symbol may be used as the **missing-symbol**. If **MISSING** is not specified, it defaults to '?'. Whitespace is illegal as a missing data symbol, as are the following:

```
( ) [] {} / , ; := * ' ` " <> ^
```

**GAP** = **symbol**

The **symbol** a character used to represent alignment gaps, corresponding to insertions and/or deletions. For example, **gap**=− would assign the hyphen as the gap character. The **GAP** setting is ignored unless **DATATYPE** is DNA, RNA, or PROTEIN.

Alignment gaps may be treated either as missing data or as an additional character-state (fifth base or 21st amino acid) using the **GAPMODE** option. Whitespace is illegal as a gap symbol, as are the following:

```
( ) [] {} / , ; := * ' ` " <> ^
```

**SYMBOLS** = "**symbol symbol..."*

The **symbol** list defines a set of permissible symbols that may be used to designate character states. The default **SYMBOLS** list is "01" for the **STANDARD** data type (see below), which means that the only (non-missing) character-state symbols permitted are '0' and '1'. If you want to use any other symbols to designate character states, you must explicitly define an alternate **SYMBOLS** list.

The format of a **symbols-list** is a sequence of single-character
"symbols"; the entire list is then enclosed within double-quotes. Whitespace is not needed between elements: SYMBOLS="012" is equivalent to SYMBOLS="0 1 2".

**EQUATE = "symbol = entry"**

The EQUATE option provides a simple macro facility for translating character-state specifications in the data matrix to alternate character-state specifications. The symbol component must be a single-character. *Entry* is either a valid character-state or a character-state set.

Any number of EQUATE macros may be specified following the equal sign, but only one pair of double-quotes is used. For example:

```plaintext
format equate="U=T R={AG} .=- X=??;
```

EQUATE macros may not be defined recursively. That is, you cannot equate A to B and B to C, expecting A to be expanded to C. If you equate the same symbol to more than one expansion, the last definition applies. Case is significant in equate symbols. That is, MISSING=? EQUATE="E=(012) e=??" means that E will be interpreted as 0, 1, and 2, e as missing data.

**MATCHCHAR = symbol**

If a symbol is specified, any occurrence of that symbol in the data matrix is translated to the state (or state-set) occurring in the first row of the matrix. For example:

```plaintext
format datatype=dna gap=- matchchar=.;
matrix
 One  ATGCT ATCCG TCATG ACCTA
 Two  ..C... .G... .--A. ..GG.
 ThreeC.... .G... .GGA. T.....
 Four C..AA ----. A...A .GTC.
```

Whitespace is illegal as a matching character symbol, as are the following:

```
() [] {} , ; = * " / <>^`
```

**LABELS = { NO | LEFT | RIGHT }**

If LABELS = LEFT, taxon names (or character names, if the data matrix is transposed) begin each row of the data matrix (i.e., precede the character-state data). If LABELS = RIGHT, then these names end each row of the data matrix. The default is LABELS = LEFT. The LEFT and RIGHT options are PAUP* extensions. We recommend the use of LABELS or NOLABELS for compatibility with other Nexus programs. LABELS with no other qualifier is equivalent to LABELS = LEFT.

Example input format:
begin data;
  dimensions ntax=4 nchar=5;
  format label = right;
  matrix
    00111 taxon1
    0111? taxon2
    11001 taxon3
    10000 taxon4
  ;
end;

TRANSPOSE

If TRANSPOSE is specified, rows of the data matrix correspond to characters and columns correspond to taxa. Otherwise, rows correspond to taxa and columns to characters. The following is an example of a transposed data matrix:

begin data;
  dimensions ntax=4 nchar=5;
  format transpose;
  taxlabels taxon1 taxon2 taxon3 taxon4;
  matrix
    char1   0011
    char2   0110
    char3   1100
    char4   1100
    char5   1?10
  ;
end;

INTERLEAVE

Specification of allows the data to be entered in "blocks" of characters. If the data is not transposed, then each "block" contains information for some of the characters, for all taxa. Taxa in each section must occur in the same order. This format is especially useful for molecular sequence data, where the number of characters can be large. A small interleaved matrix follows:

matrix
taxon1   A C C T C G G C
taxon2   A C C T C G G C
taxon3   A C G T C G C T
taxon4   A C G T C G C T
taxon1   T T A A C G A
taxon2   T T A A C C A
taxon3   C T C A C C A
taxon4   T T C A C C A
;

The interleaved sections need not all be of the same length. In an
interleaved matrix, new line characters are significant; they indicate that the next character information encountered applies to a different taxon (for non-transposed matrices).

[NO]TOKENS

The TOKENS subcommand is currently not supported by PAUP* 4.0 beta; however, this subcommand is described here because it will be supported in the final release 4.0. This subcommand specifies whether or not data matrix entries are single symbols, or can be tokens. If TOKENS is specified, then the data values must be full NEXUS tokens, separated by whitespace or punctuation as appropriate, as in the following example:

```
begin characters;
dimensions nchar=3;
format tokens;
matrix
taxon_1 absent red big
taxon_2 absent blue small
taxon_3 present blue small;
end;
```

[NO]TOKENS is the default and is not allowed for DATATYPES DNA, RNA, and NUCLEOTIDE. If TOKENS is invoked, the standard 3-letter amino acid abbreviations can be used with DATATYPE = PROTEIN, and defined state names for DATATYPE = STANDARD.

ELIMINATE

This command allows one to specify a list of characters that are to be excluded from consideration. PAUP* will completely ignore eliminated characters. (This is similar to the ZAP subcommand in version 3.1 of PAUP.) For example;

```
eliminate 4-100;
```

tells the program to skip over characters 4 through 100 when the matrix is read. Character-set names are not allowed in the character list. This command does not affect character numbers.

TAXLABELS

This command allows one to specify the names of the taxa. It serves to define taxa, and is only allowed in a CHARACTERS block if the NEWTAXA token is included in the DIMENSIONS statement.
**CHARSTATELABELS**

CHARSTATELABELS allows one to specify both the names of the characters and names of the states. This command was developed as an alternative to the older commands CHARLABELS and STATELABELS. Here is an example:

```
charstatelabels
  1 eye_color/red blue green,
  3 head_shape/round square,
  5 pronotum_size/small medium large
;
```

A forward slash (/) separates the character name and the state names, with a comma separating the information for different characters. If no state names are to be specified, the slash may be omitted; if no character names are to be specified, the slash must be included, but no token needs to be included between the character number and the slash. If state x is the last state to be named, then subsequent states need not be named but states 1 through x must be. If no name is to be applied to a state, enter a single underscore for its name. Character names must not correspond to another character name or number; thus, 1 is not a valid name for the second character listed. PAUP* does not use character-state label information; however, it will extract the name from a CHARSTATELABELS command.

**CHARLABELS**

This command allows one to specify names of characters:

```
charlabels
  flange microsculpture body_length
  hind_angles #_spines spine_size
  _ _ head_size pubescent_intervals
  head_color clypeal_margin;
```

Character labels are listed consecutively. If character x is the last character to be named, then subsequent characters need not be named, but characters 1 through x need to be. If no name is to be applied to a character, a single underscore can be used for its name. Character names must not correspond to another character name or number; thus, 1 is not a valid name for the second character listed.

The command should be used only for non-transposed matrices (in transposed matrices, the character labels are defined in the MATRIX command).

**STATELABELS**

Use this command to assign names to character states. PAUP* does not use this information in any way, however, the information is used by MacClade and possibly other NEXUS programs.
statelabels
1 absent present,
2 isodiametric transverse,
3 '4.5–6.2mm' '6.3–7.0mm' '7.7–11.0mm',
4 rounded subangulate angulate,
10 0 '1–4' '6–9' '7–9' '8–9' 7 8 9,
11 black rufous metallic flavous,
12 straight concave, 
;

State labels need not be specified for all characters. A comma must separate state labels for each character. State labels are listed consecutively within a character. If state x is the last state to be named, then subsequent states need not be named, but states 1 through x must be. If no name is to be applied to a state, enter a single underscore for its name.

**MATRIX**

In its standard format, the **MATRIX** command contains a sequence of taxon names and state information for that taxon. The matrix itself may appear in a variety of forms. For example:

```
begin data;
  dimensions nchar=5;
  matrix
    taxon1  00111
    taxon2  0111?
    taxon3  11001
    taxon4  10000
  ;
end;
```

```
begin data;
  dimensions nchar=5;
  matrix
    taxon1
      001
      11
    taxon2
      011
      1?
    taxon3
      110
      01
    taxon4
      100
      00
  ;
end;
```
Commands used in the DATA Block

The DATA block contains the data matrix and other associated information. This block is equivalent to a CHARACTERS block in which the NEWTAXA subcommand is included in the DIMENSIONS command. In versions 3.0-3.07 of MacClade and 3.0-3.1.1 of PAUP, both the data matrix and taxa were saved in a DATA block. However, in some instances the character matrix is not needed, making the option to input only taxa labels useful. All of the options described in the TAXA and CHARACTERS blocks are still permitted under the DATA block; however, we strongly encourage the use of the TAXA and CHARACTERS blocks for the sake of compatibility with other programs using the NEXUS-format.

The following CHARACTER and TAXA blacks are equivalent to the single DATA block:

begin taxa;
  dimensions ntax=3;
  taxlabels taxon_1 taxon_2 taxon_3;
end;

begin characters;
  dimensions nchar=12;
  format datatype=DNA;
  matrix
    taxon_1  CCATGGTACGT
    taxon_2  TCCATGCTACCC
    taxon_3  TCCATGGAACCC;
end;

begin data;
  dimensions ntax = 3 nchar=12;
  format datatype=DNA;
  matrix
    taxon_1  CCATGGTACGT
    taxon_2  TCCATGCTACCC
    taxon_3  TCCATGGAACCC;
end;

Taxa need not be in same order as in the TAXA block, and the matrix need not contain all taxa. For interleaved matrices, all sections must have the same taxa in the same order.
Commands used in the ASSUMPTIONS Block

The ASSUMPTIONS block houses assumptions about the data, or gives general directions as to how to treat it (e.g., which characters are to be excluded from consideration). Its syntax is:

```
BEGIN ASSUMPTIONS;
[OPTIONS
  [ DEFType = type-name ]
  [ POLYTCount = { MINSteps | MAXSteps }]
  [ GAPMode = { MISSING | NEWState | INDEL } ] ]
[ USERType type-name
  [ ( { stepMatrix | CSTree } ) ] = usertype-description; ]
[ TYPESet[*] typeset-name [ ( { STANDARD | VECTOR } ) ] =
typeset-definition; ]
[ WtSET[*] wtset-name [ ( { STANDARD | VECTOR } { TOKENS | NOTOKENS } ) ] = wtset-definition; ]
[ ExSET[*] exset-name [ ( { STANDARD | VECTOR } ) ] = character-set; ]
[ ANCStates[*] ancstates-name [ ( { STANDARD | VECTOR } ) ] =ancstates-definition; ]
END;
```

In earlier versions of PAUP, the CHARSET and TAXSET commands also appeared in the ASSUMPTIONS block; now they appear in the SETS block. The GAPMODE subcommand of the OPTIONS command of this block was originally housed in an OPTIONS command in the DATA block. As this subcommand dictates how data are to be treated, rather than provide details about the data themselves, it was moved into the ASSUMPTIONS block.

**OPTIONS**

This command houses a number of disparate subcommands. They are all of the form subcommand = option.

**DEFType = type-name**

This specifies the default character type for parsimony analyses. Whenever a character's type is not explicitly stated, its type is taken to be the default type. The default DEFType is UNORD, but may be changed to one of the following: ORD, UNORD, DOLLO, DOLLO.UP, DOLLO.DN, IRREV, IRREV.UP, or IRREV.DN.

**POLYTCount = { MINSteps | MAXSteps }**

This option specifies whether polytomies are treated as "hard" or "soft" (see Maddison (1989)) when counting the number of steps required by a character and when reconstructing ancestral states. PAUP* currently supports only POLYTCount = MAXSteps ("hard" polytomies), and will ignore the POLYTCount specification.
Commands used in the ASSUMPTIONS Block

**GAPMODE** = {**MISSING** | **NEWSTATE** | **INDEL** }

Specifies how gaps are to be treated. GAPMODE = **MISSING** designates gaps to be treated in the same way as missing data; GAPMODE = **NEWSTATE** specifies that gaps are to be treated as an additional state (for DNA/RNA data, as a fifth base).

**USERTYPE**

The **USERTYPE** command defines a character transformation type, as used in parsimony analysis to designate the cost of changes between states. **USERTYPES** must be defined before they are referred to in any **TYPESET**. Character-type-description must follow the rules for character-state tree or stepmatrix description.

The **STEPMATRIX** format is as follows:

```
usertype mymatrix (stepmatrix)=n
   s  s  s  s
   .  k  k  k
   k  .  k  k
   k  k  .  k
   k  k  k  .;
```

where n is the number of rows and columns in the step matrix, the s's are state symbols, and the k's are the cost for going between states. n can take any value ≥ 2. Diagonal elements may be listed as periods. If a change is to be prohibited, then one enters an "i" for infinity. Typically, the state symbols will be in sequence, but they need not be. The following matrices assign values identically:

```
usertype mymatrix (stepmatrix)=4
   0  1  2  3
   .  1  5  1
   1  .  5  1
   5  5  .  5
   1  1  5  .;
```

```
usertype mymatrix2 (stepmatrix)=4
   2  0  3  1
   .  5  5  5
   5  .  1  1
   5  1  .  1
   5  1  1  .;
```

The **CSTREE** format is very similar to the **TREE** format in a **TREES** block. That is, character state trees are described in the parenthesis notation following the rules given for Trees of taxa. Instead of taxon labels, character state symbols are used. Thus

```
usertype cstree-name (cstree) = [(list of subtrees)][state-symbol];
```
where each subtree has the same format as the overall tree and the subtrees are separated by commas.

**TYPESET**

A **TYPESET** specifies a set of character-type assignments for each character as used in parsimony analysis. Any characters not listed in the character-set have the default character type. The type names to be used are either the predefined ones or those defined in a **USERTYPE** command. Each value in a definition in VECTOR format must be separated by whitespace. The following are equivalent type sets:

```plaintext
typeset mytypes = Ord: 1 4 6, Unord: 2 3 5;
typeset mytypes (vector) = Ord Unord Unord Ord Unord Ord;
```

**WTSET**

A **WTSET** specifies a set of character-weight assignments for each character. Any characters not listed in the character-set have weight 1. The weights may be either integers or real numbers. Each value in a definition in VECTOR format must be separated by whitespace, unless the NOTOKENS option is invoked, in which case no whitespace is needed, and all weights must be integers in the range 0-9. The following are equivalent weight sets:

```plaintext
wtset mywts = 3: 1 4 6, 1: 2 3 5;
wtset mywts (vector) = 3 1 1 3 1 3;
```

**ExSET**

**ExSET** specifies a set of characters that may be jointly excluded. This is a standard object definition command. Any characters not listed in the character-set are included. The VECTOR format consists of 0's and 1's - a 1 indicates that the character is to be excluded; whitespace is not necessary between 0's and 1's. The following commands are equivalent, and serve to exclude characters 5, 6, 7, 8, and 12.

```plaintext
exset * toexclude = 5-8 12;
exset * toexclude (vector) = 000011110001;
```

If you precede the **exset-name** with an asterisk, any previously excluded characters are re-included and the characters specified by **character-list** are excluded.
**AncStates**

The AncStates command allows one to specify ancestral states. Any valid state symbol can be used in the description for discrete data, and any valid value for continuous data. Tokens is not allowed for DataTypes DNA and RNA. If Tokens is invoked, the standard 3-letter amino acid abbreviations can be used with DataType = Protein, and defined state names for DataType = Standard. The following commands are equivalent:

```
ancstates ancestor = 0:1-3 5-7 12, 1:4 8-10, 2:11;
ancstates ancestor (vector) = 000100011120;
```

Any number of ancstates-name:ancstates-definition pairs, separated by commas, may be specified. You may also repeat the AncStates command to define multiple ancestors, although only one ancestor can be in effect at any given time. If you precede the ancestor-name with an asterisk, that ancestor becomes the "current" ancestor. You can also assign the current ancestor with the Assume command.

**Commands used in the SETS Block**

This block stores sets of objects (characters, states, taxa, etc.). The general structure of the SETS block is as follows:

```
BEGIN SETS;
[ CHARSET charset-name [{STANDARD | VECTOR}]=character-list ;]
[ TAXSET taxset-name [{STANDARD | VECTOR}]=taxon-list; ]
[ CHARPARTITION partition-name
  [ ([ [NO]Tokens ] ]
  [ [ STANDARD | VECTOR ] ]
  = subset-name : character-set,...; ]
[ TAXPARTITION partition-name
  [ ([ [NO]Tokens ] ]
  [ [ STANDARD | VECTOR ] ]
  = subset-name : taxon-set,...; ]
END;
```

**Charset**

The Charset command specifies and names a set of characters; this name can then be used in subsequent Charset definitions or wherever a character-list is required. The Vector format consists of 0's and 1's: a 1 indicates that the character is to be included in the Charset; whitespace is not necessary between 0's and 1's. The name of a Charset cannot be equivalent to a character name or character number.
The character-set CONSTANT is predefined for all data-types; it specifies all invariant characters. The character-set REMAINDER is predefined for all DATATYPES; it specifies all characters not previously referenced in the command. The character-set GAPPED is predefined for all DATATYPES; it specifies all characters with a gap for at least one taxon.

There are four additional predefined character-sets for characters of DATATYPE = DNA, RNA, NUCLEOTIDE if a CODONS block containing a CODONPosSet is supplied.

- **Pos1**: all characters defined by current CodonPosSet as first positions.
- **Pos2**: all characters defined by current CodonPosSet as second positions.
- **Pos3**: all characters defined by current CodonPosSet as third positions.
- **Noncoding**: all characters defined by current CodonPosSet as non-protein-coding sites.

**TaxSet**

This command defines a set of taxa. A **TaxSet** name can be used in subsequent **TaxSet** definitions or wherever a taxon-set is required. The name of a **TaxSet** cannot be equivalent to a taxon name or taxon number. The taxa to be included are described in a taxon-set. For example, the following command

```plaintext
taxset beetles = Omma-.;
```

defines the **TaxSet** "beetles" to include all taxa from taxon Omma to the last defined taxon.

The VECTOR format consists of 0's and 1's: a 1 indicates that the taxon is to be included in the **TaxSet**; whitespace is not necessary between 0's and 1's.

**CharPartition, TaxPartition**

These commands define partitions of characters, taxa, and trees, respectively. The partition divides the objects into several (mutually exclusive) subsets. They follow the same format, and will be described together.

There are several formatting options. The VECTOR format consists of a list of partition names. By default, the name of each subset is a NEXUS word (this is the **Tokens** option). The **NoTokens** option is only available in the VECTOR format; this allows one to use single symbols for the subset names. Each value in a definition in VECTOR format must be separated by whitespace if the names are tokens, but not if they are **NoTokens**.
The following two examples are equivalent:

```plaintext
taxpartition populations=1:1-3, 2:4-6, 3:7 8;
taxpartition populations (vector notokens) = 11122233;
```

The following two examples are equivalent:

```plaintext
taxpartition mypartition=Chiricahua: 1-3, Huachuca: 4-6, Galiuro: 7 8;
taxpartition mypartition (vector) = Chiricahua Chiricahua Chiricahua Huachuca Huachuca Huachuca Galiuro Galiuro;
```

### Commands used in the TRESSES Block

The TRESSES block is used to input user-defined trees to PAUP*. A single `TREE` command is used for each tree; any number of `TREE` commands may be included in the block.

The syntax for the TRESSES block follows:

```plaintext
BEGIN TRESSES [ block-name ] ;
    [ TRANSLATE token taxon-name [ , token taxon-name ] … ; ]
    [ TREE [*] name = tree-specification; ]
END;
```

#### TRANSLATE

Use the `TRANSLATE` command to define mappings of arbitrary tokens appearing in the `TREE` command to valid taxon names. Ordinarily, the tokens are the integers 1 through NTAX. The tree description requires references to the taxa defined in a `TAXA`, `CHARACTERS`, `DATA`, or `DISTANCES` block.

#### TREE

Use the `TREE` command to define trees. If no rooting-specification is supplied, the default in PAUP* is to interpret the tree description as specifying a rooted tree. You can override this behavior by using a "special comment." The comment `'[&U]'` indicates that the tree should be considered unrooted and the comment `'[&R]'` indicates that the tree should be considered rooted. For example:
tree mytree = [&R] ((1,2),(3,4));

is a rooted tree, whereas

tree mytree = [&U] ((1,2),(3,4));

is an unrooted tree. You will usually define unrooted trees. These trees are then rooted for output purposes using the outgroup or Lundberg rooting procedures. However, if you wish to define an ancestor for the full tree (see ANCSTATES command), if you are using directed characters, or if you want to evaluate trees under a maximum likelihood "clock" constraint you may wish to define rooted trees instead. In any case, you can convert rooted trees to unrooted trees and vice versa using the RootTrees/DeroootTrees commands.

Note that in order to write the tree descriptions, unrooted trees may be rooted at any convenient point (including a terminal taxon or internal node); the position of the root is simply ignored when the tree is stored.

