Lab 3: Introduction to MacClade

Introduction

Today we will have a brief introduction to some of the features of the MacClade, and learn how to integrate it with PAUP*. MacClade was developed by Wayne and David Maddison as a tool for interpreting phylogenetic information. Note that MacClade is not designed for searching for cladograms, although it does have some very limited search capabilities. Instead, it can be used for creating and editing data matrices, examining the distribution of features on a phylogeny, and testing hypotheses about character evolution. MacClade is a great way to explore the data you collect for your term paper project.

MacClade is designed around two main windows, the **tree window** and the **data editor window**. Two other windows we will see today are the **chart window** and the **character status window**, although they are of less importance.

In the tree window, hypothesized phylogenetic trees are displayed and can be manipulated to visualize character evolution upon them. Tools are provided to move branches, make polytomies, re-root trees, display various character state reconstructions, display tree statistics, etc. A selection of tests used to examine phylogenetic patterns are also provided (e.g., Maddison's test), and their results are displayed in the chart window.

The data editor window allows the entry, editing, and manipulation of phylogenetic data. Both qualitative and quantitative data can be entered, and rows, columns, and blocks of data can be manipulated. The data editor also has limited capabilities for aligning molecular sequence data, and also includes options that allow weighting and ordering schemes to be designed and implemented. The character status window provides a brief summary of character weights, states, ordering, etc., and allows quick manipulations of these assumptions. MacClade can save files in nexus format, and data files created in MacClade can be read by PAUP*. Furthermore, tree files created by PAUP* can be read into MacClade and manipulated.

Most of the following exercise is a short tutorial from the MacClade manual pages 22 to 36. The example data sets can be found on your desktops. I've stuck a short section onto the end of this for you to practice using MacClade and PAUP* together.

Integrating MacClade and PAUP*

Now that you are familiar with using MacClade, we can now use it with PAUP*.

--Enter the following data matrix in MacClade:

A 0000000000

B 0000010010

C 0000011000

D 0000011100

E 0000011110

--Save the matrix to the desktop of your computer. Then open PAUP*, and execute your data set.

--Conduct an exhaustive search.

--When the computer finishes, go to the 'trees' menu and select 'save trees to file.' A dialogue box will appear from which you can save your tree file to the desktop.

--Go back to MacClade, and make sure you have your data matrix file open.

--Go to the 'display' menu and select 'tree window.' When you do this, a dialogue box will appear. When it does, select the 'open treefile' and then open your treefile. The cladogram from your analysis will appear on the screen, which you can now manipulate as you wish.

We'll spend more time examining other features of MacClade in later labs. Also, MacClade is covered in some detail in the lab portion of IB 200B.