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), NJplot (for printing phylogenetic trees), and dotter (for dot-matrix alignments).

Note: Each command written on multiple lines should be entered as a one-line command, except for multiple-line commands, which are delimited with semicolons.

See `http://jura.wi.mit.edu/bio/education/docs/x.html`
for more details about getting started with the VNC system.
See `http://jura.wi.mit.edu/bio/education/bioinfo-mini/unix-perl/`
for course page

#	To do / To answer	Command	Comments
0	Install the VNC client on your computer (if it's not already there)		See the web page above.
1	Connect to hebrides with SSH (secure shell).	`ssh -l username hebrides.wi.mit.edu`	Username is replaced by your's. You will be prompted for your password.
2	Move a custom configuration file to your home directory	`cp /home/george /.twmrc ~/.`	TWM is the name of the "window manager"
3	Start a VNC session on hebrides	`vncserver`	Pay attention to the message in response: New 'X' desktop is hebrides:n
4	Note: Your vncserver conection remains active even after you log out of hebrides or close your Xwindows session. So if you log on to hebrides using Xwindows another day, do <u>not</u> run the `vncserver` command again.		
4	Click on the VNC client to run it, and enter hebrides.wi.mit.edu:n		"n" is number you received after running 'vncserver'. Your hebrides desktop should appear. The open terminal is a standard "xterm" terminal
5	Open another "xterm" terminal	`xterm &` [or left click on the background and select "xterm"]	Note the scrollbar on the left; use right and left mouse buttons to scroll back and forward

6	Try moving, resizing, and minimizing the windows		Use the title bar or right top or left top buttons.
8	Open "nedit", a graphical text editor and look at one of your files.	`nedit` [or select from the menu] or `nedit filename;` *File>Open*	
9	Create a directory called "msa" in the "unix_class" directory and go there.	`cd unix_class;` `mkdir msa;` `cd msa;`	If the `unix_class` directory doesn't exist, create it: `mkdir unix_class;`
10	Get a multiple sequence file to use for an alignment	`cp /home/george/ seqs/bmps.fa .`	
11	Look at the header lines to see what sequences you have	`nedit bmps.fa`	
12	Open clustalX	`clustalx &` [or select from the menu]	This is a popular multiple alignment tool.
13	Note the help files.	*Help>…*	Like all multiple alignment tools, if you use it incorrectly, it will produce nonsense output.
14	Open the BMP file	*File>"Load Sequences"…*	Select your file.
15	Perform a default alignment.	*Alignment>"Do Complete Alignment"*	
16	Select the last sequence (BMP7), remove it, and realign	*Edit>"Cut Sequences"; Alignment>"Do Complete Alignment"*	
17	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.
18	Save clustalX's color alignment	*File>"Write Alignment as PostScript"*	Ignore any postscript errors.
19	Convert from .ps to .pdf	`ps2pdf bmps.ps`	This does what Acrobat Distiller does on a desktop computer.
20	Look at the PDF file (or download it first if you prefer)	`acroread bmps.pdf`	Acrobat Reader command. New versions (5.*) let you rotate the image.
21	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
22	Look at the tree file	*nedit bmps.ph*	

23	Use NJplot to draw the tree.	*njplot &;* *File>Open* [and select bmps.ph]	
24	Print the tree displayed by Njplot	*File>"Save plot"*	Select a name like tree_1.ps
25	Convert from .ps to .pdf and look at the result	`ps2pdf tree_1.ps;` `acroread file.pdf`	As before.
26	Disconnect from VNC (unless you want to keep the same desktop)	`vncserver -kill :n`	Where n is the number of your original connection