Unix, Perl and BioPerl

Session 1: Introduction to Unix for Bioinformatics

Exercise 2: Intro to X Windows with some graphical applications

Goal: Learn X Windows while trying out some common sequence-based graphical applications such as ClustalX (for multiple sequence alignment) and NJplot (for printing phylogenetic trees), and try converting between graphical formats with Ghostscript and ImageMagick.

Windows users should use the Cygwin/X system, and Macintosh users can use X11.

See `http://jura.wi.mit.edu/bio/education/docs/x.html`
for more details about getting started with the Cygwin/X and the X11 systems.
See `http://jura.wi.mit.edu/bio/education/bioinfo2006/unix-perl/`
for course page

#	To do / To answer	Command	Comments
0	**Windows only**: Open Cygwin and enter the command `startx &` This should open up a new window with X Windows capability. Use that new window for subsequent commands.		
1	Connect to hebrides from Cygwin/X (Windows) or X11 (Macintosh; the dock or Applications > Utilities > X11) using the following command: `ssh -Yl username hebrides.wi.mit.edu` "username" is replaced by yours. Note "Y", which lets you connect with X Windows. You will be prompted for your password. Without the "Y", you can connect, but will not be able to access any graphical interfaces.		
2	Open "nedit", a graphical text editor and look at one of your files: `nedit &` *File > Open* This is a much more powerful editor than pico, and it can show programming syntax with color-coding.		

3	Entering commands in the terminal, create a directory called "msa" in the "unix_class" directory and go there:
	 `mkdir unix_class  # If you didn't already create this`
	 `cd unix_class`
	 `mkdir msa`		

	```cd msa```
4	Get the file of sequences that you want to align: ```cp /home/george/seqs/bmps.fa .```
5	Look at the header lines to see what sequences you have: ```nedit bmps.fa &```
6	Open ClustalX: ```clustalx &``` This is a popular multiple alignment tool (also available for Windows and Mac).
7	Note the help files: *Help>…* Like all multiple alignment tools, if you use it incorrectly, it will produce nonsense output.
8	Open the BMP file: *File>"Load Sequences"…* Select your file.
9	Perform a default alignment: *Alignment>"Do Complete Alignment"*
10	Select the last sequence (BMP7) by highlighting the name, remove it, and realign: *Edit>"Cut Sequences";* *Alignment>"Do Complete Alignment"*
11	Look at the two other files that have been produced: ```nedit &``` (as above) One is obviously an alignment, and the other describes the guide tree.
12	Save ClustalX's color alignment *File>"Write Alignment as PostScript"* Postscript errors can be safely ignored.
13	Going back to your Unix terminal, convert the alignment figure from .ps to .pdf format using Ghostscript: ```ps2pdf bmps.ps``` This does what Acrobat Distiller does on a desktop computer, creating bmps.pdf
14	Look at the PDF file: ```acroread bmps.pdf``` Acrobat Reader command. The .pdf and .ps files can also edited in Illustrator
15	Back in ClustalX, create a phylogenetic tree based on this alignment: [select from the menu] *Trees>Draw N-J Tree…* The output file should have the ```.ph``` extension
16	Look at the tree file: *nedit bmps.ph*

	You may be able to figure out the tree structure, but it's often easiest to let a program draw it for you.
17	Use NJplot to draw the tree. *njplot &* *File>Open* [and select bmps.ph]
18	Print the tree displayed by Njplot *File>"Save plot"* Select a name like tree_1.ps

19	Convert from .ps to .pdf and look at the result
	`ps2pdf tree_1.ps`
	`acroread file.pdf`
	As before.

20	(Optional) Use ImageMagick to view images and convert between formats. Start by opening a postscript or PDF file with the 'display' command: display myImage & Clicking on the image should make the menu appear. You can experiment with some interesting graphical effects – as long as the menu works on your system (which can be a problem). To save your image, select on the menu *File>Save>Format* and you'll get a big choice of vector and bitmap formats. Try converting to another format and then viewing the new file with "display".
21	Any questions? Delete any files you downloaded to the laptop.