

Command line Practical

Basic Unix Command Line Skill

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

1. Using terminal in Virtual Box

- Open the Terminal application in the Virtual Machine window
- Set up `Shared Clipboard` in virtual box. Navigate to the `Devices` tab on the menu bar and set it to `bidirectional`.

2. Change to `/home/<virtual_box_name>/Desktop/` and make a folder

- `$ cd /home/<virtual_box_name>/Desktop/`
- `$ mkdir workshop` This will be where your workshop documents will be stored.
- `$ ls` to your folder and everyone else's
- `$ cd workshop` change into your directory

3. Download and Copy the sample data

- Today's sample data can be downloaded here:

```
https://github.com/gonzalezvl/Microbial_Metagenomics_Workshop_UCLA_2015/
```

- use `cp` to copy the directory `Command_line_practical` and its contents to your new folder `/home/<virtual_box_name>/workshop/`
 - *We're not giving the exact command line here. Hint: 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.

4. Viewing file contents

- Use `cd` to change the directory to `Command_line_practical` 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.

5. 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.*

6. 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 4 to view your new file's contents.
- After viewing your file delete it with the `rm` command

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.

UCLA Microbial Metagenomics Workshop 2015

Modified from Hydra Workshop 2015