Getting started with Unix and Perl

Feeling overwhelmed by it all? You're not in this alone! Rea d this SEQanswers post about biologists starting to analyze NGS data : http://seqanswers.com/forums/showthread.php?t=4589

That post mentions a great resource for biologists beginning to work in the Unix enviornment: the Unix and Perl for Biologists website. These kind folks have put together a tutorial that you can work (with some modifications) on TACC. This page shows you how to do just that.

First, login to TACC:

```
ssh <userid>@lonestar.tacc.utexas.edu
```

In your home directory, create a directory for the tutorial. This name "Volumes/USB" is an attempt to match the pathnames in the tutorial as much as possible.

```
mkdir -p Volumes/USB
```

Prepare the tutorial resources in this directory:

```
cd Volumes/USB
cp /corral-repl/utexas/BioITeam/downloads/unix_and_perl_v3.0.zip .
unzip unix_and_perl_v3.0.zip
```

This creates a directory **Unix_and_Perl_course** that contains the tutorial files.

It is important to note that this tutorial was designed to run on a Mac, so some things in it will not be quite the same on TACC. In fact, in order for things to work at all, you must replace names in the tutorial that start with **/Volumes/USB** with **~/Volumes/USB**. For example, instead of:

```
cd /Volumes/USB/Unix_and_Perl_course
```

you should type

```
cd ~/Volumes/USB/Unix_and_Perl_course
```

The reason this is necessary is that the tutorial was designed to run on an Apple PC where you can install new devices in the root file system (under the **/** directory). We cannot do that at TACC, so the next best thing is to install it in a similar looking pathname in your home directory (signified by **~**).

Before you start the tutorial, it might help to have this Cheat sheet of useful Unix commands open in a browser window.

Now you're ready to dive in. Open the Unix and Perl primer for biologists and start on p 15. Remember, don't expect everything to work exactly like the tutorial docs indicate.