

# While you are waiting

- **No Food or Drink in this room**
- **Logon to Windows machine**
  - Username/password on right-hand monitor
    - Not the username/password I gave you earlier
- We will walk through connecting to the workshop Linux machine from Windows

**Ask questions at any point**

# **Logging onto Sequencing Workshop Linux Machine & Linux Introduction**

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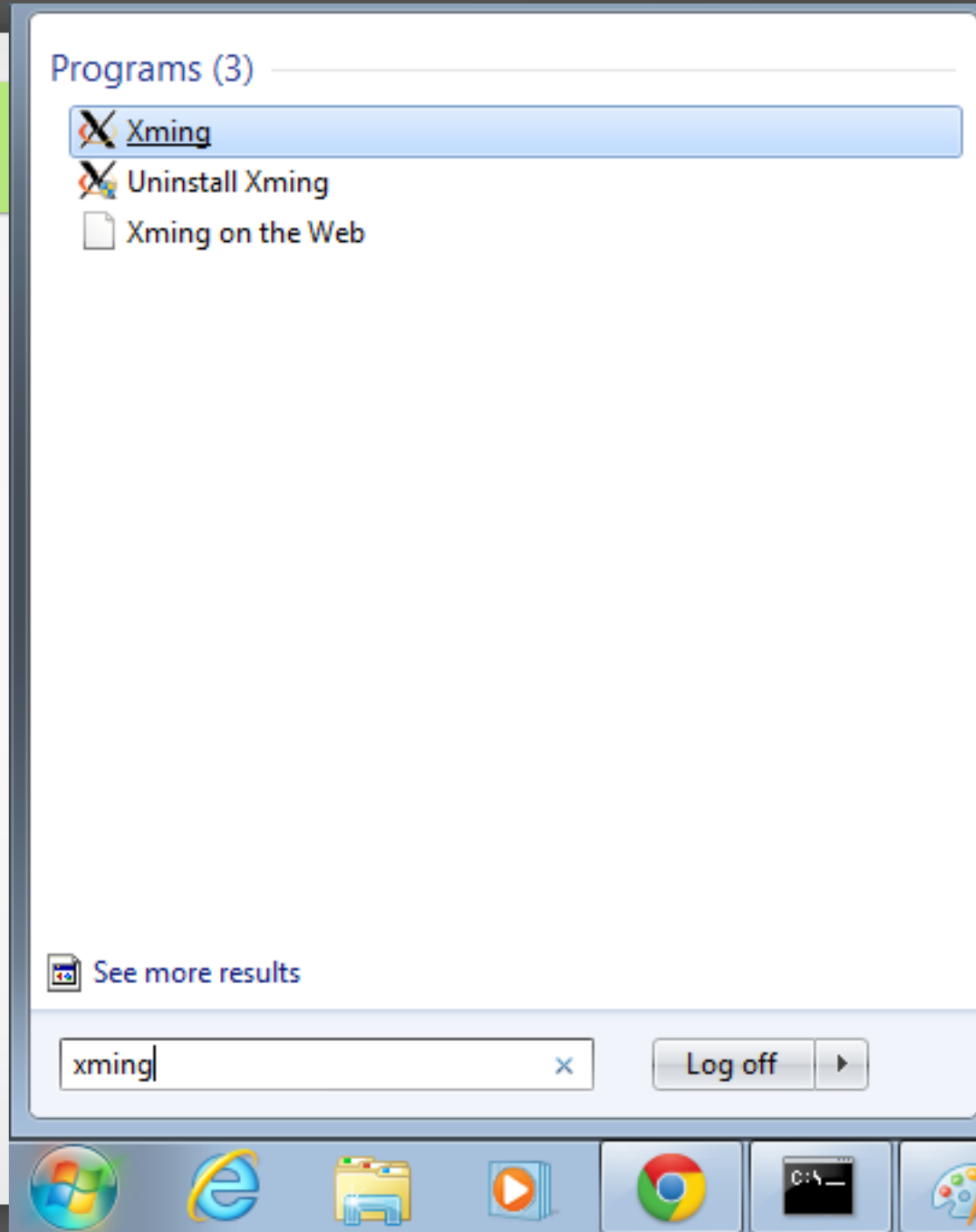
# Connecting to Workshop Machine

- PuTTY - connect to Linux machine
  - terminal emulator
  - run commands
- xming - X11 display server
  - Allows you to open pdfs, etc from putty
- Instructions at start of each practical
  - So don't worry about memorizing it