Another "special comment" stored in the TREES block and used by PAUP* is the tree weight comment. Tree weights are the reciprocal of the number of trees found in either a Bootstrap or Jackknife replicate. This option allows the combination of bootstrap results from runs performed at different times or on different machines and the recovery of results obtained prior to a system crash. For example the TREEFILE created by the Bootstrap command might look like this:

[Trees found in bootstrap replicate #1]
tree B_1.1 = [&W 1] (1,(((2,4),5),3),6));

[Trees found in bootstrap replicate #2]
tree B_2.1 = [&W 1/2] (1,(((2,4),5),6),3));
tree B_2.2 = [&W 1/2] (1,(((2,4),(5,6)),3));

An example tree with branch lengths is

tree PAUP_1 = [&U] (1:22,(2:12,3:9):9,4:72);

PAUP* currently ignores the tree names; trees are referred to subsequently only by number, in the order in which they are presented in the TREES block. (MacClade uses the tree names, however.) If the name is preceded by an asterisk (*), the tree becomes the "default" tree. (E.g., a DescribeTrees command with no tree list will result in the description of the default tree.)

If a taxon is omitted from the tree specification, it is assumed to descend from the root of the tree described by the remaining taxa.
Commands used in the CODONS Block

The CODONS block contains information about the genetic code, the regions of DNA and RNA sequences that are protein coding, and the location of triplets coding for amino acids in nucleotide sequences. Numerous other commands used by other NEXUS-compliant programs may be included in the CODONS block. Currently only the CODONPOSSET command is implemented in PAUP*; all other CODONS block commands will be ignored.

```
BEGIN CODONS;
  [ CODONPOSSET [*] name [[] STANDARD | VECTOR]] =
    N: character-set,
    1: character-set,
    2: character-set,
    3: character-set;]
END;
```

CODONPOSSET

The CODONPOSSET command stores information about protein coding regions and the codon positions of nucleotide bases in protein-coding regions.

Those characters designated as 1, 2, or 3 are coding bases which are specified as being of positions 1, 2, and 3, respectively. Those characters designated as N are considered non-protein-coding. Those characters designated as ? are of unknown nature. Any unspecified bases are considered of unknown nature (equivalent to ?). If no CODONPOSSET statement is present, all bases are presumed of unknown nature.

For example, the following command

```
codonposset * coding=
  N:1-10,
  1:11-.\3,
  2:12-.\3,
  3:13-.\3;
```

designates bases 1-10 as noncoding, and positions of the remaining bases in the order 123123123....

Commands used in the DISTANCES Block

This block contains distance matrices. Taxa are usually not defined in a DISTANCES block; rather, this block should be preceded by a block that
defines taxon labels and ordering (e.g., TAXA). The syntax of the block is as follows:

```
BEGIN DISTANCES;
[ DIMENSIONS [ NEWTAXA ] NTAX = number-of-taxa
    NCHAR = number-of-characters;]
[ FORMAT
    [ TRIANGLE = { LOWER | UPPER | BOTH } ]
    [ [No] DIAGONAL ]
    [ [No] LABELS ]
    [ MISSING = SYMBOL ]
    [ INTERLEAVE ]; ]
[ TAXLABELS taxon-name taxon-name...]
MATRIX distance-matrix ;
END;
```

Commands must appear in the order listed. Only one of each command is allowed per block.

**DIMENSIONS**

The NTAX subcommand of this command is needed to process the matrix when some defined taxa are omitted from the distance matrix. The NCHAR subcommand is optional, and can be used to indicate the number of characters for those analyses that need to know how many characters (if any) were used to calculate the distances. NCHAR is not required for successful reading of the matrix.

As for the CHARACTERS block, taxa can be defined in a DISTANCES block if NEWTAXA precedes the NTAXA subcommand in the DIMENSIONS command. It is advised that new taxa not be defined in a DISTANCES block, for the reasons discussed in the description of the DATA block. NEWTAXA, if present, must be appear before the NTAX subcommand.

**FORMAT**

This command specifies the formatting of the MATRIX. The [No]LABELS and MISSING subcommands are as described in the CHARACTERS block.

```
TRIANGLE = { LOWER | UPPER | BOTH }
```

This subcommand specifies whether only the lower left half of the matrix is present, or only the upper right, or both halves. Below is one example of an upper triangular matrix and one of a matrix with both halves included.
begin distances;
    format triangle = upper;
    matrix
        taxon_1  0.0  1.0  2.0  4.0  7.0
        taxon_2  0.0  3.0  5.0  8.0
        taxon_3  0.0  6.0  9.0
        taxon_4  0.0 10.0
        taxon_5  0.0;
end;

begin distances;
    format triangle = both;
    matrix
        taxon_1  0  1.0  2.0  4.0  7.0
        taxon_2  1.0  0  3.0  5.0  8.0
        taxon_3  2.0  3.0  0  6.0  9.0
        taxon_4  4.0  5.0  6.0  0 10.0
        taxon_5  7.0  8.0  9.0 10.0  0;
end;

DIAGONAL

If DIAGONAL is turned off, the diagonal elements are not included

    format nodiagonal;
    matrix
        taxon_1
        taxon_2  1.0
        taxon_3  2.0  3.0
        taxon_4  4.0  5.0  6.0
        taxon_5  7.0  8.0  9.0 10.0;

If TRIANGLE is not BOTH, then there will be one row that contains only
the name of a taxon. This row is required. If TRIANGLE = BOTH, then
the diagonal must be included.

INTERLEAVE

The INTERLEAVE subcommand in the DISTANCE block is currently not
supported by PAUP* 4.0 beta; however, this subcommand is
described here because it will be supported in the final release 4.0.
The INTERLEAVE format is similar to that described in the
CHARACTERS block, although the interleaved distance matrices take
a slightly different form:
As in the CHARACTERS block, new line characters in interleaved matrices are significant, in that they indicate a switch to a new taxon.

**TAXLABELS**

TAXLABELS allows one to specify the names and ordering of the taxa. This command serves to define taxa, and is allowed only if the NEWTAXA token is included in the DIMENSIONS statement.

**MATRIX**

The MATRIX command contains the distance data.

### Commands used in the PAUP Block

Commands described in this section are specific to PAUP*. They may be included in the PAUP block of a NEXUS file or typed from the command line.

Unless otherwise specified, options specified in these commands are "persistent;" i.e., they retain their values between successful invocations of the command. Persistence of options simplifies typing of commands because one a command requiring a large number of options has been entered once, subsequent invocations of the command need not respecify all of the options. The drawback is that you can become temporarily confused if you forget that a previously specified option remains in effect until you explicitly override it.

**OPTIONS AND SUBCOMMANDS AFFECTING MULTIPLE COMMANDS**

Several options apply to a number of commands. Specification of these options on one command affects all commands that use the same options. To minimize redundancy, these options are described in the following sections rather than in the description for each individual command to which the option applies.
Tree-searching options

These options pertain to the commands that request searching for trees.

**KEEP** = *real-value*

If *real-value* is zero, only the best trees found will be saved. If *real-value* ≥ zero, all trees of score ≤ *real-value* will be saved. By default, *real-value* = 0, so that only the best trees found will be saved.

**ENFORCE** = { YES | NO }

ENFORCE requests that topological constraints be enforced; i.e., trees that are not compatible with the constraint tree are not evaluated. If the CONSTRAINTS option (see below) is not used to specify a constraint tree, the "current" constraint tree is used.

**DSTATUS** = { integer-value | NO }

Information on the progress of the search (number of trees examined, number of trees saved, etc.) may output to the display buffer using the DSTATUS setting. Specify an *integer-value* to control how frequently (in seconds) information is output to the display or specify DSTATUS = NO to suppress this information. The default setting for the Macintosh versions of PAUP* is DSTATUS = NO and DSTATUS = 60 for all other versions.

**CONSTRAINTS** = constraint-tree-name

The specified constraint tree, which must have been defined in a previous CONSTRAINTS command, becomes the current constraint tree. You must also specify ENFORCE if you want to search under constraints.

**CONVERSE** = { YES | NO }

If CONVERSE is specified in conjunction with ENFORCE, only trees that are not compatible with the constraint tree are evaluated. CONVERSE = NO reverses the effect of a previous CONVERSE specification.

**STATUS** = { YES | NO }

Information on the progress of the search (number of trees examined, number of trees saved, etc.) is output to a status window. STATUS = NO suppresses this window.

Tree-rooting options

**ROOT** = { OUTGROUP | LUNDBERG | MIDPOINT }

The ROOT option is used to specify how unrooted trees are to be rooted prior to output. You can choose OUTGROUP rooting, using whichever outgroup you have selected; MIDPOINT rooting, which roots the tree at its midpoint; or LUNDBERG rooting, which requires that a previous ANCSTATES command has been issued. By default, OUTGROUP rooting is in effect.
OUTROOT = { POLYOMY | PARAPHYL | MONOPHYL }

If outgroup-rooting is currently selected, there are three options for output. The outgroup can make up a polytomy next to the ingroup (POLYOMY, the default); or it can be made to be paraphyletic relative to the ingroup (PARAPHYL); or the monophyletic sister group to the ingroup (MONOPHYL).

Tree output options

TCOMPRESS = { YES | NO }

Specify TCOMPRESS to output tree diagrams in a "vertically compressed" format. The resulting diagram is not as aesthetically appealing, but it allows more of a large tree to be seen on one screen (or in one window), and it takes less paper to print.

Options for character-matrix listings

SHOWEXCLUDED = { YES | NO }

Unless SHOWEXCLUDED is specified, "excluded" characters are not shown in character-matrix listings.

CMLABELS = { YES | NO }

By default, character names are used to label the columns of character-matrix listings. If you want to use numbers even when character names are available, specify CMLABELS = NO.

CMCSTATUS = { YES | NO }

If CMCSTATUS is specified, characters that are constant, "zapped," uninformative, or excluded are identified by asterisks at the top of each column of a character-matrix listing.

CMCOLWID = column-width

The value specified for column-width determines the number of columns used for each character in the data matrix. The default is CMCOLWID=2, so that one blank column appears between each column of character state data. For sequence data, you may want to use CMCOLWID=1 in order to fit more characters onto each line of output.

CMSHOWEQ = { YES | NO }

Unless CMSHOWEQ has been specified, if the possible state assignments to an interior node correspond to a multistate taxon code specified in an EQUATE macro, the corresponding EQUATE character is shown rather than the equivalent set of character states.

Other options

OPT = { ACCTRAN | DELTRAN | MINF }

The OPT= subcommand determines how the characters are optimized on the tree(s) in memory. ACCTRAN (the default) uses "accelerated transformation", DELTRAN uses "delayed transformation", while MINF optimizes so as to minimize the "f-
value" (Farris, 1972; Swofford and Maddison, 1987). See the section on character-state optimization for detailed discussion of these options.

ANCSTATES = ancestral-states-name

Change the ancestor currently in effect to the ancestral-states-name defined in an earlier ANCSTATES command (or to STANDARD). This option affects searching and character-state reconstruction algorithms.

? 

The "?" command is a synonym for HELP. "?" with no arguments requests a list of the available commands. See help on HELP for further information.

[PAUP command] ?

! 

Use the ! command to execute a UNIX command from within PAUP*. You can type a command that contains a semicolon by enclosing the entire command within single-quotes. You can open a temporary UNIX shell by typing, for example, !csh or !sh. When you are ready to resume your PAUP* session, type exit or Ctrl-D to exit the shell and return to PAUP*. Note, some shells respond differently to this command.

! [ unix-command ] ;

AGREE

Use the AGREE command to calculate agreement subtrees.

AGREE [tree-list] [/options] ;

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALL</td>
<td>{NO</td>
<td>SETS</td>
</tr>
<tr>
<td>SHOWTree</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>FILE</td>
<td>tree-file-name</td>
<td>none</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>APPEND</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TCOMPRESS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>
Description of options:

\texttt{ALL = \{ NO \mid SETS \mid TREES \mid BOTH \}}

Use ALL to calculate agreement subtrees for the trees specified in the \texttt{AGREE [tree-list]}. If \texttt{ALL = SETS}, a list of the agreement sets and the taxa included within each set is given. If \texttt{ALL = TREES}, all of the agreement subtrees are printed, overriding \texttt{SHOWTREE = NO} if this option was specified.

\texttt{SHOWTREE = \{ YES \mid NO \}}

Shows the agreement subtree(s) given in the \texttt{[tree-list]}.

\texttt{FILE = tree-file-name}

If FILE is specified, a description of all agreement subtrees is output to a file containing a NEXUS-format TREES block. This option is not persistent; you must specify it on every \texttt{AGREE} command for which you want a tree file to be saved. (See "Input/Output files" on page 9 for more details).

The following options apply only if FILE is specified

\texttt{REPLACE = \{ YES \mid NO \}}
\texttt{APPEND = \{ YES \mid NO \}}

If the specified file already exists, you will be prompted for confirmation that the existing file should be replaced. Explicit specification of REPLACE suppresses this prompt; the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND, in which case a new TREES block will be concatenated to the end of an existing file.

\texttt{TCOMPRESS = \{ YES \mid NO \}}

See "Tree output options" on page 31 under "Options Affecting Multiple Commands".

\textbf{ALLTREES}

Use the \texttt{ALLTREES} command to perform an exhaustive search of all possible tree topologies. The syntax is:

\texttt{ALLTREES [options] ;}
Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default Settings</th>
</tr>
</thead>
<tbody>
<tr>
<td>KEEP</td>
<td>{ real-value</td>
<td>NO }</td>
</tr>
<tr>
<td>ENFORCE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CONSTRAINTS</td>
<td>constraint-name</td>
<td>NONE</td>
</tr>
<tr>
<td>CONVERSE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>FD</td>
<td>{ NO</td>
<td>BARCHART</td>
</tr>
<tr>
<td>NCLASSES</td>
<td>integer-value</td>
<td>20</td>
</tr>
<tr>
<td>FDFILE</td>
<td>frequency-distribution-file-name</td>
<td>NONE</td>
</tr>
<tr>
<td>SCOREFILE</td>
<td>file-name-for-scores</td>
<td>NONE</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>STATUS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>DSTATUS</td>
<td>{ integer-value</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*Option is nonpersistent

Description of options:

FD = { NO | BARCHART | HISTOGRAM }

Unless FD = No is specified, a frequency distribution of tree scores is output. (Normally, obtaining the frequency distribution is the only reason for doing an exhaustive rather than branch-and-bound search, so you will probably never specify this option.) FD = BARCHART is the default so that the number of trees at each score is output. If FD = HISTOGRAM, tree scores are pooled into classes, the size of which is specified by the NCLASSES option.

NCLASSES = integer-value

Integer-value specifies the number of class intervals for the frequency distribution of tree scores. By default, NCLASSES=20, so that adjacent tree scores are pooled into 20 classes of tree scores. This option is only relevant when FD = HISTOGRAM.

FDFILE = frequency-distribution-file-name

If FDFILE is specified, the data for the frequency distribution of tree scores are saved to a text file for input to other programs. The FDFILE option is not persistent. Frequency-distribution-file-name specifies the name of the file to receive the frequency distribution. (See "Input/Output files" on page 9 for more details).
REPLACE = \{ YES | NO \}

If FDFILE is used and the specified file already exists you will be prompted for confirmation that the existing file should be replaced. REPLACE suppresses this prompt; the existing file will be quietly overwritten by the new data.

SCOREFILE = file-name-for-scores

Use SCOREFILE to save a text file of tree scores found during the exhaustive search.

See "Tree-searching options" on page 30 under "Options Affecting Multiple Commands" for a description of the following options:

KEEP = keep-score
ENFORCE = \{ YES | NO \}
CONSTRAINTS = constraint-tree-name
CONVERSE = \{ YES | NO \}
STATUS = \{ YES | NO \}
DSTATUS = \{ integer-value | NO \}

ANCSTATES

The ANCSTATES command, used to define ancestral states, is ordinarily issued from within the ASSUMPTIONS block. You may also issue it from the command line or from within a PAUP block. See "Commands used in the ASSUMPTIONS Block" on page 19 for the description of this command.

ASSUME

Use the ASSUME command to invoke a type set, weight set, or exclusion set, or to select an ancestor. The options under this command are described in the "Commands used in the ASSUMPTIONS Block" on page 19. The syntax is:

ASSUME \{ options \} ;

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>TYPESET</td>
<td>typeset-name</td>
<td>none</td>
</tr>
<tr>
<td>WTSET</td>
<td>wtset-name</td>
<td>none</td>
</tr>
<tr>
<td>EXSET</td>
<td>exset-name</td>
<td>none</td>
</tr>
<tr>
<td>ANCSTATES</td>
<td>ancstates-name</td>
<td>none</td>
</tr>
</tbody>
</table>
**BANDB**

Use the **BANDB** command to search for trees using the branch-and-bound algorithm. The syntax is:

```
BANDB [options] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>UPBOUND</td>
<td>real-value</td>
<td>0</td>
</tr>
<tr>
<td>KEEP</td>
<td>{real-value</td>
<td>NO }</td>
</tr>
<tr>
<td>ENFORCE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CONSTRAINTS</td>
<td>constraint-name</td>
<td>none</td>
</tr>
<tr>
<td>CONVERSE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>FDONLY</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>FDTYPE</td>
<td>{ BARCHART</td>
<td>HISTOGRAM }</td>
</tr>
<tr>
<td>NCLASSES</td>
<td>integer-value</td>
<td>20</td>
</tr>
<tr>
<td>FDFILE</td>
<td>frequency-distribution-file-name</td>
<td>none</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>ADDSEQ</td>
<td>{ FURTHEST</td>
<td>ASIS</td>
</tr>
<tr>
<td>MULTREES</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>STATUS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>DSTATUS</td>
<td>{integer-value</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*OPTION IS NONPERSISTENT

Option descriptions:

**UPBOUND = upper-bound**

Use this option to specify an upper bound on the score of the best tree(s). If you do not specify an upper bound on the score of the best tree (or if you specify UPBOUND=0), PAUP* computes a starting upper bound via the stepwise addition algorithm.

**FDONLY = { YES | NO }**

If FDONLY = YES, then a frequency distribution of tree scores is
output for all trees less than or equal to the score specified by the
KEEP option. This option is not permitted unless it is used in
conjunction with the KEEP score option.

**FDTYPE = \{ BARCHART | HISTOGRAM \}**

The default FDTYPE specifies that the number of trees at each tree
score is output as a BARCHART. If FDTYPE = HISTOGRAM, tree scores
are pooled into classes, the size of which is specified by the NCLASSES
option.

**NCLASSES = integer-value**

*Integer-value* specifies the number of class intervals for the frequency
distribution of tree scores. By default, NCLASSES = 20, so that
adjacent tree scores are pooled into 20 classes of tree scores. This
option is only available when FDTYPE = HISTOGRAM.

**FDFILE = frequency-distribution-file-name**

If FDFILE is specified, the data for the frequency distribution of tree
scores are saved to a text file for input to other programs. The FDFILE
option is not persistent. *Frequency-distribution-file-name* specifies the
name of the file to receive the frequency distribution. (See "Input/
Output files" on page 9 for more details).

**REPLACE = \{ YES | NO \}**

If FDFILE is used and the specified file already exists you will
be prompted for confirmation that the existing file should be
replaced. REPLACE suppresses this prompt; the existing file
will be quietly overwritten by the new data.

**ADDSEQ = \{ FURTHEST | ASIS | SIMPLE | MAXMINI | KMAXMINI \}**

ADDSEQ specifies the way in which taxa are selected for next
addition to the tree at the current node of the search tree. FURTHEST
is usually the fastest, although it is not permitted unless all
characters are of type ORD or UNORD (it will automatically be
overridden by SIMPLE in this case).

**MULTREES = \{ YES | NO \}**

Ordinarily, PAUP* saves all minimal trees it finds during the branch-
and-bound search. You can use MULTREES = NO to save only one of
the best trees found. If you only want to know the score of the best
tree(s), use this option. The single tree found is guaranteed to be of
minimum score and the search often runs much faster.

See "Tree-searching options" on page 30 under "Options Affecting Multiple
Commands" for a description of the following options:

**KEEP = keep-score**

**ENFORCE = \{ YES | NO \}**
**BASEFREQS**

Use the `BASEFREQS` command to show base frequencies for each taxon. In addition, this command gives the expected base frequencies for each taxon and the Chi-square test of homogeneity of base frequencies across taxa. The syntax is:

```
BASEFREQS ;
```

**BOOTSTRAP**

Use the `BOOTSTRAP` command to perform a bootstrap analysis using either a branch-and-bound or a heuristic search. The syntax is:

```
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSEED</td>
<td>integer-value</td>
<td>0</td>
</tr>
<tr>
<td>NREPS</td>
<td>integer-value</td>
<td>100</td>
</tr>
<tr>
<td>SEARCH</td>
<td>{ HEURISTIC</td>
<td>BANDB</td>
</tr>
<tr>
<td>CONLEVEL</td>
<td>integer-value</td>
<td>50</td>
</tr>
<tr>
<td>KEEPALL</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>WTS</td>
<td>{ NO</td>
<td>SIMPLE</td>
</tr>
<tr>
<td>NCHAR</td>
<td>{ CURRENT</td>
<td>number-of-characters }</td>
</tr>
<tr>
<td>GRPFREQ</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TREEFILE</td>
<td>bootstrap-tree-file-name</td>
<td>none</td>
</tr>
<tr>
<td>FORMAT</td>
<td>{ Nexus</td>
<td>ALTNexus</td>
</tr>
<tr>
<td>BRLENS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>
*OPTION IS NONPERSISTENT

Description of options:

**BSEED = integer-value**

By default, PAUP* references the system clock to obtain a value used to seed a random number generator. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)

**NREPS = integer-value**

Use NREPS to specify the number of bootstrap replications (resamplings) to be performed. The default is 100.

