Mac Classic OS Directions

Prior to running DT_ModSel, you ll have to do the following:

1) Install MacPerl:
   It is available (free) at the following web site:
   http://www.macperl.com

2) Download the following three files: You can cut and paste them into a word processor or BBEdit. Make sure you save them as flat text files.

   a. Model_Commands
   b. DT_MacModSel
   c. ParmFile.txt

   It may be helpful to create a folder called DTModSel to contain the files you need.

3) Obviously, you ll need PAUP to 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

   It s often convenient to rename these to coincide with the name of the data file. For example if the sequences are in the file Plethodon.nex, score_file & tree_file.tre could be renamed Plethodon.score & Plethodon.tre, respectively.

3) Make sure to transfer the score and tree files to the folder where DT_ModSel resides.

4) The file ParmFile.txt contains three lines that must be modified as follows.

```
Score_File name: Plethodon.score
Tree_File name: Plethodon.tre
Sample_Size: 711
```

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

5) Open MacPerl by double clicking on the icon.

6) Go to the Script option on the menu bar at the top of the screen and pull down to Run, or simply type command-R. Navigate to DT_MacModSel and hit return

7) The output of the program is the model selected following Minin et al (2003).