# Start xming

1. Start->search
2. Type:  
xmingSelect :  
Xming

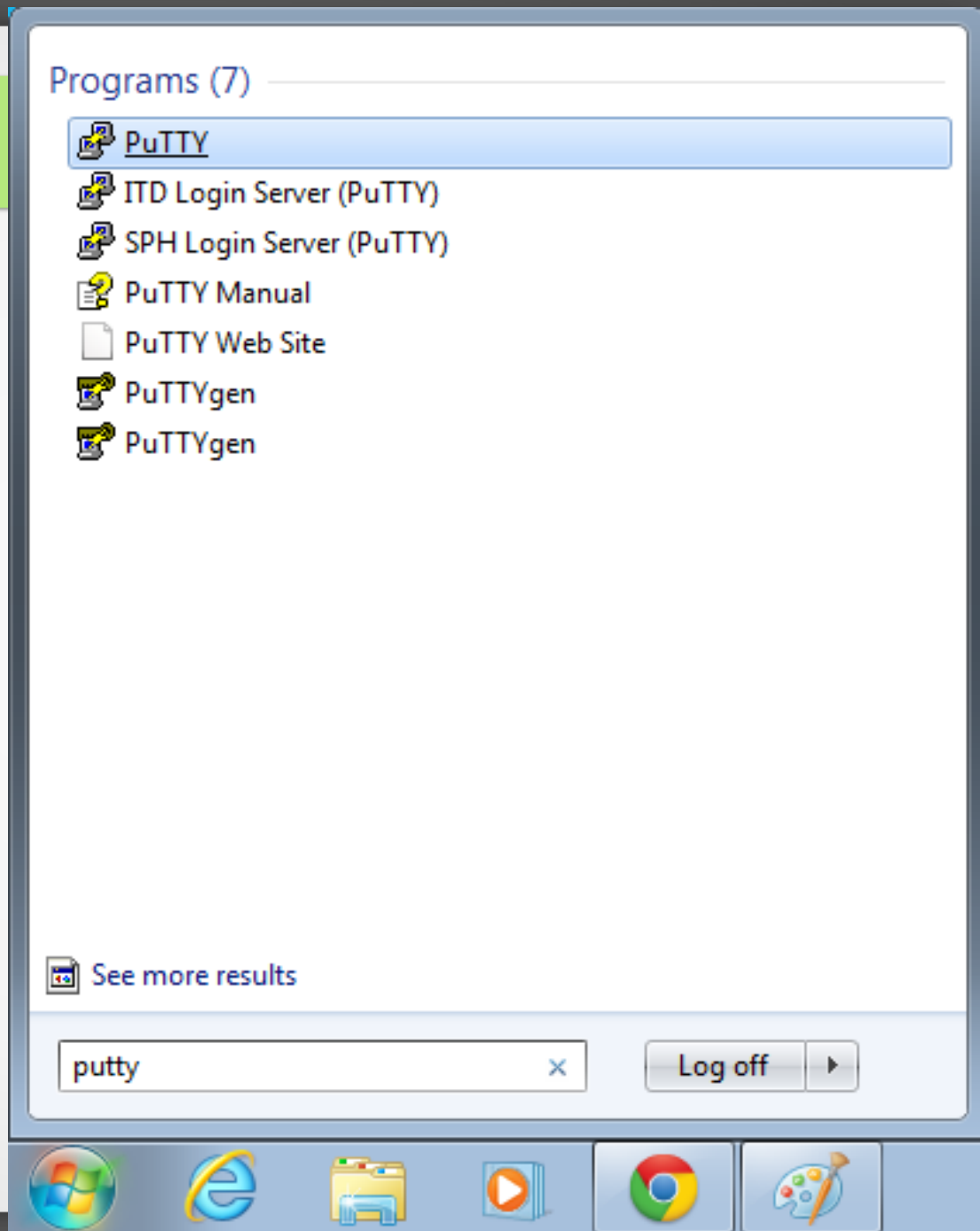
Nothing will  
happen, but it is  
started