**SEARCH = { HEURISTIC | BANDB | FASTSTEP | NJ | UPGMA }**

A tree search is performed for each bootstrap resampling of the characters using the options specified under SEARCH. If SEARCH = FASTSTEP, tree searches in each replication are performed using one random-sequence-addition replication and no branch swapping. SEARCH = NJ | UPGMA may be used only if the distance criterion has been selected (see the "Set" command described on page 103).

**CONLEVEL = integer-value**

Use CONLEVEL to specify the minimum proportion of the bootstrap replicates (expressed as a percentage) in which a group must appear if it is to be included in the bootstrap consensus tree. For example, to obtain a bootstrap consensus tree that shows only those groups which occurred on more than 80% of the trees, you would specify CONLEVEL=80.

CONLEVEL must be at least 50, which is the default.

**WTS = { NO | SIMPLE | REPEATCNT }**

If WTS = NO, any previously applied character weights are ignored. If WTS = SIMPLE, then characters are sampled with equal probability but any character weights are applied. If WTS = REPEATCNT, then weights are treated as repeat counts. WTS = REPEATCNT option is only allowed if all weights are integers.

**NCHAR = { CURRENT | number-of-characters }**

Use NCHAR to specify the number of characters to sample in each replicate. You will almost always want to use NCHAR = CURRENT,
however, the option to sample more or fewer than the number of currently included characters may be useful in certain specialized contexts. Using character weights is not allowed when NCHAR is set to a value other than the number of included characters.

GRPFREQ = { YES | NO }

Unless GRPFREQ = NO, a table of bootstrap partition frequencies is output to the display buffer.

KEEPALL = { YES | NO }

If you request KEEPALL, groups occurring at frequencies less than CONLEVEL will also be retained in the bootstrap consensus as long as they are compatible with all groups that are already included in the consensus. Effectively, this forces CONLEVEL=50, because any group occurring in 50% or more of the replicates will automatically be compatible with all more frequently occurring groups.

TREEFILE = bootstrap-tree-file-name

If TREEFILE is specified, a description of all trees found in each bootstrap replicate is given in the NEXUS tree format. Trees contain a weight comment for the purposed of combining bootstrap results from runs performed at different times or on different machines and for recovering results obtained prior to a system crash. The weight is the reciprocal of the number of trees found in a replicate. The bootstrap-tree-file-name must follow the conventions described under "Input/Output files" on page 9

REPLACE = { YES | NO }

If TREEFILE is used and the specified file already exists you will be prompted for confirmation that the existing file should be replaced. REPLACE suppresses this prompt and the existing file will be quietly overwritten by the new data.

FORMAT = { NEXUS | ALTNEX | FREQPARS | PHYLIP | HENNIG }

Specifies the type of treefile to be produced. NEXUS requests a file containing the standard NEXUS TREES block using a translation table (which greatly reduces the amount of disk space required to store the trees). ALTNEX also specifies a NEXUS TREES block, but no translation table is used (the full taxon names are included in each tree description). FREQPARS requests a treefile for the FREQPARS program described by Swofford and Berlocher (1987). PHYLIP requests a treefile for input to version 3.x of Felsenstein's (1991) PHYLIP package. HENNIG requests a treefile for version 1.5 of Farris's (1988) Hennig86 program.

BRLENS = { YES | NO }

If BRLENS = YES is specified, tree descriptions will include branch lengths if the program corresponding to the FORMAT setting
supports them.  `BRLENS = NO` reverses the effect of a previous `BRLENS` specification.

**CUTOFFPCT** = integer-value

Use `CUTOFFPCT` to specify the minimum bootstrap partition frequency to be displayed in the partition frequency table. Partitions occurring at a frequency below this value are not shown.

---

**CHARPARTITION**

Use the `CHARPARTITION` to define a partition of the characters. The syntax is:

```
CHARPARTITION partition-name = partition-definition ;
```

The `CHARPARTITION` command is ordinarily issued from within the `SETS` block. However, you may also issue it from the command line or from within a PAUP block.

---

**CHARSET**

Use the `CHARSET` command to define a "character set." Character sets are simply groups of characters that can be referred to by a single name in other commands. The syntax is:

```
CHARSET character-set-name = character-list ;
```

The `character-set-name` must not be identical to any of the original character names.

The `CHARSET` command is ordinarily issued from within the `SETS` block. However, you may also issue it from the command line or from within a PAUP block.

---

**CLEARTREES**

Use the `CLEARTREES` command to empty the tree buffer. Ordinarily you will be prompted for conformation. If you specify `NOWARN = YES`, the tree buffer is silently emptied. The syntax is:

```
CLEARTREES [NOWARN] ;
```

---

**CONDENSE**

Use the `CONDENSE` command to collapse zero-length branches into polytomies for all trees and then keep only those trees that are unique after the collapsing is accomplished. The syntax is:
CONDENSE [options] ;

Available options:

**Keyword** | **Option type** | **Default setting**
--- | --- | ---
COLLAPSE | { NO | MAXBRLEN | MINBRLEN | AMBEQUAL } | MAXBRLEN
DEL DUPES | { YES | NO } | YES

Description of Options:

**COLLAPSE** = { NO | MAXBRLEN | MINBRLEN | AMBEQUAL }

Unless COLLAPSE = NO is specified, branches are collapsed according to the specified criterion.

**DEL DUPES** = { YES | NO }

Unless DEL DUPES is specified, duplicate trees will be eliminated.

**CONSTRAINTS**

Use the **CONSTRAINTS** command to define a constraint tree. The syntax is:

```
CONSTRAINTS constraint-name [ (BACKBONE) | (MONOPHYLY) | (CONVEXITY) ] = tree-specification | taxpartition-name ;
```

The tree-specification must follow the format for "TREE" on page 24. The taxpartition-name must follow the format described under **TAXPARTITION** on page 23.

**CONTREE**

Use the **CONTREE** command to request computation of strict, semistrict (combinable component), Adams, and/or majority-rule consensus trees. The syntax is:

```
CON TREE [tree-list] [ / options ] ;
```

The tree list specifies which trees to include in the consensus; the default is "ALL."

Available options:

**Keyword** | **Option type** | **Default setting**
--- | --- | ---
PERCENT | integer-value | 50
LE50 | { YES | NO } | No
Description of options:

**STRICT** = { **YES** | **NO** }

By default, a strict consensus tree is computed. Use STRICT = **NO** to suppress this computation.

**SEMISTRUCT** = { **YES** | **NO** }

Specify SEMISTRUCT = **YES** to request computation of a semistrict (combinable component) consensus tree. SEMISTRUCT = **NO** reverses the effect of a previous SEMISTRUCT specification.

**MAJRULE** = { **YES** | **NO** }

Specify MAJRULE = **YES** to request computation of a semistrict (combinable component) consensus tree. MAJRULE = **NO** reverses the effect of a previous MAJRULE specification.

The following options apply only if MAJRULE is in effect:

**PERCENT** = integer-value

The integer-value specifies the percentage of the trees on which
a group must appear in order to be retained in the majority-rule consensus. A group must appear on more than this percentage of the trees before it is retained. The default is 50.

LE50 = { YES | NO }

If LE50 = YES is specified, groups occurring on less than 50% of the trees are retained in the consensus if they are compatible with the groups already on the tree. LE50 = NO reverses the effect of a previous LE50 specification.

GRPfreq = { YES | NO }

By default, a table is output that shows all partitions (or groups) occurring on at least one tree and the frequency of each such group. GRPfreq = NO can be used to suppress this output.

ADAMS = { YES | NO }

Specify ADAMS = YES to request computation of an Adams consensus tree. ADAMS = NO reverses the effect of a previous ADAMS specification.

USETreeWts = { YES | NO }

Trees output to a treefile in bootstrap and jackknife contain a weight comment. These weights are the reciprocal of the number of trees found in a replicate. The GETTREES command will optionally store these weights, and the majority-rule consensus calculator will use them when USETreeWts = YES. This allows calculation of majority-rule consensus trees that correspond exactly to the consensus tree output by the original bootstrap or jackknife command. This option allows the combination of bootstrap results from runs performed at different times or on different machines and the recovery of results obtained prior to a system crash. Also, it permits graphics-quality output of bootstrap trees after redefining an outgroup or otherwise changing rooting options by rereading the trees (with weights) and computing/printing a majority-rule consensus tree.

INDICES = { YES | NO }

Specify INDICES to request calculation of a variety of consensus indices. The following indices are computed by PAUP* and are described in Rohlf (1982) and Swofford (1991):

- Component information (consensus fork)
- Nelson-Platnick term information
- Nelson-Platnick total information
- Mickevich's consensus information
- Colless weighted consensus fork (proportion max. information)
- Schuh-Farris levels sum
- Rohlf's CI(1)
- Rohlf's -ln CI(2)
SHOWTREE = { YES | NO }

Unless SHOWTREE = NO, the consensus tree (or trees if more than one consensus method is specified) is printed to the display buffer.

TREEFILE = file-specification

If TREEFILE is specified, a description of all consensus trees computed is output to a file containing a NEXUS-format TREES block. This option is not persistent; you must specify it on every CONTREE command for which you want a tree file to be saved. (See "Input/Output files" on page 9)

APPEND = { YES | NO }
REPLACE = { YES | NO }

If the specified file already exists, you will be prompted for confirmation that the existing file should be replaced. Explicit specification of REPLACE suppresses this prompt and the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND, in which case a new TREES block will be concatenated to the end of an existing file.

See "Options And Subcommands Affecting Multiple Commands" on page 29 for a description of the following options:

ROOT = { OUTGROUP | LUNDBERG | MIDPOINT }
OUTROOT = { POLYTOMY | PARAPHYL | MONOPHYL }
TCOMPRESS = { YES | NO }

CSTATUS

Use the CSTATUS command to request a listing of character-status information for all characters. Currently only a single option is available for this command. Use FULL = {YES | NO } to specify whether the full status of each character is output or only a brief summary. The syntax is:

CSTATUS [ options ];

For each character, the following information is output if FULL = YES:

1. The number and name (if any) of the character.
2. The character’s current type.
3. If the character is constant (invariant), excluded, or uninformative.
4. The character’s current weight. The weight value is put into parentheses if the character is excluded.
5. A list of the states observed for the character.
**CTYPE**

Use the **CTYPE** command to assign character types to characters. The syntax is:

```
CTYPE  type-name: character-list [, type-name:
         character-list] . . . ;
```

The `type-name` must be one of the standard character types (ORD, UNORD, DOLLO, DOLLO.UP, DOLLO.DN, IRREV, IRREV.UP, or IRREV.DN) or the name of a user-defined character type (see, "Commands used in the ASSUMPTIONS Block" on page 19 for details). Each `character-list` consists of one or more character numbers, character names, or character-set names. The characters specified by `character-list` are assigned the immediately preceding character-type. Any number of character-type:character-list pairs, separated by commas, may be specified.

**DEFAULTS**

Use the **DEFAULTS** command to specify default option settings for another command. The syntax is:

```
DEFAULTS  command-name default-option-setting . . . ;
```

Options for the following commands may be set:

- ALLTREES
- BANDB
- BOOTSTRAP
- CONTREE
- DESCRIBE
- HSEARCH
- LAKE
- LENFIT
- RANDTREES
- SAVETREES

For example,

```
defaults hsearch swap=nni addseq=closest;
    hsearch;
```

is equivalent to:

```
hsearch swap=nni addseq=closest;
```

**DELETE**

Use the **DELETE** command to delete a taxon from subsequent analyses. The syntax is:

```
**DELETE** *taxon-list* */ [ONLY] [options] * ;

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>PRUNE</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td><strong>CLEARTrees</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td><strong>CONDENSE</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*Option is nonpersistent

Description of options:

Unless ONLY is specified, taxa specified in the taxon-list are simply added to the set of currently deleted taxa. If taxa have already been deleted and you want only those taxa specified in taxon-list to remain deleted, specify ONLY; any currently deleted taxa not explicitly specified in the list will be restored.

The following three commands pertain if there are trees in memory that will become invalidated by the deletion of taxa.

**CLEARTrees** = { YES | No }  

If CLEARTrees is specified, any trees currently in memory are simply deleted.

**PRUNE** = { YES | No }  

If PRUNE = Yes is specified, newly deleted taxa will be removed ("pruned") from the trees currently in memory, which otherwise remain unmodified.

**CONDENSE** = { YES | No }  

If CONDENSE is specified, any duplicate trees that result from the removal of taxa (PRUNE option) are deleted.

If you do not specify PRUNE or CLEARTrees, the program will prompt for your desired action. PRUNE and CLEARTrees are mainly useful for batch file processing, where you do not want the program to stop and wait for a response from the user before continuing.

---

**DEROOTTrees**

Use the DEROOTTrees command to convert all trees in memory from a rooted to an unrooted representation. The syntax is:

**DEROOTTrees** ;
There are no options.

The circumstances under which you would need to use this command are rather unlikely.

**DESCRIBETREES**

Use the **DESCRIBETREES** command to output tree diagrams and associated information. The syntax is:

**DESCRIBETREES**  
.tree-list  
/  
.options  
;

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>PLOT</td>
<td>{ NONE</td>
<td>CLADOGRAM</td>
</tr>
<tr>
<td>ROOT</td>
<td>{ OUTGROUP</td>
<td>LUNDBERG</td>
</tr>
<tr>
<td>OUTROOT</td>
<td>{ POLYTOMY</td>
<td>PARAPHYL</td>
</tr>
<tr>
<td>BRLENS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>LABELNODE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>XOUT</td>
<td>{ NONE</td>
<td>TERMINAL</td>
</tr>
<tr>
<td>MPRSETS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>APOLIST</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CHGLIST</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>PATRISTIC</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>HOMOPLASY</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>FVALUE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>DIAG</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TCOMPRESS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CMLABELS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CMSHOWEQ</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CMCOLWID</td>
<td>integer-value</td>
<td>1</td>
</tr>
<tr>
<td>CMCSTATUS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>
The tree-list specifies the numbers of the trees you wish to describe. If this is the first `DESCRIBETREES` command and you do not specify a tree list, only the first tree is described.

Description of options:

**PLOT = { NONE | CLADOGRAM | PHYLOGRAM | BOTH }**

If PLOT = CLADOGRAM, branch lengths on the tree have no meaning, and taxa are aligned at the right edge of the diagram. If PLOT = PHYLOGRAM, branch lengths are drawn proportionally to the number of changes assigned to each branch. PLOT = BOTH requests output of the tree diagram in both CLADOGRAM and PHYLOGRAM formats.

**BRLENS = { YES | NO }**

Requests output of a table of assigned, minimum-possible, and maximum-possible branch lengths.

**CHGLIST = { YES | NO }**

Requests output of a list of changes in each character.

**APOLIST = { YES | NO }**

List of changes along each branch.

**DIAG = { YES | NO }**

Requests output of character diagnostics, including the minimum-possible, assigned, and maximum-possible length of each character, and goodness-of-fit measures based on these quantities.

**PATRISTIC = { YES | NO }**

Requests output of the patristic distance matrix.

**HOMOPLASY = { YES | NO }**

Requests output of the pairwise homoplasy matrix.

**LABELNODE = { YES | NO }**

Ordinarily, internal nodes on the tree diagram are labeled with a node number that is referenced by other output information (change lists, apomorphy lists, etc.). `LABELNODE = NO` can be used to suppress the labeling of internal nodes.

**XOUT = { NONE | TERMINAL | INTERNAL | BOTH }**

Requests output of a table of character-state assignments for each tree. `XOUT = INTERNAL` requests output of the character-states assigned to internal nodes for each tree. `XOUT = TERMINAL` requests
a listing of the original data matrix. (This option is not particularly useful, as you would ordinarily use the \texttt{SHOWMATRX} command to list the data matrix.) \texttt{XOUT = BOTH} requests a listing of the original data matrix plus the states assigned to internal nodes.

\texttt{MPRSETS = \{ YES | NO \}}

Requests a listing of the possible character-state assignments (MPR-sets) for each tree (parsimony criterion only).

\texttt{FVALUE = \{ YES | NO \}}

Requests output of the F-value and F-ratio.

See "Options And Subcommands Affecting Multiple Commands" on page 29 for details.

\texttt{ROOT = \{ OUTGROUP | LUNDBERG | MIDPOINT \}}
\texttt{OUTROOT = \{ POLYTOMY | PARAPHYL | MONOPHYL \}}
\texttt{TCOMPRESS = \{ YES | NO \}}
\texttt{CMLABELS = \{ YES | NO \}}
\texttt{CMSHOWEQ = \{ YES | NO \}}
\texttt{CMCSTATUS = \{ YES | NO \}}
\texttt{CMCOLWID = column-width}

\textbf{DOS}

Use the \texttt{DOS} command to execute a DOS command and return immediately to PAUP* or to enter a DOS shell. The syntax is:

\begin{verbatim}
DOS [ dos-command ] ;
\end{verbatim}

If you do not specify a command, PAUP* will open a DOS shell. Type \texttt{exit} at the DOS prompt when you want to return to PAUP*. If you specify a command, control is returned to PAUP* immediately after the command has finished. You can type a command that contains a semicolon by enclosing the entire command within single-quotes.

\textbf{DSCORES}

Use the \texttt{DSCORES} command to calculate scores of trees in memory according to distance criterion. The \texttt{tree-list} indicates which trees are to be evaluated. The syntax is:

\begin{verbatim}
DSCORES [ tree-list ] [/ options ] ;
\end{verbatim}
Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>DISTANCE</td>
<td>{ USER</td>
<td>TOTAL</td>
</tr>
<tr>
<td>RATES</td>
<td>{ EQUAL</td>
<td>GAMMA }</td>
</tr>
<tr>
<td>SHAPE</td>
<td>real-value</td>
<td>0.5</td>
</tr>
<tr>
<td>PINVAR</td>
<td>real-value</td>
<td>0</td>
</tr>
<tr>
<td>REMOVEFREQ</td>
<td>{ PROPORTIONAL</td>
<td>EQUAL }</td>
</tr>
<tr>
<td>ESTFREQ</td>
<td>{ ALL</td>
<td>CONSTANT }</td>
</tr>
<tr>
<td>ALLSITESMEAN</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>SUBST</td>
<td>{ ALL</td>
<td>TV</td>
</tr>
<tr>
<td>CLASS</td>
<td>(cAC cAG cAT cCG cCT cGT)</td>
<td>(a a a a a a)</td>
</tr>
<tr>
<td>BASEFREQ</td>
<td>{ EQUAL</td>
<td>EMPIRICAL }</td>
</tr>
<tr>
<td>MISSDIST</td>
<td>{ INFER</td>
<td>IGNORE }</td>
</tr>
<tr>
<td>OBJECTIVE</td>
<td>{ ME</td>
<td>LSFIt }</td>
</tr>
<tr>
<td>POWER</td>
<td>integer-value</td>
<td>2</td>
</tr>
<tr>
<td>NEGBrLEN</td>
<td>{ PROHIBIT</td>
<td>ALLOW</td>
</tr>
<tr>
<td>DCOLLAPSE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>MAXPass</td>
<td>integer-value</td>
<td>20</td>
</tr>
<tr>
<td>SMaxPass</td>
<td>integer-value</td>
<td>20</td>
</tr>
<tr>
<td>DELTA</td>
<td>real-value</td>
<td>1e-06</td>
</tr>
<tr>
<td>SDELTA</td>
<td>real-value</td>
<td>1e-06</td>
</tr>
<tr>
<td>LOGIter</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

The options for this command are the same as those used under the PSet command. See page 52 for a description of these options.
**DSET**

Use the **DSET** command to set options for distance analysis. The syntax is:

```
DSET [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>DISTANCE</strong></td>
<td>{ USER</td>
<td>TOTAL</td>
</tr>
<tr>
<td><strong>RATES</strong></td>
<td>{ EQUAL</td>
<td>GAMMA }</td>
</tr>
<tr>
<td><strong>SHAPE</strong></td>
<td>real-value</td>
<td>0.5</td>
</tr>
<tr>
<td><strong>PINVAR</strong></td>
<td>real-value</td>
<td>0</td>
</tr>
<tr>
<td><strong>REMOVEFreq</strong></td>
<td>{ PROPORTIONAL</td>
<td>EQUAL }</td>
</tr>
<tr>
<td><strong>ESTFreq</strong></td>
<td>{ ALL</td>
<td>CONSTANT }</td>
</tr>
<tr>
<td><strong>ALLSitesMean</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td><strong>SUBST</strong></td>
<td>{ ALL</td>
<td>TV</td>
</tr>
<tr>
<td><strong>CLASS</strong></td>
<td>(cAC cAG cAT cCG cCT cGT)</td>
<td>(a a a a a a)</td>
</tr>
<tr>
<td><strong>BASEFreq</strong></td>
<td>{ EQUAL</td>
<td>EMPIRICAL }</td>
</tr>
<tr>
<td><strong>MISSDist</strong></td>
<td>{ INFER</td>
<td>IGNORE }</td>
</tr>
<tr>
<td><strong>OBJECTIVE</strong></td>
<td>{ ME</td>
<td>LSFIT }</td>
</tr>
<tr>
<td><strong>POWER</strong></td>
<td>integer-value</td>
<td>2</td>
</tr>
<tr>
<td><strong>NEGBrLen</strong></td>
<td>{ PROHIBIT</td>
<td>ALLOW</td>
</tr>
<tr>
<td><strong>DCOLLAPSE</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td><strong>MAXPass</strong></td>
<td>integer-value</td>
<td>20</td>
</tr>
<tr>
<td><strong>SMAXPass</strong></td>
<td>integer-value</td>
<td>20</td>
</tr>
<tr>
<td><strong>DELTA</strong></td>
<td>real-value</td>
<td>1e-06</td>
</tr>
<tr>
<td><strong>SDELTA</strong></td>
<td>real-value</td>
<td>1e-06</td>
</tr>
</tbody>
</table>
Description of options:

\[
\text{DISTANCE} = \{ \text{USER} | \text{TOTAL} | \text{MEAN} | \text{ABS} | \text{P} | \text{JC} | \text{F81} | \text{TAJNEI} | \\
\text{K2P} | \text{F84} | \text{HKY85} | \text{K3P} | \text{TAMNEI} | \text{GTR} | \\
\text{CUSTOM} | \text{ML} | \text{LOGDET} | \text{UPHOLT} | \text{NEIL}\}
\]

