Day 1, AM Practical
Basic Unix Command Line Skill
Prerequisites:
- Hydra account- Paul will be setting up Hydra accounts for and giving initial passwords. Your username will be the same as your SI email username but the passwords are not synchronized.
- A connection to si-staff wireless, a wired connection on the SI LAN, or an active VPN connection.

Goals:
- Log into Hydra with your new user account
- Get experience with the command line for manipulation and viewing of files
- Get experience finding help on Hydra and the web for commands

Note: Lines that start with a `$` should be entered on the command line without the `$`

Want answers? We don't give the exact command for all exercises. We encourage you to spend time figuring these out, but if you get stuck on a step, a complete log of all the exercises is here: https://gist.github.com/mkweskin/52626f5320e899e191d4 (or bit.ly/hydra-day1am-answers).

1a. **Hydra login (Mac users)**
- Open the Terminal application (in /Applications/Utilities/)
- `$ ssh <username>@hydra-login01.si.edu` (<username> is your hydra username)
- If prompted about the "authenticity of the host" type "yes"
- Enter your hydra password when prompted (Paul will tell you your initial password)
- Questions: How can you tell you are now on hydra? What folder are you in when you first login?

1b. **Hydra login (Windows users)**
- Start PuTTY (http://the.earth.li/~sgtatham/putty/latest/x86/putty.exe)
- In the configuration window for "Host Name" enter hydra-3.si.edu and click "Open"
- If prompted about the "server's host key" click "yes"
- At the "login as: " prompt enter your hydra username and then your hydra password when prompted
- You're now at the same screen that Mac users see from their terminal application
- Question: How can you tell you are now on hydra? What folder are you in when you first login?

2. Change your password (first login and then every 90 days)
- `$ passwd` Enter your current password and then your new password two times. Password rules are the same as your SI email account (≥8 characters, ≥1 number, ≥1 special character, not previously used).
- On Hydra *you need to change you password in two locations*.
    - `$ ssh hydra-3`

- ○ `$ passwd` use your initial password and then the same new password as the previous step.
- ○ `$ exit` to return to hydra-login-01. We'll be talking about the two servers later.

3. Change to `/pool/cluster0/workshop` and make a folder

- Your data are stored in one of the `/pool` folders rather than your home folder. /pool is connected to the network storage on Hydra for high-speed access to all the computers on the cluster. For this training we will be using `/pool/cluster0`
- `$ cd /pool/cluster0/workshop`
- `$ mkdir <username>` This will be where your workshop documents will be stored.
- `$ ls` to your folder and everyone else's
- `$ cd <username>` change into your directory

4. Copy the sample data

- This directory has today's sample data:
`/pool/cluster0/workshop/Hydra_workshop_2015/Day1`
- use `cp` to copy the directory `Day1` and its contents to your new folder
`/pool/cluster0/workshop/<username>`
  - ○ *We're not giving the exact command line here.* Use your cheat sheet to find the `cp` option to copy an entire directory. The format of the `cp` command is `cp [options] source destination` For the destination use `.` to copy to the current folder. Did you use an absolute path or a relative path for source and destination?
- `$ ls -l` to confirm that the folder copied successfully. You should see the `Day1` folder.
- Error about `…omitting directory…`? Check the cheat sheet for the `cp` option to copy a whole directory.

5. Viewing file contents

- Use `cd` to change the directory to `Day1` and then change again into `data` which has the sequence files we'll be using. Use `$ ls -l` to confirm that the two `sequences.fa` and `sequences.fq` are there.
- Try all four of these commands to examine the file `sequences.fa`
  - a) `$ cat sequences.fa`
  - b) `$ head sequences.fa`
  - c) `$ tail sequences.fa`
  - d) `$ less sequences.fa` (Remember, `q` is quit in less)
- e) Use `less` to *find the sequences* that contains the description EAS20_8_6_1_5_388 (Type `h` in less for help screen, look for "Search forward…" in the "SEARCHING" section.).

f) Use `head` to display *the first sequence only* (first two lines). Type `$ man head` (or Google) to find the option to limit the number of lines `head` displays (man pages open in `less`, use the arrow keys to navigate and `q` to quit).

g) Use `tail` and wildcard globbing to display the last 10 lines *of the two sequences files* (`sequences.fa` and `sequences.fq`) with one command.

6. Edit a file with `nano`

• Open `sequences.fa` with `nano`

• Change some bases in one of the sequences. We'll need this file in the afternoon so keep it valid fasta.

• Save and close the file

Remember in `nano` shortcuts are at the bottom of the screen and `^` is the control key.

7. Create a new text file and delete it

• `$ nano newfile` If the filename doesn't exist, an empty document will be opened.

• Enter some text into the file, save it and exit.

• Use one of the text viewing commands we used in Step 5 to view your new file's contents.

• After viewing your file delete it with the `rm` command

8. Find the hidden file! (extra credit)

• Return to the "parent" folder, `Day1` (remember that `..` refers to the parent directory). Use the `ls` option that shows hidden files and then cat the file a pre-lunch treat.

9. Exit the hydra ssh session

• `$ exit` to close the connection to hydra. It's best practice to always do this.

Digging deeper (optional for more advanced users):

1. Want to learn the `vi` editor? Enter the command `$ vimtutor` on Hydra or your Mac for a tutorial. To exit type `:q`

2. Want to learn the `emacs` editor? Do the `emacs` tutorial by starting `$ emacs` and then `<control+h>` and then `t`. To exit type `<control+x>` and then `<control+c>`.

3. Using `$ ls -l` Compare the creation date of the original file and the one you copied. Check the `cp` man page or online resources to learn how to copy the file and preserve the original create date.

4. When you use `less` to view the fasta file, the lines automatically wrap ("fold" in `less` lingo) which can be annoying for fasta files with long sequences. What flag for less will stop this so the lines don't wrap ("chop" in `less` lingo)? Hint: this is an option when starting `less` rather than a command when `less` is already running.