

DRAWING TREES IN UNIX**1 Using our tree drawing script**

We have written a UNIX script to allow you to plot phylogenies (using the output from PAUP*, GARLI, or MrBayes) and get the results in pdf format. To use the script, you'll need to do the following:

1. After connecting to a stat department computer using ssh, issue the following commands at the UNIX prompt:

```
cp /home/lkubatko/WWW/stat882/drawtree.r drawtree.r
cp /home/lkubatko/WWW/stat882/message.txt message.txt
```

The step above only needs to be done once.

2. Place the trees you want to plot into a file called `treefile.tre`. You can do this using the `cp` command (e.g., if the output from a GARLI run was saved in a file called `primates.tre`, you would type `cp primates.tre treefile.tre` at the UNIX prompt.
3. Issue the following command the UNIX prompt:

```
R CMD BATCH drawtree.r
```

This is the tree drawing script – it will open the software R, read the tree(s) in the file `treefile.tre`, and plot them using the “Ape” package. The plotted trees will be stored in a file called `tree.pdf` in your UNIX directory.

4. If you are familiar with `ftp`, you can move the file from your UNIX account to your computer in this way. If not, you can mail the tree pdf file to yourself by issuing the following command at the UNIX prompt:

```
pine youremail@osu.edu -attach tree.pdf < message.txt
```

where `youremail@osu.edu` can be any e-mail address to which you'd like your results sent. After issuing this command, you need to hit the “control” and X keys together, and then answer “y”, to send the message.

5. Check your e-mail – a pdf file containing the pictures of your trees should be included as an attachment.

2 Ignorable details

R is a wonderful software package for carrying out a wide variety of statistical analyses. R is freeware, and can be downloaded for any platform. R users can contribute packages to the R software repository that carry out specialized types of analyses. One such package for phylogenetics is called Ape (see <http://ape.mpl.ird.fr/>). Ape contains many nice functions and is what is being used to plot the trees in the script we've prepared.

We have written the script to use the default tree-drawing. However, Ape includes many options to make your trees prettier. If you're familiar with R, these commands are fairly intuitive, and I encourage you to check the Ape package out. If you're not familiar with R and would like to be, feel free to set up some time to meet with me!

3 Other Tree Drawing Programs

There are many other tree drawing programs, and you may wish to download these to your own computer to use instead (most are free). A comprehensive list is given here: <http://evolution.genetics.washington.edu/phylip/software.html#methods> – scroll down to “Tree plotting/drawing”.