Use the \text{DISTANCE} option to specify the distance measure used to calculate the scores of the trees in memory. The following distances may be used:

- **USER**: user-defined distance (see "Commands used in the DISTANCES Block" on page 26)
- **TOTAL**: total number of pairwise character differences
- **MEAN**: mean number of pairwise character differences (adjusted for missing data)
- **ABS**: absolute distances
- **P**: uncorrected distance often referred to as the p-distance or dissimilarity (D) distance.
- **JC**: Jukes and Cantor (1969); equal base frequencies, one substitution type
- **F81**: Felsenstein (1981); unequal base frequencies, one substitution type
- **TAJNEI**: Tajima and Nei (1984); unequal base frequencies, one substitution type
- **K2P**: Kimura (1980); equal base frequencies, unequal Ti:Tv
- **F84**: Felsenstein (1984); unequal base frequencies, unequal Ti:Tv
- **HKY85**: Hasegawa, Kishino, and Yano (1985); unequal base frequencies, unequal Ti:Tv
- **K3P**: Kimura (1981); equal base frequency; 3 substitution types
- **TAMNEI**: Tamura and Nei (1993); unequal base frequency; 3 substitution types
- **GTR**: general time-reversible model (Lanave et al. 1984, and Rodríguez et al. 1990); unequal base frequencies, 6 substitution types.
- **CUSTOM**: user defines the base frequencies and number of substitution types
The following set of options apply only to the calculation of pairwise distances:

\[ \text{RATES} = \{ \text{EQUAL} \mid \text{GAMMA} \} \]

Unless \text{RATES} = \text{GAMMA}, rates across all characters are assumed to be equal. If \text{RATES} = \text{GAMMA}, rates across sites are assumed to follow a continuous gamma distribution. The shape of the gamma distribution is equal to the value specified for the \text{SHAPE} option. This option is not available for the \{ \text{ABS} \mid \text{P} \mid \text{LOGDET} \mid \text{ML} \} distance criterion. To specify gamma distributed rates for ML distances use the "LSet" command described on page 79.

\[ \text{SHAPE} = \text{real-value} \]

Use \text{SHAPE} to specify the shape of the gamma distribution used to accommodate among-site rate variation. Again, this option is not available for the \{ \text{ABS} \mid \text{P} \mid \text{LOGDET} \mid \text{ML} \} distance criterion. To specify the gamma-shape parameter for ML distances use the "LSet" command described on page 79.

\[ \text{PINVAR} = \text{real-value} \]

Use \text{PINVAR} to specify the proportion of invariable sites (i.e., sites that are unable to accept substitutions); the remaining sites are assumed to vary at the same rate.

The following options are available only if a \text{real-value} has been specified under \text{PINVAR}:

\[ \text{REMOVEFREQ} = \{ \text{PROPORTIONAL} \mid \text{EQUAL} \} \]

If \text{REMOVEFREQ} = \text{EQUAL}, the same number of identical sites is removed from each nucleotide in a given pairwise comparison. If \text{REMOVEFREQ} = \text{PROPORTIONAL}, then the number of identical sites removed is proportional to the frequency of each base.

\[ \text{ESTFREQ} = \{ \text{ALL} \mid \text{CONSTANT} \} \]

If \text{REMOVEFREQ} = \text{PROPORTIONAL}, then the frequency of each base may be estimated from the entire data set (Est-
FREQ = ALL) or only the invariable sites (ESTFREQ = CONSTANT).

**ALLSITESMEAN = { YES | NO }**

Adjust the distance so that it represents the mean number of substitutions over all sites, rather than over only the variable sites.

**SUBST = { ALL | TV | TI | TRATIO }**

By default PAUP* counts or estimates substitutions of all types (SUBST = ALL). For many DNA distances, the distance represents the mean number of substitutions per site that have accumulated since a pair of taxa last shared a common ancestor. You can restrict the PAUP* to count or estimate changes representing transition (i.e., between purines or pyrimidines) (SUBST = TI) or transversion (between purines and pyrimidines) (SUBST = TV) substitutions.

**CLASS = ( CAC CAG CAT CCG CCT CGT )**

If DISTANCE = CUSTOM, then substitution types may be assigned to any of six classes. For example, substitution types may be pooled into common classes to reflect changes between structurally similar molecules (e.g. transitions and transversions). A user is free to decide among the many possible ways that substitution types may be divided or combined.

**BASEFREQ = { EQUAL | EMPIRICAL }**

If DISTANCE = CUSTOM, base frequencies used to estimated pairwise distances may be based on either the empirical base frequency or equal base frequencies (i.e., frequency of each base equals 1/4).

**MISSDIST = { INFERENCE | IGNORE }**

Unless MISSDIST = IGNORE, PAUP* infers "missing-data" sites (including gaps) and ambiguity codes by distributing them proportionately to unambiguous changes. You may also choose to ignore sites for the affected pairwise comparison (IGNORE).

The following set of options apply to the calculation of branch lengths and tree scores:

**OBJECTIVE = { ME | LSFIT }**

Choose between minimum evolution (ME) and least-squares (LSFIT) as the objective function used to calculate pairwise distances. See Swofford et al. (1996) for a discussion of these objective functions.

**POWER = integer-value**

Sums of squared deviations in least-squares analyses (OBJECTIVE = LSFIT) may be unweighted (POWER = 0),
weighted by the inverse (POWER = 1) of the distance, or
weighted by the squared inverse (POWER = 2). POWER = 2
corresponds with the method of Fitch and Margolish (1967).

NEGBRLEN = { PROHIBIT | ALLOW | SETZERO | SETABSVAL }

Use NEGBRLEN to specify negative branch length handling. If
NEGBRLEN = PROHIBIT, then PAUP* constrains branch lengths to be
nonnegative. By default, PAUP* allows but sets to zero negative
branch lengths when computing the value of the objective function
(SETZERO). You may also allow negative branch lengths (ALLOW) or
an absolute value (SETABSVAL) when computing the value of the
objective function.

DCOLLCAPSE = { YES | NO }

Use DCOLLAPSE to collapse branches of effectively zero length when
searching. If a branch has a length greater than or equal to $1 \times 10^{-8}$,
it is eliminated from the tree.

MAXPASS = integer-value

Use MAXPASS to set the maximum number of smoothing passes.

SMAXPASS =integer-value

Use SMAXPASS to set the maximum number of branch-length
smoothing passes when a tree search is in progress. Setting
SMAXPASS to a smaller value can speed search times, but the
objective function may not be fully optimized.

DELTA = real-value

Use DELTA to set the value for stopping smoothing passes. In other
words, when a score changes less than the real-value specified,
PAUP* assumes that the branch lengths have converged to their
optimal values for a given tree.

SDELTA =real-value

Use SDELTA to set the value used to stop smoothing passes for
operations when a tree search is in progress.

LOGITER = { YES | NO }

If LOGITER = YES, then the progress of the branch-length iterations
will be output to the display buffer. This output can be extensive and
it is ordinarily not useful.

EDIT

Use the EDIT command to edit a file using PAUP*’s editor. The syntax is:
EDIT  [file-specification]  ;

This command is only valid in implementations of PAUP* that provide built-in editing capabilities.

EXCLUDE

Use the EXCLUDE command to exclude one or more characters from tree-score calculations. The syntax is:

EXCLUDE  character-list  [/ONLY]  ;

Unless /ONLY is specified, characters specified in the character-list are simply added to the set of currently excluded characters. If some characters have already been excluded but you want only those characters specified in character-list to remain excluded, specify /ONLY; any currently excluded characters not explicitly specified in the list will be re-included.

EXECUTE

Use the EXECUTE command to request processing of an input file. The input file should be a valid NEXUS file. The syntax is:

EXECUTE  file-specification  ;

See "Input/Output files" on page 9 for details regarding the format of file-specification.

The input file may contain any or all of the following: TAXA blocks, CHARACTERS blocks, DATA blocks, ASSUMPTIONS blocks, TREES blocks, DISTANCES blocks, CODONS blocks, and valid PAUP commands. Although not required, you should place PAUP commands inside of a PAUP block so that other programs (e.g., MacClade) can use the same file. PAUP commands are processed exactly as if they had been entered from the command line, with only a few exceptions (e.g., the EDIT command cannot be issued from a file). Commands are processed until the end of the file is reached, or a QUIT command is encountered.

EXSET

The EXSET command, used to define "exclusion sets," is ordinarily issued from within the ASSUMPTIONS block. However, you may also issue it from the command line or from within a PAUP block. See "Commands used in the ASSUMPTIONS Block" on page 19 for the description of this command.

FILTER

Use the FILTER command to filter trees according to score, constraints, or other criteria. The syntax is:
**FILTER** [ options ] | OFF ;

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>REVERSE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>MAXSCORE</td>
<td>real-value</td>
<td>none</td>
</tr>
<tr>
<td>MINSCORE</td>
<td>real-value</td>
<td>none</td>
</tr>
<tr>
<td>NUMLE</td>
<td>integer-value</td>
<td>none</td>
</tr>
<tr>
<td>NUMGE</td>
<td>integer-value</td>
<td>none</td>
</tr>
<tr>
<td>CONSTRAINTS</td>
<td>constraint-name</td>
<td>none</td>
</tr>
<tr>
<td>SD</td>
<td>integer-value</td>
<td>none</td>
</tr>
<tr>
<td>FROM</td>
<td>integer-value</td>
<td>none</td>
</tr>
<tr>
<td>LESSRESOLV</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>PERMDEL</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>ALWAYS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>BINARY</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*OPTION IS NONPERSISTENT

Description of options:

Any combination of the following filtering criteria can be specified.

**REVERSE = { YES | NO }**

If REVERSE = YES, the condition of the specified filter is reversed. For example:

```
filter maxscore=500;
```

retains trees with scores less then or equal to 500, and

```
filter maxscore=500 reverse = yes;
```

retains trees with scores greater then or equal to 500.

**MAXSCORE = real-value**

Use MAXSCORE to specify the maximum score of trees retained by the filter. Trees with higher (worse) scores are not kept.
MINSCORE = real-value

Use MINSCORE to specify the minimum score of trees retained by the filter. Trees with lower (better) scores are not kept.

NUMLE = integer-value

Keep trees only if their position in memory (tree number) is less than or equal to the specified integer-value.

NUMGE = integer-value

Keep trees only if their position in memory (tree number) is greater than or equal to the specified integer-value.

CONSTRAINTS = constraint-name

Only those trees that are compatible with the specified constraint tree are retained.

SD = integer-value  FROM = integer-value

Only those trees within integer-value symmetric difference distance units of the specified tree number are retained.

LESSRESOLV = { YES | NO }

Keep a tree only if more highly resolved compatible trees do not exist.

PERMDEL = { YES | NO }

Permanently delete those trees not retained by the filter.

ALWAYS = { YES | NO }

Apply filter even when no trees satisfy the filtering criteria.

BINARY = { YES | NO }

Keep a tree only if none of its internal nodes are greater than degree three.

If OFF is specified, trees that do not satisfy the specified filtering criteria are retained.

FACTORY

Use the FACTORY command to reset all options to factory default settings. The syntax is:

FACTORY ;
**FSTATUS**

Use the **FSTATUS** command to show current status of data, log, and tree file. The syntax is:

```
FSTATUS ;
```

**GAMMAPLOT**

Use the **GAMMAPLOT** command to show a gamma-distribution plot. The syntax is:

```
GAMMAPLOT [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>SHAPE</td>
<td>{real-value</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>NCat</td>
<td>integer-value</td>
<td>4</td>
</tr>
<tr>
<td>REPRate</td>
<td>{ MEAN</td>
<td>MEDIAN }</td>
</tr>
</tbody>
</table>

If SHAPE = PREVIOUS, the plot of the gamma distribution is drawn using the most recently estimated shape parameter (see the "LSet" command described on page 79). To obtain a plot of the gamma distribution with a user-defined shape parameter specify SHAPE = *real-value*. PAUP* uses the default value of 0.5 for this option.

NCat = integer-value

Use NCat to specify the number of categories into which the continuous gamma distribution is divided in order to obtain a discrete approximation.

REPRate = { MEAN | MEDIAN }

Use REPRate to specify whether the mean or the median is used to represent the rates within each category of the gamma distribution.

**GENERATE TREES**

Use the **GENERATE TREES** command to generate a set of random trees or all-possible trees. The syntax is:

```
GENERATE TREES { ALL | RANDOM } [ options ] ;
```
Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>MODEL</td>
<td>{ EQUIPROBABLE</td>
<td>MARKOVIAN }</td>
</tr>
<tr>
<td>NTREES</td>
<td>integer-value</td>
<td>100</td>
</tr>
<tr>
<td>SEED</td>
<td>integer-value</td>
<td>0</td>
</tr>
<tr>
<td>ROOTED</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>NONBINARY</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

Descriptions of options:

**MODEL = { EQUIPROBABLE | MARKOVIAN }

The EQUIPROBABLE model dictates that every possible tree has the same probability. The MARKOVIAN model assumes that trees are generated by a random (pure-birth) branching process.

**NTREES = integer-value

Use NTREES to specify the number of trees to be generated.

**SEED = integer-value

If RANDOM is specified, PAUP* references the system clock to obtain a value used to seed a random number generator. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)

**ROOTED = { YES | NO }

If ROOTED = YES, rooted trees will be generated, otherwise, the generated trees will be unrooted.

**NONBINARY = { YES | NO }

If NONBINARY = YES is requested, then trees are drawn from the set of all possible binary and nonbinary trees. By default (NONBINARY = NO), only binary trees are generated.

**GETTREES

Use the GETTREES command to load trees into memory from a file containing a NEXUS-format TREES block. The syntax is:

```
GETTREES [ options ] ;
```
Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>FILE</td>
<td>tree-file-name</td>
<td>paup.trees</td>
</tr>
<tr>
<td>FROM</td>
<td>integer-value</td>
<td>none</td>
</tr>
<tr>
<td>TO</td>
<td>integer-value</td>
<td>none</td>
</tr>
<tr>
<td>MODE</td>
<td>{ 1</td>
<td>2</td>
</tr>
<tr>
<td>ALLBLOCKS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>ROOTED</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>UNROOTED</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>DUPTREES</td>
<td>{ KEEP</td>
<td>ELIMINATE }</td>
</tr>
<tr>
<td>STOREBRLENS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>STORETREEWTS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>WARNTREE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*OPTION IS NONPERSISTENT

Description of options:

FILE = tree-file-name

Specify the tree-file-name containing a NEXUS-format TREES block. (See "Input/Output files" on page 9 for details regarding the file-name format)

FROM = integer-value

If nonzero, integer-value specifies the number of the first tree in the file to get.

TO = integer-value

If nonzero, integer-value specifies the number of the last tree in the file to get.

ALLBLOCKS = { YES | NO }

If ALLBLOCKS = YES, then all of the TREES blocks contained within the specified file will be processed.

MODE = { 1 | 2 | 3 | 4 | 5 | 7 }

By default (MODE=3), any preexisting trees in memory are replaced by the trees read from the file. The MODE setting allows you to alter
this behavior. Let $M$ = the set of trees originally in memory and $T$ =
the set of trees from the tree file. The following mode values are then
available:

1 = replace $M$ by $T - M$ (i.e., keep trees from the file that are not
originally in memory)

2 = replace $M$ by $T \cap M$ (keep trees from the file that are *also*
originally in memory)

3 = replace $M$ by $T$ (i.e., replace all trees in memory by all trees
from the file)

4 = replace $M$ by $M - T$ (i.e., keep trees in memory that are *not*
also in the file)

5 = replace $M$ by $M \oplus T$ (i.e., keep trees that are either currently in
memory or in the file, but not both places)

7 = replace $M$ by $M \cup T$ (i.e., append trees from file to trees
originally in memory, with elimination of duplicates)

**ROOTED = { YES | NO }**

If directed character types are in effect for one or more characters and
the trees being input are unrooted, you will ordinarily be asked if
you want to convert the trees to rooted trees (otherwise, you will not
be able to use the new trees unless you change the character types or
root them later). If you specify ROOTED explicitly, this conversion
will occur automatically without a prompt.

**UNROOTED = { YES | NO }**

If the trees being input are rooted but all character types are
currently undirected, you will ordinarily be asked if you want to
convert the trees to unrooted trees. If you specify UNROOTED
explicitly, this conversion will occur automatically without a
prompt.

**DUPTREES = { KEEP | ELIMINATE }**

Duplicate trees from the TREEFILE are eliminated if DUPTREES =
ELIMINATE.

**STOREBRLENS = { YES | NO }**

If branch lengths are present in the TREES block, then STOREBRLENS =
YES stores branch lengths.

**STORETREEWTS = { YES | NO }**

If tree weights are present in the TREES block, then STORETREEWTS =
YES stores tree weights. Tree weights are typically the reciprocal of
the number of trees found in either a **BOOTSTRAP** or **JACKKNIFE**
replicate. This option allows the combination of bootstrap results from runs performed at different times or on different machines and the recovery of results obtained prior to a system crash. (See "UseTreeWts = { Yes | No }" on page 44 for more details)

**WARN TREE** = { Yes | No }

If **WARN TREE** = No, trees currently in memory will be quietly overwritten by the trees in the tree-file. Otherwise, you will be prompted for confirmation.

**HELP**

Use the **HELP** command to obtain help on using PAUP*’s command-line interface. The syntax is:

```
HELP [{COMMANDS | command-name }]
```

If invoked with no arguments, **HELP** produces a list of the available commands. If **COMMANDS** (or CMDS) is specified, a one-line description of each command is output. If a command-name is specified, **HELP** provides information of that command.

Examples:

```
help;[requests a list of available commands]

help commands;[requests a list of available commands, with a one-line description of each]

help bandb;[requests help on the BANDB command]
```

Note: The help file distributed with this beta test version is out-of-date at this time.

**HOMPART**

Use the **HOMPART** command to perform test for homogeneity of partitioned data sets. This test was described as the incongruence-length difference test by Farris et al. (1995). The syntax is:

```
HOMPART [ options ] [ / heuristic-search-options | branch-and-bound-search-options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>PARTITION</td>
<td>character-partition-name</td>
<td>-</td>
</tr>
</tbody>
</table>
Description of options:

**PARTITION = character-partition-name**

Use **PARTITION** to specify the *character-partition-name* to be used in the analysis. To learn how to setup Character-partitions see **CHARPARTITIONS page 23**.

**NREPS = integer-value**

Use **NREPS** to specify the number of homogeneity replicates to be performed.

**SEED = integer-value**

By default, PAUP* references the system clock to obtain a value used to seed a random number generator. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)

**SEARCH = { HEURISTIC | BANDB }**

A search is performed for each data partition replicate using the option specified for **SEARCH**. Options for either of the search options may be specified after a slash. (See the "BandB" command described on page 36 and the "HSearch" command described on page 65 for a description of the available options.)