# Open PuTTY

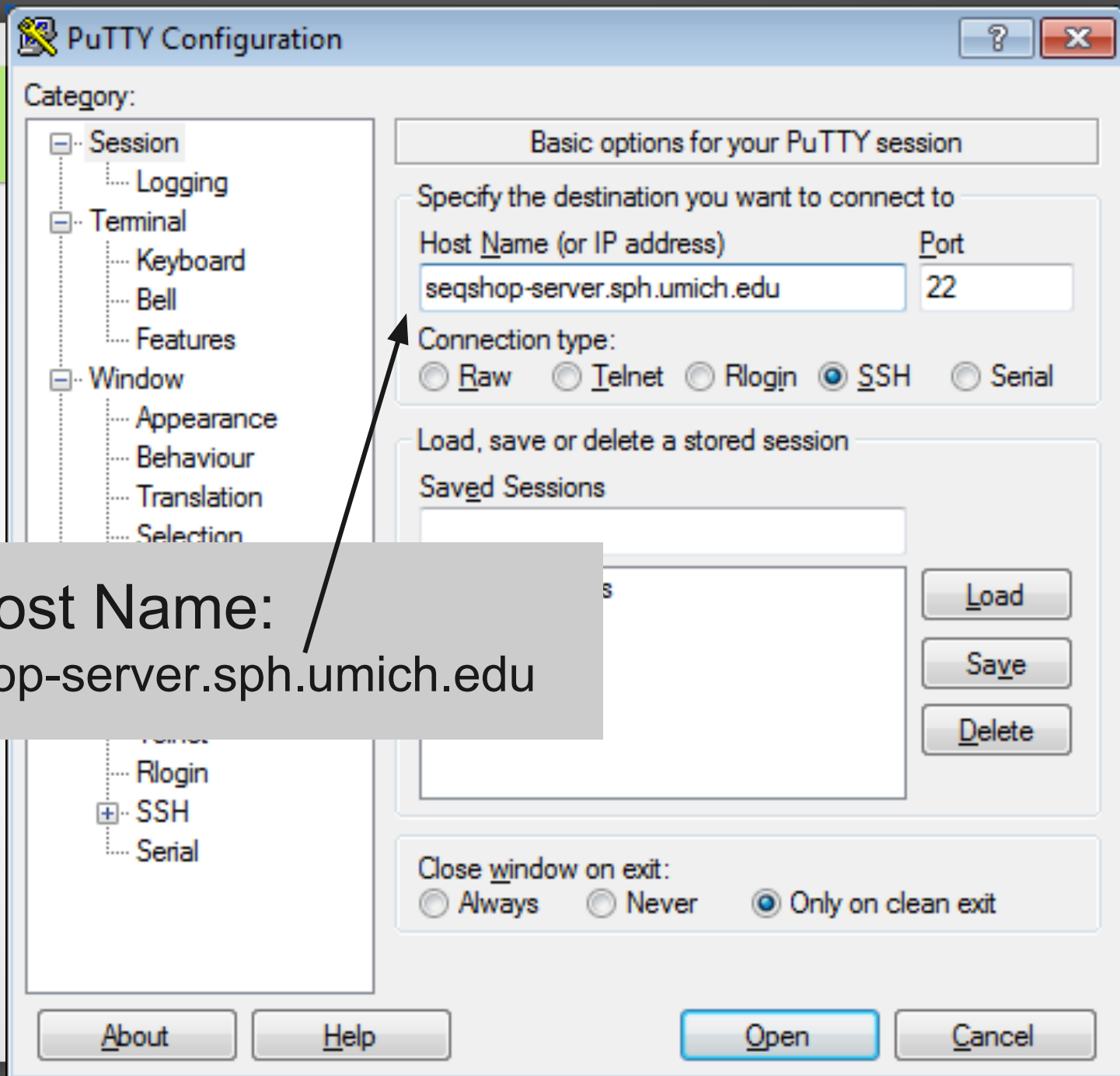
1. Start->search
2. Type: putty
3. Select : PuTTY

