Short Introduction to Linux

Bioinformaticists are knowledgeable of both biology and computers. UNIX is most popular computer operating system for science, and Linux is a flavor of UNIX. It offers the most power and flexibility, but it requires its users to know how to run commands in the terminal application.

Notes

1. Words in brackets <> means words you should replace.
2. A dot (.) means the current directory. For example, to see what is in the current directory: ls .
3. Two dots (..) means the parent directory. For example, to move to the parent directory: cd ..
4. Tilde (~) means your home directory. For example, to move to your home directory: cd ~
5. Star (*) means all files. For example, to copy all text files to your home directory: cp * ~

To log out, System -> Log out <username>.
To open a Terminal, right-click on the Desktop and click 'Open in Terminal'.
To create or edit a document: Applications -> Office -> LibreOffice Writer.

How to Run Bioinformatics Software

1. First step: in a terminal session, use the 'module' command to load the software.
   module load <software>
   e.g.,
   > module load matlab
   > module load weka
   > module load cytoscape
   > module load igv
2. Second step: run the software program
   matlab
   weka
   bash /panfs/roc/msisoft/cytoscape/2.8.3/cytoscape.sh
   bash /panfs/roc/msisoft/igv/2.3.9/igv.sh