---

**HSearch**

Use the **HSearch** command to search for optimal trees using heuristic algorithms. The syntax is:

```
HSearch [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>START</td>
<td>{ Stepwise</td>
<td>NJ</td>
</tr>
<tr>
<td>ADDSEQ</td>
<td>{ Simple</td>
<td>Closest</td>
</tr>
<tr>
<td>Option</td>
<td>Description</td>
<td>Default Value</td>
</tr>
<tr>
<td>-----------------</td>
<td>--------------------------------------------------</td>
<td>---------------</td>
</tr>
<tr>
<td>NREPS</td>
<td>Integer value</td>
<td>10</td>
</tr>
<tr>
<td>RSEED</td>
<td>Integer value</td>
<td>0</td>
</tr>
<tr>
<td>SAVEREPS</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>RSTATUS</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>REFTax</td>
<td>Integer value</td>
<td>0</td>
</tr>
<tr>
<td>HOLD</td>
<td>{ integer-value</td>
<td>NO }</td>
</tr>
<tr>
<td>SWAP</td>
<td>{ NONE</td>
<td>NNI</td>
</tr>
<tr>
<td>MULTREES</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>KEEP</td>
<td>{ real-value</td>
<td>No }</td>
</tr>
<tr>
<td>NBEST</td>
<td>{ integer-value</td>
<td>NO }</td>
</tr>
<tr>
<td>ALLSWAP</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>QUICKSWAP</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>ENFORCE</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>CONSTRAINTS</td>
<td>constraint-name</td>
<td>none</td>
</tr>
<tr>
<td>CONVERSE</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>USENonMin</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>STEEPEST</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>ABORTREP</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>NCHUCK</td>
<td>Integer value</td>
<td>0</td>
</tr>
<tr>
<td>CHUCKSCORE</td>
<td>{ real-value</td>
<td>NO }</td>
</tr>
<tr>
<td>RETAIN</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>STATUS</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>DSTATUS</td>
<td>{ integer-value</td>
<td>NO }</td>
</tr>
<tr>
<td>RANDOMIZE</td>
<td>{ AddSeq</td>
<td>TREES }</td>
</tr>
</tbody>
</table>

*Option is nonpersistent

Description of options:

\[ \text{START} = \{ \text{STEPWISE} \mid \text{NJ} \mid \text{CURRENT} \mid \text{tree-number} \mid \text{-tree-number} \} \]

By default, starting trees for branch swapping are obtained via a
stepwise addition procedure. Alternatively, you can request that all of the trees currently in memory (START = CURRENT) or a subset of the current trees (START = tree-number [-tree-number]) be used as a starting points for branch swapping. If the optimality criterion is set to maximum likelihood or distance, neighbor joining (START = NJ) may also be used to obtain starting trees.

**ADDSEQ = { SIMPLE | CLOSEST | ASIS | RANDOM | FURTHEST }**

Use ADDSEQ to specify the addition sequence to be used in the stepwise addition procedure.

Options for ADDSEQ = SIMPLE:

**REFTAX = reference-taxon-number**

By default, the first taxon in the data file is used as the reference taxon. Use REFTAX to specify an alternate reference taxon. This option is relevant only for unrooted-tree searches. For rooted-tree searches, the hypothetical ancestor (see "Ancstates" on page 35 and "Assume" on page 35) is used as the reference taxon.

Options for ADDSEQ = RANDOM:

**NREPS = integer-value**

Use NREPS to specify the number of random-addition-sequence replications to be performed. The default is 10.

**RSEED = integer-value**

By default, PAUP* references the system clock to initialize the seed used to generate pseudorandom numbers used to obtain random-addition-sequences. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)

**SAVERePS = { YES | NO }**

If SAVERePS = YES, then optimal trees from each repetition are saved even if they are not optimal over all repetitions.

**RANDOMIZE = { ADDSEQ | TREES }**

If RANDOMIZE = TREES, initial trees are random trees rather than trees found by random-addition-sequence.

**RSTATUS = { YES | NO }**

If you specify RSTATUS = YES, a status report showing the results of each random-addition-sequence replication is output. The status report can be useful in evaluating the effectiveness of the heuristic search while the search is...
HOLD = \{integer-value \mid NO\}

Specifies the number of trees to be held at each cycle of the stepwise-
addition procedure. By default, HOLD = 1, so that a single tree is held
at each step. However, setting \(n > 1\) sometimes improves the score
of the tree found by stepwise addition.

SWAP = \{TBR \mid SPR \mid NNI \mid NONE\}

Specifies the algorithm used by branch-swapping: TBR = tree
bisection-reconnection, SPR = subtree pruning-regrafting, NNI =
nearest-neighbor interchange, NONE = NO branch swapping
performed. NNI rearrangements are a subset of those done by SPR,
and SPR rearrangements are a subset of those done by TBR.
Ordinarily, you will use TBR, but SPR or NNI can be used to reduce
search times.

MULTREES = \{YES \mid NO\}

Ordinarily, PAUP* saves all minimal trees it finds during branch
swapping. You can use MULTREES = NO to save only one of the best
trees found. Use of MULTREES is not recommended, as it can
drastically reduce the ability of branch swapping to find the best tree.
(This option is synonymous with MULPARS option in earlier versions
of PAUP.)

NBEST = \{integer-value \mid NO\}

Use NBEST to save the N best trees discovered during the search
according to the optimality criterion in effect.

ALLSWAP = \{YES \mid NO\}

Unless ALLSWAP = YES is specified, the trees saved by setting
NBEST > 1 will include only those trees encountered during a
search for optimal trees; no special effort is made to find
additional trees that might be still better. If ALLSWAP = YES is
requested, then all trees saved are themselves input to the branch
swapping procedure, making it much more likely that the
optimal NBEST trees will be found. Setting ALLSWAP = YES can
dramatically increase the search time, however.

QUICKSWAP = \{YES \mid NO\}

Unless QUICKSWAP = NO, trees found by step-wise addition are input
to a round of NNI rearrangements before going on to more extensive
rearrangements. Only one tree is maintained during this phase.

USENONMIN = \{YES \mid NO\}

It is possible that the trees in memory at the time branch-swapping
begins are not all equal in score. Ordinarily, only the best available
trees are input to the branch-swapping procedure. If you want to swap on nonminimal trees as well, specify USENONMIN. USENONMIN = NO reverses the effect of a previous USENONMIN specification.

STEEPEST = { YES | NO }

Specify STEEPEST to request use of the steepest-descent modification in the branch-swapping procedure. STEEPEST = NO reverses the effect of a previous STEEPEST specification.

NCHUCK = integer-value
CHUCKSCORE = { real-value | NO }

If this pair of options is used, no more than the NCHUCK = integer-value of trees of score greater than or equal to the CHUCKSCORE = real-value will be retained in a search (or in a random-addition-sequence replicate).

ABORTREP = { YES | NO }

If ABORTREP is requested and NCHUCK and CHUCKLEN values have been specified, the current random-addition-sequence replicate will be aborted if the "chucking" limits are hit.

RETAIN = number-of-trees-to,retain

The first number-of-trees-to,retain will be retained in memory throughout the search. (Ordinarily, all trees initially in memory will be replaced by trees found during the search.) The RETAIN option is not persistent; you must reset it for every HSEARCH command if you want to continue retaining the same set of initial trees.

See "Options And Subcommands Affecting Multiple Commands" on page 29 for a description of the following options:

KEEP = keep-score
ENFORCE = { YES | NO }
CONSTRAINTS = constraint-name
CONVERSE = { YES | NO }
STATUS = { YES | NO }
DSTATUS = { integer-value | NO }

INCLUDE

Use the INCLUDE command to re-include characters that were previously excluded. The syntax is:

INCLUDE character-list [/ONLY] ;

Unless /ONLY is specified, characters specified in the character list are simply removed from the set of currently excluded characters. If you want
only those characters specified in the list to be included, specify /ONLY; characters not explicitly specified in the list will then be excluded.

**INGROUP**

Use the **INGROUP** command to return one or more taxa to the ingroup. The syntax is:

```
INGROUP taxon-list [/ONLY] ;
```

Unless /ONLY is specified, taxa specified in the taxon-list are simply removed from the current outgroup. If you want only those taxa specified in taxon-list to be included in the ingroup, specify /ONLY; any taxon that is not explicitly specified in the list will be transferred to the outgroup.

**JACKKNIFE**

Use the **JACKKNIFE** command to perform jackknife analysis. The syntax is:

```
```

Available options:

<table>
<thead>
<tr>
<th><strong>Keyword</strong></th>
<th><strong>Option type</strong></th>
<th><strong>Default setting</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>PCTDELETE</td>
<td>real-value</td>
<td>50</td>
</tr>
<tr>
<td>JSEED</td>
<td>integer-value</td>
<td>0</td>
</tr>
<tr>
<td>NREPS</td>
<td>integer-value</td>
<td>100</td>
</tr>
<tr>
<td>SEARCH</td>
<td>{ HEURISTIC</td>
<td>BANDB</td>
</tr>
<tr>
<td>RESSAMPLE</td>
<td>{ NORMAL</td>
<td>JAC }</td>
</tr>
<tr>
<td>CONLEVEL</td>
<td>integer-value</td>
<td>50</td>
</tr>
<tr>
<td>KEEPALL</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>WTS</td>
<td>{ NO</td>
<td>SIMPLE</td>
</tr>
<tr>
<td>GRPFREQ</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TREEFILE</td>
<td>tree-file-name</td>
<td>none</td>
</tr>
<tr>
<td>FORMAT</td>
<td>{ NEXUS</td>
<td>ALTNEXUS</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>
CUTOFFPCT

*Option is nonpersistent

Description of options:

PCTDELETE = real-value

Use PCTDELETE to specify the percentage of the data set to be deleted for each jackknife replicate.

JSEED = integer-value

By default, PAUP* references the system clock to initialize the seed used to generate pseudorandom numbers for character resampling. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)

NREPS = integer-value

Use NREPS to specify the number of jackknife replications to be performed.

SEARCH = { HEURISTIC | BANDB | FASTSTEP | NJ | UPGMA }

A tree search is performed for each jackknife sample using the method specified under SEARCH. If SEARCH = FASTSTEP, tree searches in each replication are performed using one random-sequence-addition replication and no branch swapping. SEARCH = { NJ | UPGMA } may be used only for the distance criterion.

RESAMPLE = { NORMAL | JAC }

If RESAMPLE = JAC, then the JAC program in Hennig86 (Farris) is emulated.

CONLEVEL = integer-value

Use CONLEVEL to specify the minimum proportion of the bootstrap replicates (expressed as a percentage) in which a group must appear if it is to be included in the bootstrap consensus tree. For example, to obtain a bootstrap consensus tree that shows only those groups which occurred on more than 80% of the trees, you would specify CONLEVEL=80. CONLEVEL must be at least 50, which is the default.

KEEPALL = { YES | NO }

If you request KEEPALL, groups occurring at frequencies less than CONLEVEL will also be retained in the jackknife consensus as long as they are compatible with all groups that are already included in the consensus. Effectively, this forces KEEPALL=50, because any group occurring in 50% or more of the replicates will automatically be compatible with all more frequently occurring groups.
WTS = { NO | SIMPLE | REPEATCNT }

If WTS = NO, any previously applied character weights are ignored.
If WTS = SIMPLE, then characters are sampled with equal probability
but character weights are applied. If WTS = REPEATCNT, then
weights are treated as repeat counts. This option is only allowed if
all weights are integers.

GRPfreq = { YES | NO }

Unless GRPfreq = NO, a table of jackknife partition frequencies is
shown.

TREEFILE = tree-file-name

If TREEFILE is specified, a description of all trees found in each
jackknife replication is given in the NEXUS tree format. Trees
contain a weight comment for the purpose of combining jackknife
results from runs performed at different times or on different
machines and for recovering results obtained prior to a system crash.
The weight is the reciprocal of the number of trees found in a
replicate. The tree-file-name must follow the conventions described
under "Input/Output files" on page 9

REPLACE = { YES | NO }

If TREEFILE is used and the specified file already exists you will be
prompted for confirmation that the existing file should be
replaced. REPLACE suppresses this prompt and the existing file
will be quietly overwritten by the new data.

FORMAT = { NEXUS | ALTNEX | FREQPARS | PHYLIP | HENNIG }

Specifies the type of treefile to be produced. NEXUS requests a
file containing the standard NEXUS TREES block using a
translation table (which greatly reduces the amount of disk space
required to store the trees). ALTNEX also specifies a NEXUS
TREES block, but no translation table is used (the full taxon
names are included in each tree description). FREQPARS requests
a treefile for the FREQPARS program described by Swofford and
Berlocher (1987). PHYLIP requests a treefile for input to version
3.4 of Felsenstein's (1991) PHYLIP package. HENNIG requests a
treefile for version 1.5 of Farris's (1988) Hennig86 program.

CUTOFFPCT = integer-value

Use CUTOFFPCT to specify the minimum jackknife partition
frequency to be displayed in the partition frequency table. All
partitions below this integer-value are pooled into a single class.
**LAKE**

Use the **LAKE** command to perform an analysis using Lake's (1987b) method of linear invariants. This command is available only when **DATATYPE = DNA | RNA | NUCLEOTIDE**. The syntax is:

```
LAKE [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>MODE</td>
<td>{ CHOOSE4</td>
<td>ALLQUART</td>
</tr>
<tr>
<td>SPECTDIST</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>BRLENS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>SUMTabONLY</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>EXACTN</td>
<td>integer-value</td>
<td>30</td>
</tr>
<tr>
<td>TAXA</td>
<td>taxon-list for MODE=CHOOSE4</td>
<td>-</td>
</tr>
<tr>
<td>GRPA</td>
<td>taxon-list 1 for MODE=FOURGRPS</td>
<td>-</td>
</tr>
<tr>
<td>GRPB</td>
<td>taxon-list 2 for MODE=FOURGRPS</td>
<td>-</td>
</tr>
<tr>
<td>GRPC</td>
<td>taxon-list 3 for MODE=FOURGRPS</td>
<td>-</td>
</tr>
<tr>
<td>GRPD</td>
<td>taxon-list 4 for MODE=FOURGRPS</td>
<td>-</td>
</tr>
</tbody>
</table>

Description of options:

**MODE = { CHOOSE4 | ALLQUART | FOURGRPS }**

If there are more than 4 (non-deleted) taxa in the data set, this option specifies whether you want to choose 4 taxa for analysis (MODE=CHOOSE4), analyze all possible quartets (MODE=ALLQUART), or divide the taxa into four groups and analyze all quartets containing one member from each group (MODE=FOURGRPS).

**SPECTDist= { YES | NO }**

SPECTDist requests the output of the spectral distribution (the number of positions falling into each of the 36 possible patterns considered informative by Lake's method).

**BRLENS= { YES | NO }**

BRLENS requests output of branch-lengths calculated by Lake's "operator metric" (Lake, 1987a).
SUMTabONLY = { YES | NO }

SUMTabONLY limits the output to a summary table of results rather than outputting results for each quartet.

EXACTN = integer-value

An exact binomial test (rather than the chi-square approximation) will be used to test the significance of deviations of invariant scores from 0 if the number of informative positions is less than n.

If MODE = CHOOSE4, you must specify exactly four taxa using the following option:

TAXA = taxon-list

The taxon-list must contain exactly four taxa.

If MODE = ALLQUART, you may limit the number of included taxa by selecting at least four taxa using the following option:

TAXA = taxon-list

If MODE = FOURGRPS, you must assign at least one taxon to each of the four groups using the following options:

GRPA = taxon-list-for-first-group
GRPB = taxon-list-for-second-group
GRPC = taxon-list-for-third-group
GRPD = taxon-list-for-fourth-group

LEAVE

Use the LEAVE command to terminate processing of an input file. Ordinarily, PAUP* continues processing until the end of an input file is reached. If, for whatever reasons, you do not want some of the commands in the input file to be processed, insert a LEAVE command into the file at the point where you want execution to stop. PAUP* then continues as if the end of the file were reached at that point. LEAVE has no effect if issued interactively. The syntax is:

LEAVE ;

LOADConstr

Use the LOADConstr command to load constraints from treefile. The syntax is:

LOADConstr [ options ] ;
Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>FILE</td>
<td>tree-file-name</td>
<td>paup.trees</td>
</tr>
<tr>
<td>APPEND</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>ASBACKBONE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*Option is nonpersistent

Description of options:

FILE = tree-file-name

Use FILE to specify the tree-file-name containing constraint trees.

APPEND = { YES | NO }

If APPEND = YES, then the constraints contained in the input file are added to any constraints already in memory.

ASBACKBONE = { YES | NO }

Use ASBACKBONE to load the trees as backbone constraints. Backbone constraint trees should contain only a subset of the taxa currently in memory.

LOG

By default, output generated by PAUP* goes only to the "display buffer," a region of memory set aside exclusively for this purpose. PAUP*'s main display window is used to view this information. The LOG command may be used to request direction of PAUP output to a file (e.g., for subsequent printing). The syntax is:

\[ \text{LOG [ options ] ;} \]

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>FILE</td>
<td>log-file-name</td>
<td>paup.log</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>APPEND</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>START</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>STOP</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>
FLUSHLOG \{ YES | NO \}  NO

*Option is nonpersistent

Description of options:

If START is specified (the default), logging is initiated to the named file. If FILE is not specified explicitly, a default name is assigned. If APPEND is specified, subsequent output is appended to the previous contents (if any) of the file. Otherwise, subsequent output will overwrite the original contents of the file. The APPEND/REPLACE setting is retained between invocations of the LOG command, unless the file is changed by a FILE= directive. If REPLACE is not specified explicitly and the file already exists, you will receive a warning and will have the opportunity to cancel the command before the contents of the existing file are erased. Specification of FLUSHLOG causes the file’s buffer to be flushed after every line of output. Ordinarily, this degrades system performance and is not recommended. However, there may be situations in which immediate flushing is useful.

If the file-specification contains any of the characters equal-sign (=), semicolon (;), colon (:), or blank, it must be enclosed within single-quotes.

Examples:

log file = myoutput;

(subsequent output is saved to file ‘myoutput’)

log stop;

(subsequent output no longer saved to file)

log start append;

(resume logging, appending new output to file ‘myoutput’)

log stop;

(suspend logging once again)

log start;

(resume logging again, appending to ‘myoutput’)

log file = newoutput;

(begin logging to a different file (‘newoutput’), replacing it if it already exists)
**LSCORES**

