

BASH CHEAT SHEET

| Command | What it does | Example usage |
|---|--|--|
| <code>pwd</code> | Lists your p resent w orking d irectory (where you are) | <code>pwd</code> |
| <code>cd [dir]</code> | C hange d irectory (move from where you are) | <code>cd file_folder</code> <i>^ moves you to the file_folder directory (must be within your pwd)</i> <code>cd ..</code> <i>^ moves you back one directory level</i> |
| <code>ls [-l]</code> | Lists all files within pwd | <code>ls *.phylip</code> <i>^ lists all phylip files in your pwd</i> |
| <code>cp [file to copy] [new file]</code> | Copy a file. | <code>cp lampro_s1.slurm lampro_s2.slurm</code> <i>^ makes a copy of lampro_s1.slurm and names it lampro_s2.slurm</i> |
| <code>mv</code> | Move (or rename) a file. | <code>mv lampro_s1.slurm \$SCRATCH</code> <i>^ moves the lampro_s1.slurm file to your scratch directory. Can also do \$HOME or \$WORK2</i> <code>mv lampro_s1.slurm lampro_s2.slurm</code> <i>^ overwrites your lampro_s1.slurm file as lampro_s2.slurm</i> |
| <code>[contents of file] > [new file]</code> | Make a new file. | <code>cat lampro_s1.slurm lampro_s2.slurm > all_lampros</code> <i>^ takes the contents of both lampro_s1.slurm and lampro_s2.slurm files and lists them in a new file called all_fastqs</i> |
| <code>rm [-r] [file/directory]</code> | Deletes a file. BE CAREFUL!!! Files are not recoverable once removed. | <code>rm params-JA19529.txt</code> <i>^ deletes this txt file</i> <code>rm *.phylip</code> <i>^ deletes all phylip files from pwd</i> <code>rm -r lampro_trims</code> <i>^ deletes the entire lampro_trims folder</i> |
| <code>cat [file]</code> | View the contents of a file | <code>cat params-JA19529.txt</code> <i>^ this will show me the contents of this txt file</i> |

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| wc [file] | Word count. Calculates numbers of files, or lines within a file. -l flag is lines | wc -l params-JA19529.txt <i>^ lists number of lines in this file</i> ls *.fastq wc -l <i>^ counts the number of fastq files within your pwd</i> cat TJH3008_TX.trimmed_R1_.fastq wc -l <i>^ counts the number of lines within this particular fastq file</i> |
| head [file] | Like cat, but instead just shows you're the first few lines of a file (useful for large files) | cat TJH3008_TX.trimmed_R1_.fastq <i>^ this will show me the first 15 lines of this particular fastq file</i> |
| nano [file] | Edit the contents of a file. Navigate using arrow keys; shortcuts for other edits are at the bottom of window; useful ones are Ctrl+K which will cut an entire line and Ctrl+X which will exit. You will be asked to confirm changes to the file (type Y or N and return). | nano lampro_s1.slurm <i>^ edit the contents of lampro_s1.slurm</i> |
| [command] [command] | Pipes the result of a command into a new command. | cat lampro_s1.slurm wc -l <i>^ calculates number of lines within the lampro_s1.slurm file</i> |
| * | Wildcard. Replaces any string. | ls *.fastq > all_fastqs <i>^ takes all the fastq files in your pwd and lists them in a new file called all_fastqs</i> |