

## **Advanced PAUP\***

Today we're going to be doing some more advanced things in *PAUP\**. We're going to do it on PCs, which only have a command line interface. You're going to have to get used to using the documentation to find your commands. We're just going to use the example nexus files, but if you want to use your own data go ahead. I can help you with the analysis of your data now.

### *Basic Command Line PAUP\**

Copy the **angiosperm** and the **primate-mtdna** files from the **example nexus files** folder in the **PAUP** folder to a folder that you create on your desktop.

Open *PAUP\** in the **IB200** folder in the Start Menu.

It will ask you to open a file, but **cancel** that step for now.

As you can see there are a few pull down menus, but they don't do a lot. The one thing that these menus do OK is deal with files. You can use these menus to open and save files, although you have to use the command line to save trees. The edit and window menus have the basic features that you would expect.

Open a file **File > Open > PAUP4b10**. Select the **angiosperm.nex** file and hit **Open/Execute**.

Now I want you to open up the **Cmd\_ref\_v2**. This is a PDF file in the **PAUP** folder. Open up the **Bookmarks**. You are going to have to use the Bookmarks to find commands. Open up the **Command Reference** folder in the **Bookmarks** window.

You will see a bunch of different folders of commands for different blocks. All nexus files are made up of a combination of these different blocks. Each block starts **begin (type of block)** and finishes **end;**. Between are a number of commands that tell the program what to do, and the commands that are allowed in each block are described in the appropriate part of the document.

The **PAUP block** can be added to a nexus file. The commands allowed in the **PAUP block** can also be typed into the command line of the running program. It is nice to put them in a **PAUP block** because then you don't have to repeatedly type the same commands in, on the other hand the command line allows you the flexibility to put commands in as the program runs.

Let's run a simple heuristic search. Open up the **Commands used in the PAUP block** folder in the **Bookmarks** window. You will see a list of commands. Click on **Hsearch**, so that you go to that part of the document.

This is a description of the **Hsearch** command. Under syntax is the description of how you type the command. In this case it says **HSEARCH**

next three lines divide the coding regions into first second and third codon positions. The **exset** command defines sets of taxa that can be excluded together from the analysis. The two **usertypes** are user defined cost matrices of changes for a parsimony analysis. The last command defines a set of taxa.

Now erase all the commands in the **PAUP** block. We're going to use that space to enter our own commands. Make sure that you put a semicolon after each command line.

First type: **exclude noncoding 3rdpos**; This will limit our characters to just the first two very stable codon positions of the sequence by eliminating these two character sets.

Type: **delete hominoids**; to limit our analysis to the non-ape primates.

Type: **outgroup 12**; This sets the twelfth taxon in our analysis as the outgroup, which in this case is the tarsier. Is that the right one?

Type: **set criterion=likelihood**; This is self explanatory. The important thing to note here is the **set** command, which controls many options.

Type: **lset basefreq=equal**; Normally you would get this model from *Modeltest*, but I just chose an arbitrary one here to speed up the calculation.

So your entire PAUP block should look like this:

```
begin paup;  
exclude noncoding 3rdpos;  
delete hominoids;  
outgroup 12;  
set criterion=likelihood;  
lset basefreq=equal;  
end;
```

Pull down the **File** menu and select to execute your nexus file.

It should give a list showing all the changes that you made. Type **cstatus** to confirm that many of the characters are excluded, and that your criterion is likelihood. Type **tstatus full=yes** to see which taxa have been deleted and which are in the outgroup.

Now type **hsearch** to run the search.

When the search is done type **showtrees** to display the trees.

*Constraint trees*