

PC and Unix-Directions

Pre-running the decision (DT_ModSel) algorithm do the following:

- 1) Install Perl:
Perl is available (free) at the following web site:
<http://www.perl.com/pub/a/language/info/software.html>
- 2) Download the following two files: (Both are flat files (text))
 - a. Model_Commands
 - b. DT_ModSel
- 3) PAUP should be installed.

To run the algorithm do the following:

- 1) Append the contents of Model_Commands to the end of the Nexus file that contains the data to analyze.
- 2) Run PAUP using the new Nexus file to generate two new files:
 - a. score_file
 - b. tree_file.tre
- 3) Make sure to transfer the score and tree files to the directory where DT_ModSel resides or make sure to know their full path.
- 4) Type Perl DT_ModSel [path]/score_file [path]/tree_file.tre sample size
If the score and tree files are in the same directory as DT_ModSel adding the path is optional. Otherwise, all of the above should be typed; an error message will result if not.

Important note: the sample size is the number of nucleotides in the sequence and **NOT** the number of individuals.

- 5) The output of the program is the selected model according to the paper.

MC-Directions

Pre-running the decision (DT_ModSel) algorithm do the following:

- 1) Install MacPerl:
Perl is available (free) at the following web site:
<http://www.macperl.com/>
- 2) Down load the following two files: (Both are flat files (text))
 - a. Model_Commands
 - b. DT_MacModSel
 - c. ParmFile.txt
- 3) PAUP should be installed.

To run the algorithm do the following:

- 6) Append the contents of Model_Commands to the end of the Nexus file that contains the data to analyze.

Note: one can get the same results by loading the data to PAUP and running the commands separately after that (using PAUP as well of course).

- 7) Run PAUP using the new Nexus file to generate two new files:
 - a. score_file
 - b. tree_file.tre

Note: running PAUP again will result in two new files with the same names as above. Accordingly, to save one's results we strongly recommend renaming these files.

- 8) Make sure to transfer the score and tree files to the directory where DT_MacModSel resides.
- 9) Adjust the ParmFile.txt using a word processor. This file looks as follows:

```
score_file: <score_file>
tree_file: <tree_file.tre>
sample_size: <# of nucleotides in the sequence>
```

We recommend changing the score and tree file names to reflect the type of data underway. The number of nucleotides **HAS** to be changed depending on the data.

- 10) Run Perl DT_MacModSel
- 11) The output of the program is the selected model according to the paper.