This will open a  
PuTTY  
Configuration  
window

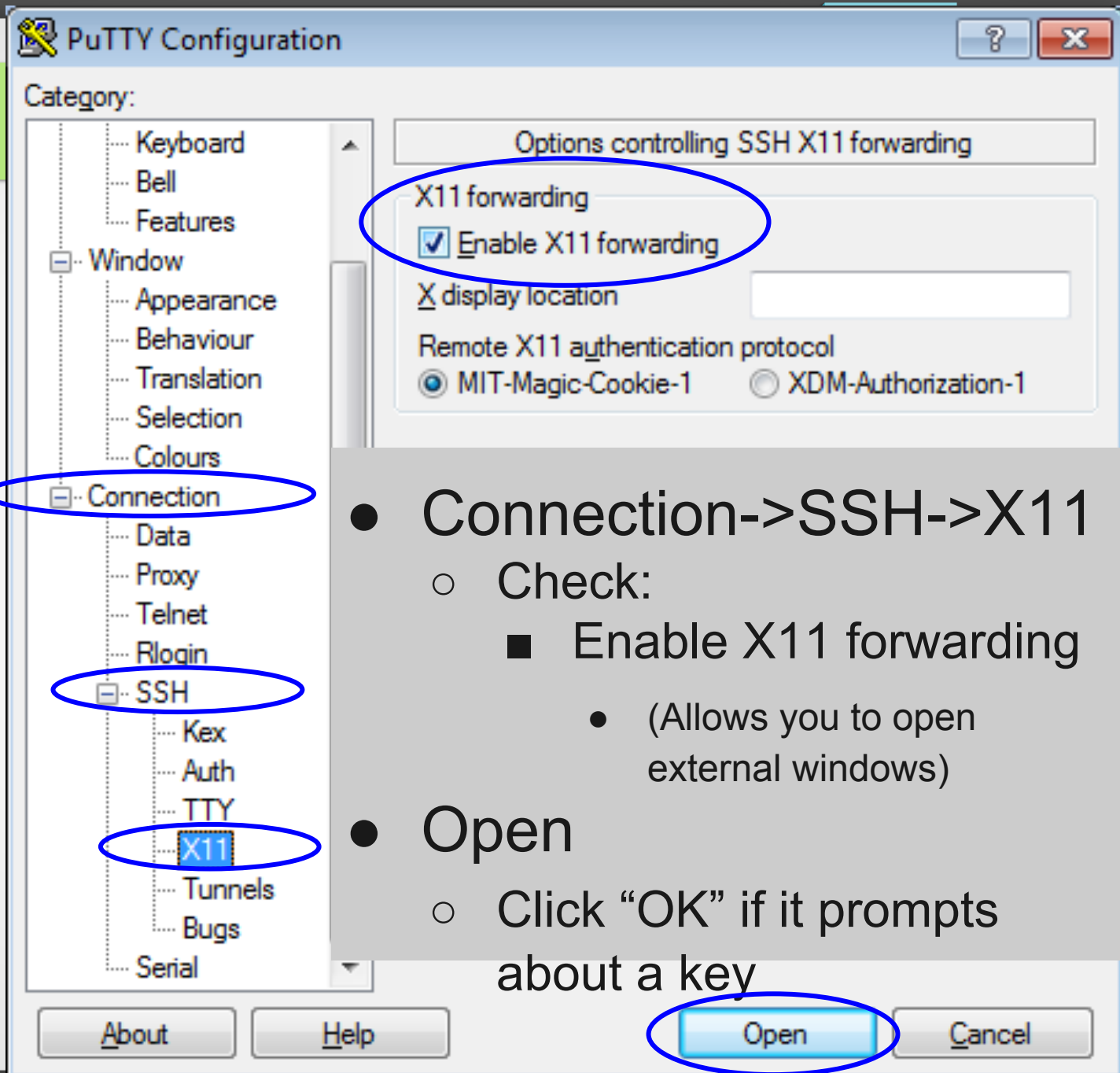


# PuTTY

- Enter Host Name:
  - seqshop-server.sph.umich.edu



# PuTTY



- Connection->SSH->X11
  - Check:
    - Enable X11 forwarding
      - (Allows you to open external windows)
- Open
  - Click "OK" if it prompts about a key

# Logon to seqshop-server

- Enter your provided Linux username and password
- You should now have a terminal on the seqshop-server Linux machine
  - If you ever want/need a 2nd terminal, redo the PuTTY steps
- Does everyone have a terminal?



# Change Your Password

- passwd
  - enter previous password
  - enter new password
  - re-enter new password

# Terminal Basics

- Command-line prompt
  - You will start in your “home” directory
    - `/net/seqshop-server/home/mktrost`
      - (your username instead)
    - `~`
  - Each have your own
    - You have permission to read/write
    - Your inputs & outputs go here
- How to figure out where you are:
  - `pwd`
    - `/net/seqshop-server/home/mktrost`

# Directory Contents

- `ls`
  - Lists files/sub-directories
  - What do you have in your directory?
    - `examples.desktop`
    - Personal Genome directory: `SampleXX/NA12878`

