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
● Enter Host Name:
  ○ seqshop-server.sph.umich.edu
- 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:
    ■ 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)