Use the **LSCORES** command to calculate the likelihoods of trees in memory. The syntax is:

```
LSCORES [ tree-list ] [/ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>SITELIKES</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>STOREASWTS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>SCOREFILE</td>
<td>file-name-for-scores</td>
<td>none</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>APPEND</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>PARSAPPROX</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>KHTEST</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>NST</td>
<td>{ 1</td>
<td>2</td>
</tr>
<tr>
<td>TRATIO</td>
<td>{ real-value</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>RMATRIX</td>
<td>{ ( rAC rAG rAT rCG rCT )</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>RCLASS</td>
<td>(cAC cAG cAT cCG cCT cGT )</td>
<td>(a b c d e f)</td>
</tr>
<tr>
<td>VARIANT</td>
<td>{ HKY</td>
<td>F84 }</td>
</tr>
<tr>
<td>BASEFREQ</td>
<td>{ EMPIRICAL</td>
<td>EQUAL</td>
</tr>
<tr>
<td>BASEFREQ</td>
<td>( frqA frqC frqG )</td>
<td></td>
</tr>
<tr>
<td>RATES</td>
<td>{ EQUAL</td>
<td>GAMMA</td>
</tr>
<tr>
<td>SHAPE</td>
<td>{ real-value</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>NCAT</td>
<td>integer-value</td>
<td>4</td>
</tr>
<tr>
<td>REPRATE</td>
<td>{ MEAN</td>
<td>MEDIAN }</td>
</tr>
<tr>
<td>INITBRLEN</td>
<td>{ ROGERS</td>
<td>LS</td>
</tr>
<tr>
<td>MAXPASS</td>
<td>integer-value</td>
<td>20</td>
</tr>
<tr>
<td>SMAXPASS</td>
<td>integer-value</td>
<td>20</td>
</tr>
<tr>
<td>DELTA</td>
<td>real-value</td>
<td>1e-06</td>
</tr>
</tbody>
</table>
Commands used in the PAUP Block

**SDelta**

*real-value*  
1e-06

**UseApprox**

{ YES | NO }  
Yes

**ApproxLim**

*real-value*  
5

**AdjustAppLim**

{ YES | NO }  
Yes

**LogIter**

{ YES | NO }  
No

**Pinvar**

{ real-value | ESTIMATE | PREVIOUS }  
0

**Recon**

{ MARGINAL | JOINT }  
MARGINAL

**AllProbs**

{ YES | NO }  
No

**SiteRates**

{ PARTITION [: charpartition-name] | RATESET [: rateset-name] | PREVIOUS }  
none

**Clock**

{ YES | NO }  
No

**UserBrLens**

{ YES | NO }  
No

**MinMemReq**

{ YES | NO }  
No

**StartVals**

{ PARSAPPROX | ARBITRARY }  
PARSAPPROX

**LCollapse**

{ YES | NO }  
Yes

**MLDistForLs**

{ YES | NO }  
No

*Option is nonpersistent

Description of options:

**SiteLikes** = { YES | NO }

Use SiteLikes to output single-site likelihood scores.

**StoreAsWts** = { YES | NO }

Use StoreAsWts to store the site-likelihood scores as character-weights. The reason for doing this are esoteric; there would ordinarily be no reason to use this option.

**ScoreFile** = *file-name-for-scores*

If ScoreFile is specified, likelihood scores and parameter estimates for each tree evaluated are saved to a text file. The *file-name-for-scores* must follow the conventions described under "Input/Output files" on page 9.

**Replace** = { YES | NO }

**Append** = { YES | NO }
If the file-name-for-scores already exists, you will be prompted for confirmation before the existing file is replaced. Use REPLACE = YES to suppress this prompt; the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND, in which case a new TREES block will be concatenated to the end of an existing file.

**PARSAPPROX = { YES | NO }**

Use PARSAPPROX to specify parsimony-based approximations of likelihood model parameters (i.e., the gamma shape parameter and the parameters used in the instantaneous rate matrix).

**KHTEST = { YES | NO }**

Use KHTEST to request that the Kishino-Hasegawa test be used to compare pairs of topologies.

See the "LSet" on page 79 for a description of the remaining options.

---

### LSet

Use the LSet command to set options for maximum likelihood analysis. The syntax is:

\[
\text{LSet } [ \text{ options } ] ;
\]

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>NST</td>
<td>{ 1</td>
<td>2</td>
</tr>
<tr>
<td>TRATIO</td>
<td>{real-value</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>RMATRIX</td>
<td>{(rAC rAG rAT rCG rCT)</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>RCLASS</td>
<td>(cAC cAG cAT cCG cCT cG)</td>
<td>(a b c d e f))</td>
</tr>
<tr>
<td>VARIANT</td>
<td>{ HKY</td>
<td>F84 }</td>
</tr>
<tr>
<td>BASEFREQ</td>
<td>{ EMPirical</td>
<td>EQUAL</td>
</tr>
<tr>
<td>RATES</td>
<td>{ EQUAL</td>
<td>GAMMA</td>
</tr>
<tr>
<td>SHAPE</td>
<td>{real-value</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>NCAT</td>
<td>integer-value</td>
<td>4</td>
</tr>
</tbody>
</table>
Commands used in the PAUP Block

Description of options:

The following options are used to specify the substitution model parameters:

\[ NST = \{ 1 \mid 2 \mid 6 \} \]

Use NST to specify the number of substitution types. For example, if NST = 1, then all substitution types are pooled into a single rate.

\[ TRATIO = \{ \text{real-value} \mid \text{ESTIMATE} \mid \text{PREVIOUS} \} \]

Use TRATIO to specify a transition/transversion ratio. If TRATIO
= PREVIOUS, then the Transversion:Transition ratio in memory will be applied. Use TRATIO = ESTIMATE to obtain the maximum likelihood estimate for the data set and tree topology currently in memory. The default value for this option is 2. TRATIO is ignored unless NST = 2.

RMATRIX = { (rAC rAG rAT rCG rCT) | ESTIMATE | PREVIOUS }

If NST = 6, then the values for a six-parameter instantaneous rate matrix may be specified, estimated using maximum likelihood (ESTIMATE), or set to the values currently in memory (PREVIOUS).

RCLASS = (cAC cAG cAT cCG cCT cGT)

If RMATRIX = ESTIMATE, then a submodel of the six-parameter rate matrix may be specified. For example, substitution types may be pooled into common classes to reflect changes between structurally similar molecules (e.g. transitions and transversions). A user is free to decide among the many possible ways that substitution types may be divided or combined. One restriction of the GTR model is the Tamura-Nei model.

Use the following options to specify the base frequency parameters:

VARIANT = { HKY | F84 }

If TRATIO is used, then you may choose between two variants of the 2-parameter model for unequal base frequencies; that is, the model described by Felsenstein (1984) or Hasegawa-Kishino-Yano (1985).

BASEFREQ = { EMPIRICAL | EQUAL | ESTIMATE | PREVIOUS | (frqA frqC frqG) }

By default PAUP* uses the empirical base frequencies (EMPIRICAL). Base frequencies may also be estimated by maximum likelihood for a data set and tree topology (ESTIMATE), assumed equal (EQUAL), explicitly specified (frqA frqC frqG), or set the values currently in memory (PREVIOUS).

The following options are used to specify among-site rate variation parameters:

RATES = { EQUAL | GAMMA | SITESpec }

Use RATES to specify a model of among-site rate variation. By default, PAUP* assumes that all sites change at the same rate; however, many molecular studies suggest that equal rates is not a valid assumption. You may choose between two models to compensate for among site rate-variation.

SHAPE = { real-value | ESTIMATE | PREVIOUS }

Use the SHAPE option to specify the shape of the gamma
distribution used to accommodate among-site rate variation. If SHAPE = ESTIMATE, then the maximum likelihood estimate of this parameter is obtained for a given data set and tree topology. If SHAPE = PREVIOUS, then the value of SHAPE already in memory is used. The default value for this option is 0.5.

NCAT = integer-value

Use NCAT to specify the number of categories to divide the discrete approximation of the gamma distribution.

REPRATE = { MEAN | MEDIAN }

Use REPRATE to specify whether the mean or the median is used to represent the rates within each category of the discrete approximate gamma distribution.

PINVAR = { real-value | ESTIMATE | PREVIOUS }

Use PINVAR to specify the proportion of sites unable to accept substitutions; the remaining sites are assumed to vary at the same rate. The default value for this option is 0.

SITE RATES = { PARTITION [:charpartition-name] | RATESET [:rateset-name] | PREVIOUS }

Use SITE RATES to obtain a single rate estimate for a set of characters. The default for this option is none.

Use the following options to specify the starting parameter values for the likelihood estimation:

STARTVALS = { PARS APPROX | ARBITRARY }

By default, PAUP* uses parsimony-based approximations for the starting values of some parameters estimated by maximum likelihood. If STARTVALS = ARBITRARY, then arbitrary values are used. The parsimony-based starting point is usually much closer to the optimal value and convergence to the optimum will therefore occur more quickly. In some cases, however, the parsimony estimate can be a poor choice and convergence will occur more quickly from an arbitrary starting point.

INITBRLEN = { ROGERS | LS | real-value }

Use INITBRLEN to specify the method for initializing starting branch lengths. By default, PAUP* uses the Rogers-Swofford method (ROGERS); however, you may also specify a least-squared method (LS), or an arbitrary value (real-value).

MLDISTFORLS = { YES | NO }

Development of this option is in progress.
USEAPPROX = \{ **YES | NO** \}

Use USEAPPROX to reject trees if approximate likelihood exceeds the exact likelihood by more than a specified amount. By default PAUP* rejects all trees with a likelihood score greater than the five percent of the exact value. In so doing, PAUP* evaluates fewer topologies dramatically reducing overall search times.

APPROXLIM = *real-value*

Use APPROXLIM to specify the percent deviation from the exact likelihood score before a tree is no longer considered for branch swapping.

ADJUSTAPPLIM = \{ **YES | NO** \}

Use ADJUSTAPPLIM to dynamically readjust the limit specified under APPROXLIM.

Use the following options to specify performance tuning settings:

MAXPASS = *integer-value*

Use MAXPASS to set the maximum number of smoothing passes.

SMAXPASS = *integer-value*

Use SMAXPASS to set the maximum number of branch-length smoothing passes when a tree search is in progress. Setting SMAXPASS to a smaller value can speed search times, but the objective function may not be fully optimized.

DELTA = *real-value*

Use DELTA to set the value for stopping smoothing passes. In other words, when a score changes less than the *real-value* specified, PAUP* assumes that the branch lengths have converged to their optimal values for a given tree.

SDELTA = *real-value*

Use SDELTA to set the value used to stop smoothing passes for operations when a tree search is in progress.

LOGITER = \{ **YES | NO** \}

If LOGITER = **YES**, then the progress of the branch-length iterations will be output to the display buffer. This output can be extensive and it is ordinarily not useful.

MINMEMREQ = \{ **YES | NO** \}

If MINMEMREQ = **YES**, then the memory requirements will be minimized. The speed of most operations will be penalized if this
option is specified.

Miscellaneous options:

**RECON = { MARGINAL | JOINT }**

Use RECON to specify the method used to reconstruct ancestral state characters.

**ALLPROBS = { YES | NO }**

Use ALLPROBS to show marginal probabilities of all base assignments when ancestral states are reconstructed.

**CLOCK = { YES | NO }**

If CLOCK = YES, then the molecular clock model is enforced.

**USERBRLENS = { YES | NO }**

If USERBRLENS = YES, then user-input branch lengths are used when evaluating user-trees.

**LCOLLAPSE = { YES | NO }**

Use LCOLLAPSE to collapse branches of effectively zero length when searching. Branches have length less than or equal to $1 \times 10^{-8}$ are collapsed.

---

**MPRSETS**

Use the **MPRSETS** command to request output of possible character-state assignments (MPR-sets) for one or more characters on one or more trees, by superimposing the possible character-states for each node on a diagram of the tree. The syntax is:

```
MPRSETS character-list [ / options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>TREES</strong></td>
<td><code>tree-list</code></td>
<td>-</td>
</tr>
<tr>
<td><strong>TCOMPRESS</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

The *character-list* specifies the character(s) for which possible character-state assignments are shown, and consists of one or more character numbers, character names, or character-set names.

The following options are available:
TREES = TREE-LIST

The tree-list specifies the tree numbers for which possible character-state assignments are to be shown. If this is the first MPRSETS command and you do not specify a tree list, reconstructions are shown for the first tree only.

TCOMPRESS = { YES | NO }

See "Options And Subcommands Affecting Multiple Commands" on page 29 for details.

If no characters are specified for either a RECONSTRUCT or MPRSETS command, the characters are taken to be those plotted in the last invocation of either of these commands. For example, RECONSTRUCT 1 3 5 7; MPRSETS; will cause both commands to output information for characters 1, 3, 5, and 7.

NJ

Use the NJ command to calculate a tree using the neighbor-joining method. The syntax is:

    NJ [ options ] ;

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>ENFORCE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CONSTRAINTS</td>
<td>constraint-name</td>
<td>none</td>
</tr>
<tr>
<td>BRLENS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>BREAKTIES</td>
<td>{ SYSTEMATIC</td>
<td>RANDOM }</td>
</tr>
<tr>
<td>TieSeed</td>
<td>integer-value</td>
<td>0</td>
</tr>
<tr>
<td>SHOWTREE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TREEFILE</td>
<td>tree-file-name</td>
<td>none</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>APPEND</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*OPTION IS NONPERSISTENT

Description of options:
BRLENS = { YES | NO }

If BRLENS is specified, a list of branch lengths will be output to the display buffer and tree descriptions will include branch lengths. BRLENS = NO reverses the effect of a previous BRLENS specification.

BREAKTIES = { SYSTEMATIC | RANDOM }

Unless BREAKTIES = RANDOM, ties encountered during tree construction are broken systematically according to the input order of the taxa.

TIESEED = integer-value

If BREAKTIES = RANDOM, PAUP* references the system clock to initialize the seed used to generate pseudorandom numbers for breaking ties found during tree construction. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)

SHOWTREE = { YES | NO }

If SHOWTREE = YES, the neighbor-joining tree is printed to the display buffer.

TREEFILE = tree-file-name

If TREEFILE is specified, a description of the trees found by the neighbor-joining method is output to a file in the NEXUS tree format. If BRLENS = YES the tree description in the tree-file will contain branch length information. The tree-file-name must follow the conventions described under "Input/Output files" on page 9.

REPLACE = { YES | NO }
APPEND = { YES | NO }

If the specified file already exists, you will be prompted for confirmation before the existing file is replaced. Use REPLACE = YES to suppress this prompt; the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND, in which case a new TREES block will be concatenated to the end of an existing file.

See "Options And Subcommands Affecting Multiple Commands" on page 29 for a description of the following options:

ENFORCE = { YES | NO }
CONSTRAINTS = constraint-name

OUTGROUP

Use the OUTGROUP command to assign one or more taxa to the outgroup. The syntax is:
**OUTGROUP**  *taxon-list*  [/ONLY]  ;

Unless /ONLY is specified, taxa specified in the taxon-list are simply added to the current outgroup. If taxa have already been assigned to the outgroup and you want only those taxa specified in taxon-list to remain in the outgroup, specify /ONLY; any taxon that is not explicitly specified in the list will be transferred to the ingroup.

**PAIRDIFF**

Use the **PAIRDIFF** command to show nucleotide-pair frequencies. The syntax is:

```plaintext
PAIRDIFF [ taxon-list ] [ / options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>SHORTFMT</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>LONGFMT</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

Description of options:

**SHORTFMT = { YES | NO }**

If SHORTFMT is specified, then nucleotide-pair frequencies, proportion of sites differing, and apparent transition/transversion ratio is given on a single line for each sequence pair.

**LONGFMT = { YES | NO }**

If LONGFMT is specified, then a 4 X 4 matrix of nucleotide-pair frequencies, proportion of sites differing, and apparent transition/transversion ratio is given for each sequence pair both before and after adjustments are made for gaps/ambiguities.

**PERMUTE**

Use the **PERMUTE** command to perform Archie-Faith-Cranston randomization tests. The syntax is:

```plaintext
PERMUTE [ options ] [ / heuristic-search-options | branch-and-bound-search-options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>TEST</td>
<td>{ PTP</td>
<td>TPTP</td>
</tr>
</tbody>
</table>
Description of options:

**TEST = { PTP | TPTP | COMPARE2 }**

- **TEST = PTP**: does a simple permutation test for the existence of phylogenetic structure. TEST = TPTP does a "topology-dependent" PTP test; comparing the best unconstrained tree to trees forces to be compatible with a constraint tree. If TEST = COMPARE2, then the difference between two topologies is compared to a null distribution of differences.

**PSEED = integer-value**

By default, PAUP* references the system clock to initialize the seed used to generate sequences of pseudorandom numbers for randomizing characters. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)

**NREPS = integer-value**

Use NREPS to select the number of times the original data set is permuted for the null distribution of tree scores or tree score differences.

**SEARCH = { HEURISTIC | BANDB }**

Use SEARCH to select a tree searching strategy to be used on each permutation of the original data set.

**RANDOMIZE = { ALL | INGROUP }**

By default PAUP* randomizes the character states of all taxa used in the analyses. If RANDOMIZE = INGROUP, then only the character states of the ingroup taxa are randomized.

**FIRST = constraint-tree-name**
**SECOND** = constraint-tree-name

If **TEST** = **COMPARE2**, use the **FIRST** and **SECOND** options to name the constraint trees to be compared.

**CONSTRAINTS** = constraint-name

Specifies the constraint tree to be used for the T-PTP test.

See "Options And Subcommands Affecting Multiple Commands" on page 29 for a description of the following options:

**CONVERSE** = { **YES** | **NO** }

---

**PSCORES**

Use the **PSCORES** command to request a listing of tree lengths and/or fit measures for one or more trees. The syntax is:

```plaintext
PSCORES [ tree-list ] [/ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>SINGLE</td>
<td>{ NO</td>
<td>VAR</td>
</tr>
<tr>
<td>RANGE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TOTAL</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TL</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CI</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>RI</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>RC</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>HI</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>GFIT</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>KHTEST</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>NONPARAMTEST</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TESTDETAILS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

If no tree list is specified, ALL is assumed. By default, only tree lengths (for single characters, overall, or both) are output. The following options are available:
SINGLE = { ALL | VAR | NO }

The single option specifies the type of single-character output. If SINGLE = ALL, lengths (or fit measures) are output for all trees specified by tree-list. If SINGLE = VAR, lengths (or fit measures) are output only for those characters whose lengths vary among the trees specified by tree-list. If SINGLE = NO, no single-character tree lengths (or fit measures) are output.

RANGE = { YES | NO }

If RANGE is specified, only the minimum and maximum tree lengths (or best and worst fit measures) are output for each character.

TOTAL = { YES | NO }

If TOTAL = NO is specified, overall tree lengths and fit measures are not output.

TL = { YES | NO }

Unless TL = No is specified, tree lengths are output. The default is to show tree lengths and no other fit measures.

CI = { YES | NO }

Use CI to request output of consistency indices.

RI = { YES | NO }

Use RI to request output of retention indices.

RC = { YES | NO }

Use RC to request output of rescaled consistency indices.

HI = { YES | NO }

Use HI to request output of homoplasy indices.

GFIT = { YES | NO }

Use GFIT to request output of Goloboff-fits.

KHTEST = { YES | NO }

Use KHTEST to request that the Kishino-Hasegawa test be used to compare pairs of topologies.

NONPARAMTEST = { YES | NO }

Use NONPARAMTEST to request that the Templeton (Wilcoxon signed-rank) and winning-sites (sign) tests be used to compare pairs of topologies.
TESTDETAILS = \{ \text{YES} | \text{NO} \}

If \text{NONPARAMTEST} = \text{YES}, then use \text{TESTDETAILS} to display a detailed summary of the Templeton (Wilcoxon signed-rank) test calculations.

\textbf{PSet}

Use the \textbf{PSet} command to set options for parsimony analysis. The syntax is:

\begin{verbatim}
PSet [ options ] ;
\end{verbatim}

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>COLLAPSE</td>
<td>{ NO</td>
<td>\text{MAXBRLEN}</td>
</tr>
<tr>
<td>MSTAXA</td>
<td>{ UNCERTAIN</td>
<td>POLYMORPH</td>
</tr>
<tr>
<td>OPT</td>
<td>{ ACCTRAN</td>
<td>DELTRAN</td>
</tr>
<tr>
<td>STEPMATRIX</td>
<td>{ OBSONLY</td>
<td>ALLSTATES</td>
</tr>
<tr>
<td>INCLUDEANC</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>ANCSTATES</td>
<td>\text{ancstates-name}</td>
<td>none</td>
</tr>
<tr>
<td>GK</td>
<td>\text{integer-value}</td>
<td>2</td>
</tr>
<tr>
<td>GOLOBOFF</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>GUNINF</td>
<td>{ EXCLUDE</td>
<td>INCLUDE }</td>
</tr>
<tr>
<td>GPEEWEE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>MINFORFIT</td>
<td>{ MINLENGTH</td>
<td>RANGE }</td>
</tr>
<tr>
<td>GAPMODE</td>
<td>{ MISSING</td>
<td>NEWSTATE }</td>
</tr>
</tbody>
</table>

Description of options:

\textbf{COLLAPSE} = \{ \text{NO} | \text{MAXBRLEN} | \text{MINBRLEN} | \text{AMBEQUAL} \}

Use \text{COLLAPSE} to specify the criterion for collapsing branch lengths. \text{MAXBRLEN} is the method used in PAUP version 3 (and Hennig86). \text{MINBRLEN} collapses a branch if it is possible for it to have zero length. \text{AMBEQUAL} collapses a branch if the MPRset of the two incident nodes are identical. These latter two methods were introduced in Goloboff’s NONA program. We do not recommend their use, but they are available for those who wish to use them.
MSTAXA = \{ \text{UNCERTAIN} \mid \text{POLYMORPH} \mid \text{VARIABLE} \}

If one or more taxa are coded as having multiple states use MSTAXA to specify how those characters are treated. If MSTAXA = VARIABLE the punctuation used to enclose multistate characters is respected. More specifically, characters enclosed by "{}" are treated as variable and characters enclosed by "()" are treated as polymorphic.

MINFORFIT = \{ \text{MINLENGTH} \mid \text{RANGE} \}

If MSTAXA is specified, then use MINFORFIT to specify the "minimum" values used for calculating CI, RI, and RC indices. You may specify minimum-possible single-character lengths (MINLENGTH) or character "ranges" (RANGE) be used.

STEPMATRIX = \{ \text{OBSONLY} \mid \text{ALLSTATES} \mid \text{THREEPLUS1} \}

By default PAUP* allows assignment of states not observed in terminal taxa to internal nodes but only those states that can be identified as potential shortcuts by the "3+1" test (STEPMATRIX = THREEPLUS1). If STEPMATRIX = ALLSTATES, then any possible character state may be assigned to an internal node. If STEPMATRIX = OBSONLY, then internal-node state assignments are limited to states observed in the terminal data.

INCLUDEANC = \{ \text{YES} \mid \text{NO} \}

Use INCLUDEANC to include a hypothetical taxon possessing putative ancestral states for all characters in the searches. This taxon specifies the root of the tree.

GOLOBOFF = \{ \text{YES} \mid \text{NO} \}

Use GOLOBOFF to specify the Goloboff-fit criterion.

\text{GK} = \text{integer-value}

Use GK to specify the concavity parameter in Goloboff’s implied weights method. Note that this value corresponds to the definition of K given by Goloboff (1993) and not the CONC parameter in Goloboff’s Pee-Wee program; which is equal to K+1. The default value for this option is 2.

GUNINF = \{ \text{EXCLUDE} \mid \text{INCLUDE} \}

If GUNINF = INCLUDE, then fits for "uninformative" characters are included.

GPEEWEE = \{ \text{Yes} \mid \text{No} \}

Although it is not recommended, you may specify GPEEWEE to emulate results obtained by the program Pee-Wee written by P. Goloboff. Calculations are performed using integer arithmetic with weights ranging from 0 to 100, and fractional values are
truncated rather than rounded.

\[ \text{GAPMODE} = \{ \texttt{MISSING} \mid \texttt{NEWSTATE} \} \]

If \texttt{GAPMODE} = \texttt{MISSING}, gap characters in sequence data are treated as "missing." If \texttt{GAPMODE} = \texttt{NEWSTATE}, gap characters are treated as a fifth base or 21st amino acid.

See "Options And Subcommands Affecting Multiple Commands" on page 29 for a description of the following options:

\[ \text{ANCSTATES} = \texttt{ancstates-name} \]
\[ \text{OPT} = \{ \texttt{ACCTRAN} \mid \texttt{DELTRAN} \mid \texttt{MINF} \} \]

---

**PUZZLE**

Use the **PUZZLE** command to find a tree by the quartet puzzling method. This method is currently supported only for the maximum likelihood criterion. The syntax is:

```
PUZZLE [ options ];
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>NPUZZLES</td>
<td>integer-value</td>
<td>1000</td>
</tr>
<tr>
<td>SEED</td>
<td>integer-value</td>
<td>0</td>
</tr>
<tr>
<td>SHOWTREE</td>
<td>{ YES \mid NO }</td>
<td>YES</td>
</tr>
<tr>
<td>GRPFREQ</td>
<td>{ YES \mid NO }</td>
<td>YES</td>
</tr>
<tr>
<td>USEAPPROXL</td>
<td>{ YES \mid NO }</td>
<td>YES</td>
</tr>
<tr>
<td>TREEFILE</td>
<td>tree-file-name</td>
<td>none</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES \mid NO }</td>
<td>*NO</td>
</tr>
<tr>
<td>APPEND</td>
<td>{ YES \mid NO }</td>
<td>*NO</td>
</tr>
<tr>
<td>DSTATUS</td>
<td>{integer-value \mid NO }</td>
<td>NO</td>
</tr>
</tbody>
</table>

*Option is nonpersistent

Description of options:

\[ \text{NPUZZLES} = \text{integer-value} \]

Use \text{NPUZZLES} to specify the number of puzzling steps. The default value for this option is 1000
SEED = integer-value

By default, PAUP* references the system clock to initialize the seed used to generate sequences of pseudorandom numbers used to determine the order of sequence insertion during the "puzzling" step. An explicit seed may be specified to override the system clock default. (See "InitSeeds = \{ 0 | 1 \}" on page 106 for more details.)