Up-arrow will go to the previous command

# Directory/File Permissions

- `ls -l`
  - 'd' - directory; '-' - file
  - r/w/x: read, write, or execute
  - 3 sets of values
    - user/group/everyone
      - USER & GROUP are both set to you
  - Personal Data is read only by you

# Looking at a Different Directory

- Enter the path of the directory you want to look at
  - `ls ~mktrost/seqshop/`
  - `ls Sample*`
    - `*` is wildcard
- Does not change you to a different directory
  - Still in same place you were before
  - Check with `pwd`

# Change/Move to New Directory

- `cd Sample*`
  - (or `cd NA12878`)
  - `ls`
    - We will look at this more later
- `cd`
  - takes you back to your home directory

# Create New Directory

- `mkdir testDir`
- `mkdir -p testDir/dir1/dir2`
  - Create parent directories if they don't exist
  - Do not generate error if directory exists
  - `ls testDir`
  - `ls testDir/dir1`
- **Rename/Move**
  - `mv testDir testDir1`
  - `ls`

# Up a Directory

- . - current directory
- .. - up 1 directory
  - `ls ../..`
    - Lists contents of 2 directories up
  - `cd ..`
    - Move up 1 directory
  - `cd`
    - Move to home directory



# Variables

- Save from typing long path/command
  - In BASH (the shell you are running):
    - `export VARNAME=value`
      - Allows you to use `${VARNAME}` as shorthand
      - Can easily change the value without changing commands
        - Useful for scripts/seqshop copy/paste commands
    - Try it
      - `ls $TEST`
        - `${TEST}` is not set, so is blank, so just lists current directory
      - `export TEST=~ /testDir1`
      - `ls ${TEST}`
        - Should see contents of testDir1

# Look at a file

- `less`
  - Use arrow (up/down/left/right) keys to scroll through file
  - Use *space bar* to jump down a page
  - `-S` - prevents line wrap
  - Use 'q' to exit
  - `zless` - read compressed
- `cat`
  - `zcat`
- `more`

# Look at parts of a file

- `head` - look at start of the file
  - `-n K` - print first K lines (default 10)
  - `-n -K` - print all but the last K lines
- `tail` - look at end of the file
  - `-n K` - print last K lines (default 10)
  - `-n +K` - print starting with the Kth line

# Extracting Specific Columns

- `cut` - remove sections from each line of files
  - `-d DELIM` - use DELIM as delimiter rather than TAB
  - `-f N1,N2` - print fields N1 & N2 (and lines with no delimiter)

# Additional commands

- Search

- `grep` - print lines matching a pattern
  - `-v` : lines without pattern

- Word Count

- `wc`
  - `-l` : line count

# String commands together

- | - pipe - use output of previous command as input to next command
  - `tail -n+300 file | head -n 5`
    - Output starting at line 300, but only read 5 lines

# String commands together

- `zcat ${OUT}/split/chr22/chr22.filtered.PASS.vcf.gz |grep -v "^#" | cut -f 7| grep -v "PASS"`
  - `zcat ...`: uncompress the zipped VCF
  - `'|'`: takes the output of one command and sends it as input to the next
  - `grep -v "^#"`: exclude any lines that start with "#"
  - `cut -f 7`: extract the 7th column
  - `grep -v "PASS"`: exclude any rows that have a "PASS" in the 7th column

# Screen

- Leave commands running after you logout
  - Start Screen: `screen`
  - Detach from screen session: `Ctrl-a d`
  - Logout as normal
- Resume session later
  - login
  - Resume: `screen -r`
- Scroll
  - Scroll: `Ctrl-a Esc`
  - Exit Scroll: `Esc`
- Exit
  - `exit`



# Run Workshop Later

- Instructions/tutorial data will be on wiki by end of next week
  - `wget http://www.sph.umich.edu/csg/mktrost/seqshopExample.tar.gz`
  - `tar xvf seqshopExample.tar.gz`
- Build C++
  - `make`

# Useful Links

- Helpful reference to many tools:
  - <http://infoplatter.wordpress.com/2014/04/06/bioinformaticians-pocket-reference/>
    - links to "cheat-sheets", including, Unix, screen, and vi
- Our wiki with some brief description of how to do some basic commands
  - [http://genome.sph.umich.edu/wiki/Basic\\_Linux\\_Intro](http://genome.sph.umich.edu/wiki/Basic_Linux_Intro)
- Commands to use screen
  - [http://genome.sph.umich.edu/wiki/Screen\\_Commands](http://genome.sph.umich.edu/wiki/Screen_Commands)