





UNIX miscellaneous tips

Keyboard shortcuts

- Use tab to complete commands or filenames having partially typed them in e.g type sam then tab to complete this to the full command samtools or type ls /ho and then tab to complete to ls /home This is useful particularly with long filenames
- You can scroll back through previous commands you have typed using the up and down arrow keys. For example if you have just typed a very long command and pressed enter only to find that you made a mistake you can use the up arrow to select the previous command and edit it to correct the mistake and type enter again
- You can search for a previously typed command by pressing ctrl-r and then part of the command and it will search back through your history to find a command matching what you have typed e.g type wget and if you have typed this before you may see something like (reverse-i-search)`wget': wget https://gitlab.com/cgps/ghru/pipelines/snp phylogeny/raw/master/bin/filter

ed_bcf_to_fasta.py

You can then use the arrow keys to edit the command if needed and return to execute it.

Passwordless login using ssh keys

- 1. Generate a key on your local machine using
 - a. ssh-keygen on a Linux or Mac machine (see here) This will generate a file called id_rsa.pub in the hidden .ssh directory in your home directory. Type cat .ssh/id rsa.pub to show the contents which can then be shared with someone else. Never share the .ssh/id rsa file which is the private key
 - b. To do the same in Windows follow this <u>tutorial</u> to create it in Putty
- 2. Login in to the server with the username you would like passwordless access for example ssh biouser@123.456.789.001 You will have to enter your password this time Add the key to a file called .ssh/authorized_keys. If it does not exist, first add it: You have to create the .ssh directory and the authorized keys file the first time. Create the .ssh directory: mkdir ~/.ssh Set the right permissions: chmod 700 ~/.ssh Create the authorized_keys file: touch ~/.ssh/authorized keys







Set the right permissions: chmod 600 ~/.ssh/authorized_keys The permissions are important! It won't work without the right permissions!

3. Now logout of the server and back in again. For example ssh biouser@123.456.789.001 This time it will login you in without requiring a password since your private key in .ssh/id_rsa matches the public key contained in the authorized_keys file on the server

Aliases

Aliases are like shortcuts for long commands that save you typing in a frequently used command. Working with the CLI is all about doing things efficiently and bioinformaticians are lazy!

In your home directory (e.g /home/user1) there is a hidden file called .bashrc that is loaded every time you login to a terminal. This can perform many things such as

- define the way your command prompt looks
- change environmental variables such as PATH which is a list of directories that UNIX will look in for commands
- define aliases

To add a new alias open this file in an editor (for example vi)

vi ~/.bashrc

Note ~ is a shortcut for your home directory

Go to the end of the file (press 'G' in vi) or go to a section of the file where other aliases are defined and add a new line and type the new alias. The format is

<SHORT CUT>='<LONG COMMAND'> for example to add a short cut for the command that lists all files in the directory newest file last (ls -ltr) the alias might be

z='ls -ltr'

Another example might be that if you are connecting to a server from a Linux or Mac machine and therefore not using PuTTY shared sessions you will often type something like ssh ubuntu@123.456.789.001. Rather than typing this each time make an alias such as

serv1='ssh ubuntu@123.456.789.001'

To activate the new aliases you can either logout and log back in again or reload the .bashrc file using the command source .bashrc







Finding files

Finding files in UNIX can be as simple or as sophisticated as you like. The general format is

find <STARTING DIRECTOR> <OPTIONS>

For example to just find a file with the name test fas in the current directory you would type

find . -name test.fas

The name can include a wild card such as * to represent any character or a several possible characters can be specified within { }. For example to find all files ending in either _1.fastq.gz or _2.fastq.gz in /data type

find /data -name *_{1,2}.fastq.gz

To find only files or directories the -type argument can be used

The following command will find any directory from / downwards that contains data somewhere in the name find / -type d -name *data*

The following command will find in the /data directory and all sub-directories any **file** whose name contains genome

find /data -type f -name *genome*

It is also possible to search for files that have been modified within a certain time The following command will search the current directory and all subdirectories for files (including directories) modified within the last 2 days or the last 2 hours.

find . -mtime -2
find . -mmin -120m

Find files modified over 2 days ago find . -mtime +2

These commands can be combined. For example the following command will search for files ending in .vcf that have been modified in the last 12 hours

find . -type f -name *.vcf -mmin -12h







Disk Usage

Your disk is getting full!! How do you find what is taking up the space.

Firstly to find how much disk space is being used on different partitions use the df (disk free) command with the -h argument to make the output sizes human-readable

\$ df -h					
Filesystem	Size	Used	Avail	Use%	Mounted on
udev	32G	0	32G	0%	/dev
tmpfs	6.3G	908K	6.3G	1%	/run
/dev/sda1	117G	87G	30G	75%	/
tmpfs	32G	0	32G	0%	/dev/shm
tmpfs	5.0M	0	5.0M	0%	/run/lock
tmpfs	32G	0	32G	0%	/sys/fs/cgroup
/dev/sda15	105M	3.4M	102M	4%	/boot/efi
/dev/sdb	984G	365G	569G	40%	/data

In this case we can see that

- root partition has used 87G (75%) of disc space and has 30G free.
- the data partition has used 365G (40%) of disc space and has 569G free

To see what files are taking up the space we can use the du (disk usage) command again with the -h argument as well as -s to look at the usage by size. The following command will list the directories or files within /data and sort them by human-readable size

```
sudo du -sh /data/* | sort -h
. . . .
2.1G /data/mash_analysis
5.2G /data/user5 data
7.6G /data/user1 data
9.0G /data/user3_data
13G
     /data/contamination files
     /data/user2 data
15G
38G
     /data/snp analysis tutorial
46G
     /data/prodege
     /data/assembly
65G
92G
     /data/user4_data
```

Here we can see that user4_data is taking up the greatest space (92G). Looking further inside this directory we can find what subdirectories within $/data/user4_data$ are taking up the most space







- /data/user4_data/analyses/amr_analysis 51M
- /data/user4_data/analyses/etec_abricate 60M
- /data/user4 data/analyses/ETEC assembly 41G
- /data/user4_data/analyses/etec_snp_phylogeny 52G