SHOWTREE = \{ YES | NO \}

Use SHOWTREE to print the tree found by quartet-puzzling to the display buffer.

GRPFREQ = \{ YES | NO \}

Use GRPFREQ to show all observed bipartitions found during the "puzzling" step and the frequency at which they occurred.

USEAPPROXL = \{ YES | NO \}

If USEAPPROXL = YES, then approximate rather than "exact" likelihoods will be used.

TREEFILE = tree-file-name

If TREEFILE is specified, a description of the tree found at each puzzling step is output to a file in the NEXUS tree format. The tree-file-name must follow the conventions described under "Input/Output files" on page 9.

REPLACE = \{ YES | NO \}
APPEND = \{ YES | NO \}

If the specified file already exists, you will be prompted for confirmation that the existing file should be replaced. Explicit specification of REPLACE suppresses this prompt and the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND, in which case a new TREES block will be concatenated to the end of an existing file.

DSTATUS = \{integer-value | NO \}

See "Options And Subcommands Affecting Multiple Commands" on page 29 for a description of this option.

QUIT

The QUIT command causes PAUP* to terminate. Unless you specify the option WARNTSAVE = NO, PAUP* will prompt you before quitting if there are unsaved trees in memory. WARNTSAVE is the only option under this command. The syntax is:
QUIT [ options ] ;

Available options:

Keyword   | Option type   | Default setting
----------|---------------|-----------------
WARNTSave | { YES | NO }    | YES

**RANDTrees**

Use the RANDTrees command to randomly sample trees from the set of all possible trees and compute their scores under the current optimality criterion. The results are shown in the form of a frequency distribution of tree scores. The syntax is:

RANDTrees [ options ] ;

Available options:

**Keyword**  | **Option type** | **Default setting**
-------------|-----------------|---------------------
NREPS        | integer-value   | 1000
SEED         | integer-value   | 0
FDTYPE       | { BARCHART | HISTOGRAM } | BARCHART
NCLASSES     | integer-value   | 20
FDFILE       | frequency-distribution-file-name | none
REPLACE      | { YES | NO }     | *No

*Option is nonpersistent

Description of options:

NREPS = integer-value

integer-value specifies the number of random trees to be evaluated. The default is NREPS = 1000.

SEED = integer-value

By default, PAUP* references the system clock to initialize the seed used to generate sequences of pseudorandom numbers used to randomly sample tree topologies. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)
FDTYPE = { BARChart | HISTOGRAM }

The default FDTYPE specifies that the number of trees at each tree score is output as a BARChart. If FDTYPE = HISTOGRAM, tree scores are pooled into classes, the size of which is specified by the NCLASSES option.

NCLASSES = integer-value

Integer-value specifies the number of class intervals for the frequency distribution of tree scores. By default, NCLASSES=20, so that adjacent tree scores are pooled into 20 classes of tree scores.

FDFILE = frequency-distribution-file-name

If FDFILE is specified, data for the frequency distribution of tree scores are saved to a text file for input to other programs. The FDFILE option is not persistent. Frequency-distribution-file-name specifies the name of the file to receive the frequency distribution. (See "Input/Output files" on page 9 for more details).

REPLACE = { YES | NO }

If FDFILE is used and the specified file already exists you will be prompted for confirmation that the existing file should be replaced. REPLACE suppresses this prompt and the existing file will be quietly overwritten by the new data.

RATESet

Use the RATESet command to define a "rate set". The syntax is:

RATESet rate-set-name = rateset-definition ;

REconstruct

Use the REconstruct command to request output of character-state reconstructions for one or more characters on one or more trees. The reconstruction is shown by superimposing the character-states assigned to each node on a plot of the tree. Reconstructions are available under either the parsimony or likelihood criterion. The syntax is:

REconstruct [character-list] [/ options] ;

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>TREES</td>
<td>tree-list</td>
<td>-</td>
</tr>
<tr>
<td>TCOMPRESS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>
The character-list specifies the character(s) for which reconstructions are shown, and consists of one or more character numbers, character names, or character-set names.

Description of options:

TREES = TREE-LIST

The tree-list specifies the tree numbers for which reconstructions are to be shown. If this is the first RECONSTRUCT command and you do not specify a tree list, reconstructions are shown for the first tree only. If other options follow the TREES option you must the put the tree-list list in double quotes.

TCOMPRESS = { YES | NO }

See "Options And Subcommands Affecting Multiple Commands" on page 29 for details.

If no characters are specified for either a RECONSTRUCT or MPRSETS command, the characters are taken to be those plotted in the last invocation of either of these commands. For example, reconstruct 1 3 5 7; mpret; will cause both commands to output information for characters 1, 3, 5, and 7.

RESTORE

The RESTORE command is synonymous with the UNDELETE command. See "Undelete" on page 119 for a description of available options.

REVFILTER

Use the REVFILTER command to "reverse" the effect of the current filter. All trees that are currently hidden by the filter will become visible, and all trees that were previously visible will be hidden. There are no options. The syntax is:

REVFILTER ;

REWEIGHT

Use the REWEIGHT command to assign weights to the characters based on their fit to the trees currently in memory. The syntax is:

REWEIGHT [ options ] ;
Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>INDEX</td>
<td>{ RC</td>
<td>CI</td>
</tr>
<tr>
<td>FIT</td>
<td>{ MAXIMUM</td>
<td>MINIMUM</td>
</tr>
<tr>
<td>BASEWT</td>
<td>integer-value</td>
<td>1</td>
</tr>
<tr>
<td>TRUNCATE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>MINFORFIT</td>
<td>{ RANGE</td>
<td>MINLENGTH }</td>
</tr>
</tbody>
</table>

Description of options:

**BASEWT = integer-value**

Base-weight specifies the maximum possible weight that a character can be assigned, corresponding to an index value (see below) of 1. Weights are scaled from 0 to this value. The default is BASEWT=1000.

**INDEX = { RC | CI | RI }**

The INDEX option is used to specify which fit measure to use when calculating the new character weights (RC = rescaled consistency index, CI = consistency index, RI = retention index).

**FIT = { MAXIMUM | MINIMUM | MEAN }**

The FIT option is used to specify whether the new weights are based on the maximum, minimum, or mean of the fit values for each character over all of the trees in memory.

**TRUNCATE = { YES | NO }**

Because PAUP* uses integers to represent weights, they are ordinarily scaled to the nearest integer by rounding. Use the TRUNCATE option if you want to simply discard the fractional part (e.g., 8.7 goes to 8 rather than 9). I can think of no reason to use this option other than to duplicate the weights obtained using the Hennig86 program (Farris, 1988).

**MINFORFIT = { RANGE | MINLENGTH }**

If the data matrix contains polymorphic or uncertain characters, use MINFORFIT to specify the "minimum" values used for calculating CI, RI, and RC indices. You may specify minimum-possible single-character lengths (MINLENGTH) or character "ranges" (RANGE) be used.
**ROOTTREES**

Use the **ROOTTREES** command to convert all trees in memory from an unrooted to a rooted representation. Trees are rooted according to the currently specified outgroup. The syntax is:

```
ROOTTREES [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>OUTROOT</td>
<td>{ POLYTOMY</td>
<td>PARAPHYL</td>
</tr>
<tr>
<td>METHOD</td>
<td>{ OUTGROUP</td>
<td>LUNDBERG</td>
</tr>
<tr>
<td>USERBRLENS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

The circumstances under which you would need to use this command are rather unlikely.

Description of options:

**OUTROOT = { POLYTOMY | PARAPHYL | MONOPHYL }**

See "Options And Subcommands Affecting Multiple Commands" on page 29 for details.

**METHOD = { OUTGROUP | LUNDBERG | MIDPOINT }**

The **METHOD** option is used to specify how unrooted trees are to be rooted prior to output. You can choose **OUTGROUP** rooting, using whichever outgroup you have selected; **MIDPOINT** rooting, which roots the tree at its midpoint; or **LUNDBERG** rooting, which requires that a previous **ANCSTATES** command has been issued. By default, **OUTGROUP** rooting is in effect.

**USERBRLENS = { YES | NO }**

If **METHOD = MIDPOINT**, then you may specify user-defined branch lengths.

**SAVEASSUM**

Use the **SAVEASSUM** command to save the current character-type, character-weight, character-exclusion, ancestral-states, taxon-deletion, and outgroup status to a file in ASSUMPTIONS and a PAUP block. You can restore the settings in effect at the time the **SAVEASSUM** command was issued simply by executing the commands stored in the file (use the **EXECUTE** command for this purpose). The syntax is:

```
SAVEASSUM [ options ] ;
```
Available options:

**Keyword** | **Option type** | **Default setting**
--- | --- | ---
FILE | settings-file-name | none
REPLACE | { Yes | No } | *No

*Option is nonpersistent

By default, if the specified file already exists, you will be asked if you want to replace it. To suppress this warning, specify REPLACE; in this case the file will be quietly overwritten.

**SAVEDIST**

Use the SAVEDIST command to save distance matrix to a file. The syntax is:

```
SAVEDIST [ options ] ;
```

Available options:

**Keyword** | **Option type** | **Default setting**
--- | --- | ---
FILE | export-file-name | none
TRIANGLE | { LOWER | UPPER | BOTH } | LOWER
DIAGONAL | { Yes | No } | No
UNDEFINED | { TWICE_MAX | ASTERISK } | TWICE_MAX
NDECIMALS | integer-value | 8
REPLACE | { Yes | No } | *No
APPEND | { Yes | No } | *No

*Option is nonpersistent

Description of options:

**FORMAT = { TabText | OneColumn | NEXUS | PHYLIP }**

Use FORMAT to request that pairwise distances be output as tab-delimited text either as a full matrix format (TabText) or in a single-column (OneColumn) useful for saturation plots, etc.
TRIANGLE = { LOWER | Upper | BOTH }

If any FORMAT other than ONECOLUMN is selected than the distances matrix may be output as a lower half triangle (LOWER), an upper half triangle (UPPER), or full matrix (BOTH).

DIAGONAL = { YES | NO }

Use the DIAGONAL option to include the diagonal values if relevant.

UNDEFINED = { TWICE_MAX | ASTERISK }

Use UNDEFINED to specify whether undefined distances are output as twice the maximum defined distance (TWICE_MAX) or as an asterisk (ASTERISK).

NDECIMALS = integer-value

Use NDECIMALS to specify the maximum number of decimals allowed for pairwise distances.

FILE = export-file-name

Use the FILE to output pairwise distances to a file in one of two formats. The export-file-name must follow the file-name conventions described "Input/Output files" on page 9.

REPLACE = { YES | NO }
APPEND = { YES | NO }

If FILE = export-file-name option is specified and the export-file-name already exists, you will be prompted for confirmation that the existing file should be replaced. Explicit specification of REPLACE = YES suppresses this prompt; the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND = YES, in which case new distances in the specified format will be concatenated to the end of an existing file.

SAVE TREES

Use the SAVE TREES command to write trees currently in memory to a file as a NEXUS-format TREES block or as a treefile accepted by another program. The syntax is:

SAVE TREES [ options ] ;

Available options:

Keyword                        Option type  Default setting
---                            ------       ---
FILE                           tree-file-name paup.trees
**Commands used in the PAUP Block**

---

**Description of options:**

**FORMAT = { NEXUS | ALTNEXUS | FREQPARS | PHYLIP | HENNIG }**

Specifies the type of tree-file to produce. NEXUS requests a file containing the standard NEXUS TREES block using a translation table (which greatly reduces the amount of disk space required to store the trees). ALTNEX also specifies a NEXUS TREES block, but no translation table is used (the full taxon names are included in each tree description). FREQPARS requests a treefile for the FREQPARS program described by Swofford and Berlocher (1987). PHYLIP requests a treefile for input to version 3.4 of Felsenstein’s (1991) PHYLIP package. HENNIG requests a treefile for version 1.5 of Farris’s (1988) Hennig86 program.

**BRLENS = { YES | NO }**

If BRLENS is specified, tree descriptions will include branch lengths if the program corresponding to the FORMAT setting supports them. BRLENS = NO reverses the effect of a previous BRLENS specification. Branch lengths are calculated according to the current optimality criterion.

**SAVEBOOTP = { NO | BRLENS | NODELABELS | BOTH }**

Use SAVEBOOTP to include bootstrap or jackknife proportions as branch lengths (BRLENS), internal node labels (NODELABELS) (only supported by other programs), or both (BOTH).

**MAXDECIMALS = integer-value**

If branch lengths will be included in tree descriptions, use
MAXDECIMALS to specify the maximum number of decimals stored in each tree description.

FILE = tree-file-name

Specifies a name for the tree file. If you do not explicitly specify a file name, a default file name will be used.

FROM = integer-value

If nonzero, starting-tree-number specifies the number of the first tree to save.

TO = integer-value

If nonzero, ending-tree-number specifies the number of the last tree to save.

ROOT = { YES | NO }

If the current trees in memory are unrooted and ROOT is specified, trees are rooted (using the rooting options currently in effect) before they are saved. Note that the process of rooting the trees slows down the saving operation considerably. If you are saving the trees only with the intention of rereading them into PAUP*, there is no need to root the trees. However, if you are exporting the trees to another program, rooting them may be desirable.

The ROOT option has no effect if the trees in memory are already rooted. ROOT = NO can be used to reverse the effect of a previous ROOT specification.

REPLACE = { YES | NO }
APPEND = { YES | NO }

If FILE = tree-file-name option is specified and the tree-file-name already exists, you will be prompted for confirmation that the existing file should be replaced. Explicit specification of REPLACE = YES suppresses this prompt; the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND = YES, in which case a new TREES block will be concatenated to the end of an existing file.

Set

The SET command is used to set a variety of options whose scope extends beyond single commands. The syntax is:

SET [ options ] ;
Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>ROOT</td>
<td>{ OUTGROUP</td>
<td>LUNDBERG</td>
</tr>
<tr>
<td>INITSEEDS</td>
<td>{ 0</td>
<td>1 }</td>
</tr>
<tr>
<td>MONITOR</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>SEMIGRAPH</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>MAXTREES</td>
<td>integer-value</td>
<td>100</td>
</tr>
<tr>
<td>INCREASE</td>
<td>{ NO</td>
<td>PROMPT</td>
</tr>
<tr>
<td>AUTOINC</td>
<td>integer-value</td>
<td>100</td>
</tr>
<tr>
<td>SHOWEXCLUDED</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>ALLOWPUNCT</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CMLABELS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CMSHOWEQ</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CMCOLWID</td>
<td>integer-value</td>
<td>1</td>
</tr>
<tr>
<td>CMCSTATUS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>CONSTRAINTS</td>
<td>constraint-name</td>
<td>none</td>
</tr>
<tr>
<td>ERRORBEEP</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>QUERYBEEP</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>KEYBEEP</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>NOTIFYBEEP</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>ERRORSTOP</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>AUTOCLOSE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TORDER</td>
<td>{ STANDARD</td>
<td>RIGHT</td>
</tr>
<tr>
<td>CHECKEVS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>TCOMPRESS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>SHOWTAXNUM</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>BACKGROUND</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>
### Description of options:

- **MONITOR** = { *YES* | *NO* }

  MONITOR = *NO* suppresses output to the "main display" (window or terminal screen) and is useful when you want to send output to the log file and/or printer only. MONITOR reactivates the main display.

  At least one output destination must be active at all times. Consequently, if no log file is active or the "echo to printer" (ECHO) option is not set, output will be sent to the main display even if
MONITOR = NO has been requested.

INITSEEDS = \{ 0 | 1 \}

A few commands used in PAUP* require sequences of "random" numbers (i.e., BOOTSTRAP, JACKKNIFE, HOMPART, PERMUTE, RANDTREES, PUZZLE, and SURFCHECK). Other command also use "random" numbers, but only when certain options are specified (i.e., GENERATETrees, HSEARCH, NJ, and STARDECOMP). PAUP* uses a linear congruential method starting with an integer between 1 and 2,147,483,646 to seed a random number generator. By default INITSEEDS = 0, instructs PAUP* to obtain the initial seed from the system clock. If you do not specify a starting seed for subsequent runs, the seed defaults to the next number in the random number sequence initiated during the previous run. Users are always given the option to specify a value for the seed, thus overriding the PAUP* default of referencing the system clock.

ALLOWPUNCT = \{ YES | NO \}

Unless ALLOWPUNCT is specified, taxon and character names in input data matrices must conform to the NEXUS specification; namely they cannot contain special punctuation characters like parentheses, hyphens, etc. (see "Identifiers" on page 6). If ALLOWPUNCT = YES is set prior to processing of a DATA or CHARACTERS block, then taxon and character names are allowed to contain these special characters. This option applies only to the DATA and CHARACTERS blocks; names containing special characters must be enclosed within single quotes in other contexts. This option allows backward compatibility with files prepared for PAUP 3.1; new data files should always conform to the NEXUS standard to prevent incompatibilities with other programs.

SEMIGRAPH = \{ YES | NO \}

PAUP* uses special characters in its internal font to draw trees and other items. On the IBM-PC, these characters are nonstandard "high ASCII" characters. On the Macintosh, these characters are neither in the standard 128 ASCII characters nor in the set of special characters normally included with Macintosh fonts. Thus, although the trees look nice when drawn in the main display window, they may not look right when printed on some printers. Therefore, PAUP* ordinarily translates these "semigraphics" characters to standard ASCII substitutes when output is directed to a printer, file, or document window. If you want to override this behavior, specify SEMIGRAPH. (E.g., many IBM-PC printers can print the high ASCII characters, and the Apple LaserWriter can create a "bit map" version of PAUP*'s internal "PAUPMonaco" font).

This option is relevant only for IBM-PC and Macintosh versions only.

The following three options affect the setting of the maximum number
of trees that PAUP* can store at any given time:

MAXTREES = integer-value

The MAXTREES parameter specifies the maximum number of trees that can be saved. Setting MAXTREES to a large value will reduce the likelihood that the tree buffer will become full during a search or tree-file operation, at the expense of a larger chunk of memory being tied up and therefore unavailable for other purposes.

Ordinarily, if the number of trees found during a search reaches the value of MAXTREES, you will be given a chance to increase MAXTREES before proceeding. This behavior can be altered using the INCREASE option (see below). MAXTREES is initially set to 100.

INCREASE = { PROMPT | AUTO | NO }

The setting of the INCREASE option determines the action taken by PAUP* if the limit on the number of trees that can be stored (=MAXTREES, see above) is reached during a search or a tree-file operation. If INCREASE = PROMPT, you will be given the opportunity to increase MAXTREES. If INCREASE = AUTO, MAXTREES will automatically be increased by a number of trees equal to the current AUTOINC setting (see below). If INCREASE = NO, MAXTREES will not be increased, and no prompt will be issued. In this case, a "tree-buffer overflow" occurs which can affect the effectiveness of the search in progress. (The tree-buffer overflow condition will be documented in the output.)

AUTOINC = integer-value

The AUTOINC value specifies the number of trees by which MAXTREES is increased when the number of trees saved reaches MAXTREES and the INCREASE = AUTO option is in effect. AUTOINC is initially set to 100.

The following three options specify whether PAUP* sounds a "beep" when various kinds of errors occur:

ERRORBEEP = { YES | NO }

Ordinarily, PAUP* beeps to alert you that an error message has been issued. Specify ERRORBEEP = NO to suppress these beeps.

QUERYBEEP = { YES | NO }

Ordinarily, PAUP* beeps to alert you when it stops for your input before it can continue a process. Specify QUERYBEEP = NO to suppress these beeps.

KEYBEEP = { YES | NO }

Ordinarily, PAUP* beeps when you type a key that is invalid in
the current context. Specify KEYBEEP=NO to suppress these beeps.

AUTOCLOSE = { YES | NO }

After a search has ended the status window will remain in the foreground until the user closes it. Use AUTOCLOSE=YES to close the status window automatically after a run has ended.

NOTIFYBEEP = { YES | NO }

Unless NOTIFYBEEP=NO, a "beep" is sounded at the end of a search.

VISNOTIF = { NONE | SHOWALERT | FLASHONLY }

When a background job ends an alert box will be sent to the foreground and the PAUP* icon on the task-menu will flash. Use VISNOTIF to suppress the alert box (FLASHONLY) or both of the alert box and the flashing PAUP* icon (NONE).

TORDER = { STANDARD | RIGHT | LEFT | ALPHABET }

Specifies the convention used to "order" the tree.

The following two options are specific to the Macintosh version.

BACKGROUND = { YES | NO }

Ordinarily, PAUP* continues processing when it is moved to the background. Specify BACKGROUND=NO to suppress background processing, thereby giving more time to the foreground application.

CHECKEVTS = { YES | NO }

CHECKEVTS=NO disables "event-checking," causing all mouse clicks and key presses to be ignored. Speed of PAUP* searches is improved somewhat, but it will not be possible to stop the search (without restarting the computer) or to switch to a different application under MultiFinder.

FLUSHLOG = { YES | NO }

Specification of FLUSHLOG causes the file's buffer to be flushed after every line of output. Ordinarily, this degrades system performance and is not recommended. However, there may be situations in which immediate flushing is useful.

ALLOWEND = { YES | NO }

The NEXUS convention is to terminate blocks with END; however, earlier versions of PAUP used ENDBLOCK. Unless ALLOWEND=NO, PAUP* will accommodate both character strings for block termination.
ALLDIGLAB = { Prohibit | Warn | Nowarn }

By default, PAUP* issues a warning if all digit taxa or character labels are included. Use ALLDIGLAB to prohibit the use of all-digit label or to allow all-digit labels and suppress warnings. See "Identifiers" on page 6 for a description of valid taxa and character labels.

CRITERION = { Parsimony | Likelihood | Distance }

Use CRITERION to selection from the three optimality criterion.

DEFAULTMODE = { Yes | No }

By default when option settings or other information is required, a dialog box will be opened. If DEFAULTMODE = Yes, then PAUP* will take a default action. Because the default action will not be appropriate in every situation, this option is not recommended unless you know what affect the default action will have on your analyses.

STOREBRLENS = { Yes | No }

If branch lengths are present in the TREES block, then STOREBRLENS = Yes stores branch lengths for subsequent use within the program. Otherwise, the branch lengths are discarded.

STORETREETWTS = { Yes | No }

If tree weights are present in the TREES block, then STORETREETWTS = Yes stores tree weights. When tree weights are the reciprocal of the number of trees found in either a Bootstrap or Jackknife replicate, this option allows the combination of bootstrap results from runs performed at different times or on different machines and the recovery of results obtained prior to a system crash. (See "UseTreeWts = { Yes | No }" on page 44 for more details)

SHOWABBREV = { Yes | No }

Specifies whether help shows command and option names so as to indicate the shortest acceptable abbreviation.

TAXLABELS = { Full | Truncate }

If TAXLABELS = Full, then the full 32 characters of long taxon labels will be output to the display buffer. Otherwise, taxon names are truncated to 16 characters.

ERRORSTOP = { Yes | No }

Ordinarily, PAUP* stops processing an input file when unrecognized commands, OPTIONS-command keywords, or formats are encountered. If ERRORSTOP = No is specified, a warning message is issued and processing is allowed to continue.
\textbf{WARN Reset} = \{ \textbf{Yes} | \textbf{No} \}

Ordinarily, PAUP* issues a warning message when an input file containing a \texttt{DATA} block is executed and a \texttt{DATA} block has already been processed. Specification of \texttt{WARN Reset} = \texttt{NO} suppresses this warning.

\textbf{WARN Tree} = \{ \textbf{Yes} | \textbf{No} \}

Use \texttt{WARN Tree} to issue a warning about treefile operations that could delete unsaved trees.

\textbf{WARN TSave} = \{ \textbf{Yes} | \textbf{No} \}

Use \texttt{WARN TSave} to issue a warning before quitting if there are unsaved trees in memory.

\textbf{WARN Block Name} = \{ \textbf{Yes} | \textbf{No} \}

Use \texttt{WARN Block Name} to issue a warning when unrecognized blocknames are included in a data set.

\textbf{WARN Root} = \{ \textbf{Yes} | \textbf{No} \}

Use \texttt{WARN Root} to issue a warning about the rooting status of user-input trees.

\textbf{WARN Redef} = \{ \textbf{Yes} | \textbf{No} \}

Use \texttt{WARN Redef} to issue a warning about redefining names for sets, constraints, etc.

The following options are described in "Options And Subcommands Affecting Multiple Commands" command described on page 29:

\texttt{CONSTRAINTS} = \texttt{constraint-tree-name}

\texttt{STATUS} = \{ \texttt{Yes} | \texttt{No} \}

\texttt{DSTATUS} = \{ \texttt{integer-value} | \texttt{No} \}

\texttt{ROOT} = \{ \texttt{OUTGROUP} | \texttt{LUNDBERG} | \texttt{MidPoint} \}

\texttt{OUTROOT} = \{ \texttt{POLY TOMY} | \texttt{PARAPHYL} | \texttt{MONOPHYL} \}

\texttt{TCOMPRESS} = \{ \texttt{YES} | \texttt{NO} \}

\texttt{SHOW EXCLUDED} = \{ \texttt{YES} | \texttt{NO} \}

\texttt{CM SHOW EQ} = \{ \texttt{YES} | \texttt{NO} \}

\texttt{CMLABELS} = \{ \texttt{YES} | \texttt{NO} \}

\texttt{CM CSTATUS} = \{ \texttt{YES} | \texttt{NO} \}

\texttt{CM COL WID} = \texttt{integer-value}

\textbf{SHOW Anc}

Use the \texttt{SHOW Anc} command to request a listing of the ancestral character-states currently in effect. No options are available. The syntax is:

\texttt{SHOW Anc ;}
**SHOWCHARPARTS**

Use the **SHOWCHARPARTS** command to show one or all character-partition definitions.

