**# Linux Tutorial**

**# prepared for BIFX-550 --Dr. S. Ravichandran, 09/06/2018  
# comments lines are shown in green font and start with # (pound) sign**

**# let us find out where are we in the system?**

**# Make sure you are in the tcsh by typing**

**tcsh**

**# Let us check where we are now (what directory?)**

**pwd**

**# What is my username?**

**whoami  
  
# find out who else have logged in at the moment  
who**

**# let us find out what shell our administrator has assigned us**

**echo $SHELL**

**# let us go into tcsh (C-SHELL) using tcsh**

**tcsh**

**# Let us find out what shells are available for the users**

**cat /etc/shells**

**# What is today’s date/time?**

**date**

**# calendar**

**cal 10 1775**

**# What processes are running?**

**ps**

**# Help on one of the command we learned, ls   
# Let us also learn how to read man pages. Type “q” (without quotes)   
# to quit man pages**

**man ls**

**man pwd**

**# clear the screen**

**clear**

**# based on the help pages, let us add some flags to ls command. Let us  
# start with a ls command**

**ls /usr/local**

**# use “man ls” (type this without quotes) to identify what flags we can use with ls**

**ls -fla /usr/local**

**ls -fl**

**cd /tmp**   
**# find out where you are**

**pwd**  
**# Let us go home; We can also do this with   
# the following alternative, cd ~ or cd $HOME or just cd**

**cd ~**

**cd $HOME**

**# let us create a directory called foo**

**mkdir foo  
  
# Let us check the permission of the directory using “ls -l” command  
ls -l**

**# let us change the permission of the directory using chmod command  
chmod 777 foo**

**# let us check again to see that the permission of the directory   
#has changed**

**ls -ltr**

**# And let us go back to our newly created directory, foo**

**cd foo**  
  
**# let us check where we are now**  
**pwd**

**# we can echo a string   
echo hello!**

**# we can save this message in a file called bar  
echo hello! > bar**

**# check with pwd and ls  
pwd**

**ls -l**

**# Make sure you are in the foo directory   
# let us create a subdirectory called foo2**

**mkdir foo2  
  
#to go into the foo2, use cd   
cd foo2**

**# check where you are using pwd**

**pwd  
  
# to go one level up use**

**cd ../**

**# make sure you are in foo directory   
pwd**

**# to see the contents of a file, use cat  
cat bar**

**# man is the command for manual pages  
# Check to see what the command less does?**

**########**

**# we can remove directories (folders) and files ;   
# I am not going to teach you that   
# there is no way to get the removed file back.**   
**# let us again make sure you are in foo directory**  
**wget http://files.rcsb.org/download/4hhb.pdb**  
**# let us view the file using nano file editor**  
**nano 4hhb.pdb   
  
cat 4hhb.pdb**  
  
**# type “q” (without quotes) to quit; press spacebar to move forward**  
**more 4hhb.pdb  
  
head 4hhb.pdb**

**# let us copy the file into 4hhbcopy.pdb**  
**cp 4hhb.pdb 4hhbcopy.pdb**

**# use ls to see that you have two files**

**ls**

**# let us remove the file, 4hhbcopy.pdb.**   
**rm –i 4hhbcopy.pdb**

# let us clear the screen with “clear”

**clear**

**# let us get one more pdb file   
wget http://files.rcsb.org/download/1omp.pdb**

# cat command

**cat 1omp.pdb**

**# let us count the lines/words in the 4hhb.pdb**

**wc -l 4hhb.pdb**

**wc -w 4hhb.pdb**

# let us explore the pipe command   
**cat 1omp.pdb | grep -i seqres**  
  
# let us merge two files

**cat 4hhb.pdb 1omp.pdb > 4hhb-1omp.pdb**

**grep -i Fe 4hhb.pdb**

# what commands we have typed so far

**history**

**# which program; finding an executable file with which  
# has to be in your path**

**which ls**

**# Find out the difference between which and whereis**

**whereis pwd**

**# Go the following link,   
#** [**https://www.ncbi.nlm.nih.gov/protein/NP\_000509.1?report=fasta**](https://www.ncbi.nlm.nih.gov/protein/NP_000509.1?report=fasta)**, and   
# cut-and-paste the following sequence into a file called   
# np\_000509.fasta. For this step you can use the nano editor.**

1. **first open a nano editor with the following command**
2. **nano np\_000509.fasta**
3. **paste the sequence file**
4. **Use control-x to save and quit**

>NP\_000509.1 MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH

# **Let us explore the sequence file using Linux commands**

**od -b np\_000509.fasta # first col is the byte offset**

**od -c np\_000509.fasta**

**# let us create a file**   
**nano list.txt**   
**# and type the following each in one line**rat chicken monkey chimp cow ecoli human dog  
**# save the file and exit**

**# when you come out of nano editor.   
# Let us check whether the file, list.txt exists**

**Your TURN**

**# let us view the file,**   
 **Your TURN**

**# let us sort the file and save it in sortedlist.txt**

**sort < list.txt > sortedlist.txt**

**ls \*list**

**#Explore the following commands on your own**

**chmod**

**ps**

**sleep**

**df**

**du**

**quota**

**gzip**

**zcat**

**zcat**

**file**

**diff**

**find**

**# logging into other computers**

**ssh username@pronto.abc.com**

**# creating links**

**ln -s perl5.005\_03 perl**

**#filename conventions fortran: f90, C: c; C++: cc**

**# test.f90**

**# test.c**

**# test.cc**

**# test.CC**

**SHELL Tutorial**

**In this tutorial, I am going to explain some basic TCSH commands.**

**What is a SHELL?**

**How it can be useful?**

**Why I should learn at least one SHELL ?**

**#In the following tutorial, we are going to download 4 PDB structure #files from** [**www.rcsb.org**](http://www.rcsb.org) **. This process can be done for any number of #files, for now, we are going to explain this using just 4 files.**

**# make sure we are in tcsh by typing before this exercise**

**tcsh**

**foreach f ( 1stp 7lyz 2src 3v3k 4IGK 4JLU )  
wget** [**http://files.rcsb.org/download/$f.pdb**](http://files.rcsb.org/download/$f.pdb) **echo $f  
end**

**#Can we use shell programming to count the number of lines of the   
# files (Think if you can do this for millions of files?!)**

**foreach f (\*.pdb)**

**sed -e 's/REMARK/Remark/g' < $f > M$f**

**echo "Done"**