StaPH-B Linux Command Sheet v1.0 Public Health Bioinformatics

directory / file commands

pwd	- print the working directory
ls -l -alh	- list the contents of the current directory
cd dir	- change directory to <i>dir</i>
mkdir <i>dir</i>	- make directory named <i>dir</i>
touch <i>file</i>	- make a file named <i>file</i>
rm file	- remove a file named <i>file</i>
rm -r dir	- remove directory and contents named dir
rm -f <i>file</i>	- forcefully remove a file named <i>file</i>
rm -rf dir	- forcefully remove a directory <i>dir</i> and contents (careful with this)
mv file1 file2	- move file1 to file2 (used for renaming files)
mv dir1 dir2	- move dir1 to dir2 (used for renaming dirs)
cp file1 file2	- copy file1 to file2
cp -r dir1 dir2	- copy dir1 to dir2
cat file	- display the contents of <i>file</i> to stdout
less file	- display the contents of <i>file</i> fitting within the terminal screen
	- display the first 10 lines <i>file</i>
	- display the last 10 lines of <i>file</i>
sort file	- display the contents of the <i>file</i> with each line sorted
	- count the number of lines in <i>file</i>
ln -s target nam	e - create a link to the <i>target</i> file with <i>name</i>

system commands	file permission commands
w - display who is logged in	chmod 777 file - set read(r) write(w) and
whoami - display who you	execute(x) for all users
man command – display info about command	chmod 755 file - set owner to rwx and
df -h – display currant disk usage	all other users to rx
du -sh dir - display disk usage of dir	chmod 766 file - set owner to rwx and
which app - display the path to the	all other users to rw
location of the app	chmod 644 file - set owner to rw and
whereis app - display all possible paths to	all other users to r
the app	<pre>chmod +x file - make file executable for</pre>
history - display all commands that	all users
have been run	chown user file - change the owner of file
clear - clear the terminal of text	to user

compression commands

tar -cf file.tar files	- create a tar named file.tar containing files
tar -xf <i>file.tar</i>	- extract the files from <i>file.tar</i>
tar -czf file.tar.gz files	– create a tar with Gzip compression
tar -xzf file.tar.gz	– extract a tar using Gzip
	${\mathfrak s}$ – create a tar with Bzip2 compression
tar -xjf <i>file.tar.bz</i> 2	– extract a tar using Bzip2
gzip <i>file</i>	 compresses file and renames it to file.gz
gzip -d <i>file.gz</i>	– decompresses file.gz back to file

process commands

ps-e -	snapshot of processes
top –	show processes in real time
kill pid –	kill processes with id <i>pid</i>
pkill name -	kill processes with <i>name</i>
killall name-	kill all processes with name
	(careful with this)

searching

grep pattern files

grep -r pattern dir

- search for *pattern* in *dir*

- search for pattern

find dir -name "pattern" - find all files

with *pattern* in name in *dir*

in *files*

piping commands		
cmd > file cmd 2> file cmd &> file	 redirect the standard output (stdout) of cmd to file redirect the standard error (stderr) of cmd to file redirect the stdout and stderr of a cmd to file 	
<pre>cmd >> file cmd > /dev/null </pre>		
cmd < file cmd <(cmd1)	 redirect the contents of the file to the standard input (stdin) of cmd redirect the stdout of cmd1 through a file to cmd (useful if cmd takes a file input) 	
cmd1 cmd2 xargs cmd	 redirect the stdout of cmd1 to the stdin of cmd2 reads data from stdin and executes cmd one or more times depending on the input 	

useful commands

```
- count the number of unique lines in a file
     cat file.txt | sort -u | wc -l
- find all files with "assembly" in the name and copy them to a single assembly.txt file
     find . -name "*assembly*" | xargs cat > assembly.txt
- copy all ".fastq.gz" files from dir1 to dir2
     cp `find dir1 -name ".fastq.gz"` dir2
- split a multi fasta to individual fasta files
     awk '/^>/{s=++d".fa"} {print > s}' multi.fa
- convert a fastq file to fasta
      sed -n '1~4s/^@/>/p;2~4p' file.fq > file.fa
- calculate the mean length of reads in a fastq file
     awk 'NR%4==2{sum+=length($0)}END{print sum/(NR/4)}' input.fastq
- create a backup of files here all .txt files are backedup as .bak
     find . -name "*.txt" | sed "s/\.txt$//" | xargs -i echo mv {}.txt {}.bak | sh
- find these and many more at:
     https://github.com/stephenturner/oneliners
```