```
SHOWCHARPARTS [ partition-name ] ;
```

If no *partition-name* is specified, all defined partitions are output.

**SHOWCONSTR**

Use the **SHOWCONSTR** command to show one or more constraint-tree definitions. The syntax is:

```
SHOWCONSTR [ { constraint-name | ALL } ] ;
```

If you do not specify a name (or ALL), the current default constraint tree will be shown. Specify ALL to show all constraint trees that have been defined.

**SHOWDIST**

Use the **SHOWDIST** command to output a matrix of "distances" between taxa. There are no options. The syntax is:

```
SHOWDIST ;
```

Use the **DSET** command to specify the distance measure to be calculated.

**SHOWMATRIX**

Use the **SHOWMATRIX** command to list the current data matrix. The syntax is:

```
SHOWMATRIX [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>SHOWEXCLUDED</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>CMLABELS</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>CMSHOWEQ</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
<tr>
<td>CMCOLWID</td>
<td>integer-value</td>
<td>1</td>
</tr>
<tr>
<td>CMCSTATUS</td>
<td>{ Yes</td>
<td>No }</td>
</tr>
</tbody>
</table>
The options available here are described under "Options And Subcommands Affecting Multiple Commands" on page 29.

**SHOWRATESETS**

Use the **SHOWRATESETS** command to show one or all rate-set definitions. The syntax is:

```
SHOWRATESETS [ rate-set-name ] ;
```

**SHOWTAXPARTS**

Use the **SHOWTAXPARTS** command to show one or all taxon-partition definitions. The syntax is:

```
SHOWTAXPARTS [ partition-name ] ;
```

**SHOWTREES**

Use the **SHOWTREES** command to request a diagram of one or more trees with no other information (see also the **DESCRIBE** command). The syntax is:

```
SHOWTREES [ tree-list ] [/ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>TCOMPRESS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>ROOT</td>
<td>{ OUTGROUP</td>
<td>LUNDBERG</td>
</tr>
<tr>
<td>OUTROOT</td>
<td>{ POLYTOMY</td>
<td>PARAPHYL</td>
</tr>
<tr>
<td>USERBRLENS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

Description of options:

```
USERBRLENS = { YES | NO }
```

If USERBRLENS = Yes, then user-supplied branch lengths are used.

See "Options And Subcommands Affecting Multiple Commands" on page 29 for a description of the following options:

```
TCOMPRESS = { YES | NO }
ROOT = { OUTGROUP | LUNDBERG | MIDPOINT }
```
OUTROOT = \{ POLYTOMY \mid PARAPHYL \mid MONOPHYL \}

**SHOWUSERTYPE**

Use the SHOWUSERTYPE command to show all user-defined character types. There are no options for the command. The syntax is:

```
SHOWUSERTYPE ;
```

**STARDECOMP**

Use the STARDECOMP command to find a tree by star-decomposition search. The syntax is:

```
STARDECOMP [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>BREAKTIES</td>
<td>{ SYSTEMATIC \mid RANDOM }</td>
<td>SYSTEMATIC</td>
</tr>
<tr>
<td>TIESEED</td>
<td>\textit{integer-value}</td>
<td>0</td>
</tr>
<tr>
<td>ENFORCE</td>
<td>{ YES \mid NO }</td>
<td>NO</td>
</tr>
<tr>
<td>CONSTRAINTS</td>
<td>\textit{constraint-name}</td>
<td>none</td>
</tr>
</tbody>
</table>

Description of options:

**BREAKTIES = \{ SYSTEMATIC \mid RANDOM \}**

Unless BREAKTIES = RANDOM, ties encountered during tree construction are broken systematically according to the input order of the taxa.

**TIESEED = \textit{integer-value}**

If BREAKTIES = RANDOM, PAUP* references the system clock to initialize the seed used to generate pseudorandom numbers for breaking ties found during tree construction. An explicit seed may be specified to override the system clock default. (See "InitSeeds = \{ 0 \mid 1 \}" on page 106 for more details.)

See "Options And Subcommands Affecting Multiple Commands" on page 29 for details.

**ENFORCE = \{ YES \mid NO \}**
CONSTRAINTS = constraint-name

**SURFCheck**

Use the **SURFCheck** command to check likelihood surface for multiple peaks. The syntax is:

```
SURFCHECK [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>NREPS</td>
<td>integer-value</td>
<td>100</td>
</tr>
<tr>
<td>SEED</td>
<td>integer-value</td>
<td>0</td>
</tr>
<tr>
<td>TREE_NUM</td>
<td>integer-value</td>
<td>1</td>
</tr>
<tr>
<td>BRLENS</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>FILE</td>
<td>foreign-file-name</td>
<td>none</td>
</tr>
<tr>
<td>TOLER</td>
<td>real-value</td>
<td>1e-07</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>APPEND</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*OPTION IS NONPERSISTENT

Description of options:

**NREPS = integer-value**

Use NREPS to specify the number of passes ...

**SEED = integer-value**

PAUP* references the system clock to initialize the seed used to generate pseudorandom numbers for sampling "random" branch lengths. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)

**TREE_NUM = integer-value**

Use TREE_NUM to specify the tree for which the likelihood surface is checked.

**BRLENS = { YES | NO }**

If BRLENS = YES, then user-supplied branch lengths are used.
FILE = foreign-file-name

If FILE is specified the results of the surface check will be output to a text file.

REPLACE = { YES | NO }
APPEND = { YES | NO }

If FILE option is specified and the foreign-file-name already exists, you will be prompted for confirmation that the existing file should be replaced. Explicit specification of REPLACE = YES suppresses this prompt; the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND = YES, in which case a new TREES block will be concatenated to the end of an existing file.

TOLER = real-value

Use TOLER to stop smoothing passes when the likelihood score changes less than the real-value specified.

**TAXPARTITION**

Define a partition of the taxa. The syntax is:

```
TAXPARTITION partition-name = partition-definition ;
```

The TAXPARTITION command is ordinarily issued from within the SETS block. However, you may also issue it from the command line or from within a PAUP block. **TAXPARTITIONS** are needed for "convexity" constraints.

**TAXSET**

Use the TAXSET command to define a "taxon set." Taxon sets are simply groups of taxa that can be referred to by a single name in other commands. The syntax is:

```
TAXSET taxon-set-name = taxon-list ;
```

The taxon-set-name must not be identical to any of the original taxon names. The TAXSET command is ordinarily issued from within the SETS block. However, you may also issue it from the command line or from within a PAUP block.

**TIME**

Use the TIME command to output the current time and date. The syntax is:

```
TIME ;
```
**ToNEXUS**

Use the **ToNEXUS** command to convert a file to NEXUS format. The syntax is:

```
ToNEXUS [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>FORMAT</td>
<td>{ PHYLIP</td>
<td>HENNIG86</td>
</tr>
<tr>
<td>FROMFILE</td>
<td>foreign-file-name</td>
<td>none</td>
</tr>
<tr>
<td>TOFILE</td>
<td>NEXUS-file-name</td>
<td>none</td>
</tr>
<tr>
<td>DATATYPE</td>
<td>{ NUCLEOTIDE</td>
<td>PROTEIN</td>
</tr>
<tr>
<td>INTERLEAVE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>GAPSYMBOL</td>
<td>single-character-value</td>
<td>-</td>
</tr>
<tr>
<td>MISSSYMBOL</td>
<td>single-character-value</td>
<td>-</td>
</tr>
<tr>
<td>IDENTSYMBOL</td>
<td>single-character-value</td>
<td>-</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*Option is nonpersistent

Description of options:

```
FORMAT = { PHYLIP | HENNIG86 | TABText | TEXT | GCG | MEGA | PIR | FREQPars }
```

Use FORMAT to specify the import file-type. You may choose from the following formats:

1. PHYLIP (Felsenstein)
2. Hennig68 (Farris)
3. GCG MSF
4. MEGA (Kumar, Tamura, and Nei)
5. NBRF-PIR
6. Text (tab or space delimited)
7. FREQPARS (Swofford and Berlocher)
FROMFILE = foreign-file-name

Use FROMFILE to specify the foreign-file-name to be imported.

TOFILE = NEXUS-file-name

Use TOFILE to specify the NEXUS-file-name used to save the NEXUS-formatted data set.

DATATYPE = { NUCLEOTIDE | PROTEIN | RESTSITE | STANDARD | DISTANCE }

If FORMAT = { PHYLIP | TABTEXT | TEXT }, then use DATATYPE to specify the type of data being imported. If FORMAT = MEGA, then DATATYPE = { NUCLEOTIDE | PROTEIN | DISTANCE } may be selected. Note that PAUP* currently does not support distance formats.

INTERLEAVE = { YES | NO }

Use INTERLEAVE if FORMAT = PHYLIP and the data set in the PHYLIP file are interleaved.

GAPSYMBOL = single-character-value

If FORMAT = { TABTEXT | TEXT | MEGA }, then a single-character-value may be entered to represent gaps.

MISSSYMBOL = single-character-value

If FORMAT = { TABTEXT | TEXT | MEGA }, then a single-character-value may be entered to represent missing data.

IDENTSYMBOL = single-character-value

If FORMAT = { TABTEXT | TEXT | MEGA }, then a single-character-value may be entered to represent an identity character. This is equivalent to what PAUP* refers to as MATCHCHAR (see page 13).

REPLACE = { YES | NO }

If the NEXUS-file-name used under the TOFILE option already exists you will be prompted for confirmation that the existing file should be replaced. REPLACE suppresses this prompt; the existing file will be quietly overwritten by the new data.

TREEDIST

Use the TREEDIST command to request output of a matrix of tree-to-tree distances computed according to the symmetric-difference or "partition" metric (Penny and Hendy, 1985), or one of two metrics based on agreement subtrees. The syntax is:

TREEDIST [ options ] ;
Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td>METRIC</td>
<td>{ SYMDIFF</td>
<td>AGD1</td>
</tr>
<tr>
<td>FROMTREE</td>
<td>integer-value</td>
<td>0</td>
</tr>
<tr>
<td>FD</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>SHOWALL</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>FILE</td>
<td>export-file-name</td>
<td>none</td>
</tr>
<tr>
<td>REPLACE</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td>APPEND</td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*OPTION IS NONPERSISTENT

Descriptions of options:

**METRIC = { SYMDIFF | AGD1 | AGREEMENT }

Use METRIC to specific the metric used to calculate tree-to-tree distances. By default, the symmetric-difference metric (SYMDIFF) is used; however, you may also choose between two agreement-subtree metrics d (AGREEMENT) and d1 (AGD1).

**FROMTREE = integer-value

If FROMTREE is specified, then the tree given by the integer-value will be compared to all other trees retained in memory. The default (FROMTREE = 0) specifies that all pairwise tree comparison be made.

**FD = { YES | NO }

By default, the frequency distribution of tree-to-tree distances is output. Use FD=NO to suppress this output, or FD to reverse the effect of a previous FD=NO specification.

**SHOWALL = { YES | NO }

By default, a matrix of the tree-to-tree distances for all comparisons performed is output. Use SHOWALL=NO to suppress the output, or SHOWALL to reverse the effect of a previous SHOWALL=NO specification.

**FILE = export-file-name

Use the FILE option to save the tree-to-tree distances (as specified under the METRIC option) to a file.

**REPLACE = { YES | NO }

*OPTION IS NONPERSISTENT
APPEND = \{ YES | NO \}

If FILE = export-file-name option is specified and the export-file-name already exists, you will be prompted for confirmation that the existing file should be replaced. Explicit specification of REPLACE = YES suppresses this prompt and the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND = YES, in which case a new TREES block will be concatenated to the end of an existing file.

---

TREEINFO

Use the TREEINFO command to obtain information on the status of trees currently in memory. No options are available. The syntax is:

\[ \text{TREEINFO } \]

---

TREEWTS

Use the TREEWTS command to show current tree weights or specify new tree weights. The syntax is:

\[ \text{TREEWTS } \{ \text{SHOW} | \text{list-of-tree-weights} \} \]

---

TSTATUS

Use the TSTATUS command to obtain information on which taxa, if any, are deleted and which taxa have been assigned to the outgroup. No options are available. The syntax is:

\[ \text{TSTATUS } \]

---

TYPESET

The TYPESET command, used to define a type set, is ordinarily issued from within the ASSUMPTIONS block. However, you may also issue it from the command line or from within a PAUP block. See "Commands used in the ASSUMPTIONS Block" on page 19 for the description of this command.

---

UNDELETE

Use the UNDELETE command to restore previously deleted taxa (or delete taxa not in list). The syntax is:

\[ \text{UNDELETE taxon-list } [ / [ \text{ONLY} ] [ \text{CLEARTREES} ] ] ; \]
Unless /ONLY is specified, taxa specified in the taxon list are simply removed from the set of currently deleted taxa. Specify /ONLY to delete, in addition, any taxon not explicitly specified in the list.

**UPGMA**

Use the **UPGMA** command to calculate a **UPGMA** tree. The syntax is:

```
UPGMA [ options ] ;
```

Available options:

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Option type</th>
<th>Default setting</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>BRLENS</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td><strong>BREAKTIES</strong></td>
<td>{ SYSTEMATIC</td>
<td>RANDOM }</td>
</tr>
<tr>
<td><strong>TIESEED</strong></td>
<td>integer-value</td>
<td>0</td>
</tr>
<tr>
<td><strong>SHOWTREE</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td><strong>TREEFILE</strong></td>
<td>tree-file-name</td>
<td>none</td>
</tr>
<tr>
<td><strong>REPLACE</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
<tr>
<td><strong>APPEND</strong></td>
<td>{ YES</td>
<td>NO }</td>
</tr>
</tbody>
</table>

*Option is nonpersistent

Description of options:

**BRLENS = { YES | NO }**

If BRLENS = YES is specified, tree descriptions will include branch lengths. BRLENS = NO reverses the effect of a previous BRLENS specification.

**BREAKTIES = { SYSTEMATIC | RANDOM }**

Unless BREAKTIES = RANDOM, ties encountered during tree construction are broken systematically according to the input order of the taxa.

**TIESEED = integer-value**

If BREAKTIES = RANDOM, PAUP* references the system clock to initialize the seed used to generate pseudorandom numbers for breaking ties found during tree construction. An explicit seed may be specified to override the system clock default. (See "InitSeeds = { 0 | 1 }" on page 106 for more details.)
SHOWTREE = \{ YES | NO \}

If SHOWTREE = YES, the UPGMA tree is printed to the display buffer.

TREEFILE = tree-file-name

If TREEFILE is specified, a description of the UPGMA tree is output to a file in the NEXUS tree format. The tree-file-name must follow the conventions described under "Input/Output files" on page 9.

REPLACE = \{ YES | NO \}
APPEND = \{ YES | NO \}

If the specified file already exists, you will be prompted for confirmation that the existing file should be replaced. Explicit specification of REPLACE suppresses this prompt and the existing file will be quietly overwritten by the new data. Alternatively, you may specify APPEND, in which case a new TREES block will be concatenated to the end of an existing file.

\underline{USER TREE}

Use the \texttt{USER TREE} command to input a single user-defined tree. Ordinarily, you should use a TREES block (see "Commands used in the TREES Block" on page 24) to input one or more user-defined trees. This command merely provides a mechanism for quickly specifying a user-defined tree from the command line, which may be useful in certain situations.

\underline{USER TYPE}

The \texttt{USER TYPE} command, used to define a user-defined character type, is ordinarily issued from within the ASSUMPTIONS block. However, you may also issue it from the command line or from within a PAUP block. See "Commands used in the ASSUMPTIONS Block" on page 19 for the description of this command.

\underline{WEIGHTS}

Use the \texttt{WEIGHTS} command to assign weights to one or more characters. The syntax is:

\texttt{WEIGHTS character-weight: character-list [, character-weight: character-list ]... ;}

Each character-weight must be a valid character weight. Each character-list consists of one or more character numbers, character names, or character-set names (see "Character lists" on page 8 for details). The characters specified by character-list are assigned the immediately preceding
character-weight. Any number of character-weight:character-list pairs, separated by commas, may be specified.

**WTS**

The WTS command is a synonym for the WEIGHTS command. For some reason, I have a hard time typing "weights."

**WtSET**

The WtSET command, used to define a weight set, is ordinarily issued from within the ASSUMPTIONS block. However, you may also issue it from the command line or from within a PAUP block. See "Commands used in the ASSUMPTIONS Block" on page 19 for the description of this command.


Farris, J. S. 1988. Hennig86, version 1.5. Distributed by the author, Port Jefferson Station, N. Y.


Maddison, W. P. In press. Missing data versus missing characters in phylogenetic analysis. Systematic Biology


