

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.

Windows users should use the VNC system, and Macintosh users can use X11 (unless they have OS X earlier than 10.3, in which case they should use VNC too).

See <http://jura.wi.mit.edu/bio/education/docs/x.html> for more details about getting started with the VNC and the X11 systems.

See <http://jura.wi.mit.edu/bio/education/bioinfo2005/unix-perl/> for course page

#	To do / To answer	Command	Comments
VNC users: Do steps 0a – 7a; X11 users skip to step 0b			
0a	If needed, install the VNC client on your computer (if it's not already there)		See the web page above.
1a	Connect to hebrides with SSH (secure shell).	<code>ssh -l username hebrides.wi.mit.edu</code>	Username is replaced by your's. You will be prompted for your password.
2a	Move a custom configuration file to your home directory	<code>cp /home/george /.twmrc ~/.</code>	TWM is the name of the "window manager"
3a	Start a VNC session on hebrides	<code>vncserver</code>	Pay attention to the message in response: New 'X' desktop is hebrides:n
4a	Note: Your vncserver connection 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 <code>vncserver</code> command again.		
5a	Click on the VNC		"n" is number you received after

	client to run it, and enter hebrides.wi.mit.edu:n		running 'vncserver'. Your hebrides desktop should appear. The open terminal is a standard "xterm" terminal
6a	Open another "xterm" terminal	<code>xterm &</code> [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
7a	Try moving, resizing, and minimizing the windows		Use the title bar or right top or left top buttons.
X11 users: Do steps 0b-2b			
0b	If needed, install X11	Go to http://www.apple.com/macosx/features/x11/download/	X11 requires newer versions of Mac OS X (10.3 and later)
1b	Open X11	Click on X11 (Applications > Utilities > X11).	
2b	Connect to hebrides with SSH	In 'xterm', enter <code>ssh -X -l username barra.wi.mit.edu</code>	Using this command without the '-X' allows text transmission but no graphics.
All users continue from here:			
8	Open "nedit", a graphical text editor and look at one of your files.	<code>nedit</code> [or select from the menu] or <code>nedit filename;</code> <i>File>Open</i>	
9	Create a directory called "msa" in the "unix_class" directory and go there.	<code>cd unix_class;</code> <code>mkdir msa;</code> <code>cd msa;</code>	If the <code>unix_class</code> directory doesn't exist, create it: <code>mkdir unix_class;</code>
10	Get a multiple sequence file to use for an alignment	<code>cp /home/george/seqs/bmps.fa .</code>	
11	Look at the header lines to see what sequences you have	<code>nedit bmps.fa &</code>	
12	Open clustalX	<code>clustalx &</code> [or select from the menu]	This is a popular multiple alignment tool.
13	Note the help files.	<i>Help>...</i>	Like all multiple alignment tools, if you use it incorrectly, it will produce nonsense output.
14	Open the BMP file	<i>File>"Load</i>	Select your file.

		<i>Sequences"...</i>	
15	Perform a default alignment.	<i>Alignment>"Do Complete Alignment"</i>	
16	Select the last sequence (BMP7), remove it, and realign	<i>Edit>"Cut Sequences"; Alignment>"Do Complete Alignment"</i>	
17	Look at the two other files that have been produced	<code>nedit & (as above)</code>	One is obviously an alignment, and the other describes the guide tree.
18	Save clustalX's color alignment	<i>File>"Write Alignment as PostScript"</i>	Ignore any postscript errors.
19	Convert from .ps to .pdf	<code>ps2pdf bmps.ps</code>	This does what Acrobat Distiller does on a desktop computer.
20	Look at the PDF file (or download it first if you prefer)	<code>acroread bmps.pdf</code>	Acrobat Reader command. New versions (5.*) let you rotate the image.
21	Create a phylogenetic tree based on this alignment.	[select from the menu] <i>Trees>Draw N-J Tree...</i>	The output file should have the .ph extension
22	Look at the tree file	<code>nedit bmps.ph</code>	
23	Use Njplot to draw the tree.	<code>njplot &; File>Open [and select bmps.ph]</code>	
24	Print the tree displayed by Njplot	<i>File>"Save plot"</i>	Select a name like tree_1.ps
25	Convert from .ps to .pdf and look at the result	<code>ps2pdf tree_1.ps; acroread file.pdf</code>	As before.
26	Disconnect from VNC (unless you want to keep the same desktop)	<code>vncserver -kill :n</code>	Where n is the number of your original connection