

Note: Do NOT use the parentheses listed below in the actual code. But do use the quotation marks as shown (like with grep).

| Command name | Usage   | Stands for  | Definition  | Tips  |
|--------------|---|---|---|---|
| cat          | cat (in_file1) (in_file2) > (out_file)  | Concatenate   | Concatenates the content of the files by adding lines                             |   |
| cd           | cd (folder_name)<br>for example<br>cd /home/jovyan/fall2025.git   | Choose directory  | Move around directories/folders   |   |
| cp           | cp (file or folder_name) (new_location)<br>for example<br>cp Lab_02/T_sir_scn4a.fasta Lab_02/Yourname_Lab2  | Copy  | Copy a file   | Use cp -r for folders   |
| grep         | grep '(pattern_search)' (in_file)<br>for example<br>grep 'Exon' Lab_02/T_sir_scn4a.fasta  | Globally search for a Regular Expression and Print matching lines | Search patterns in a file; Use > (new_search_file) to put your search into a file | Use grep 'pattern' (in_file)   wc -l to count the # of lines that contains the search pattern |
| head         | head (file)   | Head  | Enables you to see the top of a file  | Use head -n # to define the number of lines to show   |
| less         | less (file)<br>for example<br>less Pokemon.csv  |   | Read a file   | Use less -N to add the line number  |
| ls           | ls (location)   | List  | Lists the contents of a directory   |   |
| mkdir        | mkdir (new_folder_name)<br>for example<br>mkdir Yourname_Lab2   | Make directory  | Create new folder   |   |
| mv           | mv (in_file) (new_location or out_file)<br>for example to move<br>mv Lab_02/T_sir_scn4a.fasta Lab_02/Yourname_Lab2<br>or to rename and move<br>mv Lab_02/T_sir_scn4a.fasta Lab_02/Yourname_Lab2/Tsr_whattev.fasta | Move  | Move files or rename files  |   |
| pwd          | pwd   | Print working   | Shows your current location   |   |

|      |   |               |  |   |
|------|---|---------------|--|---|
|      |   | directory     |  |   |
| rm   | rm (file)<br>for example<br>rm T_sir_scn4a.fasta_mod  | remove        | delete files and folders                               | Use rm -r to delete folders. Be careful there is NO way to recover what you have removed                              |
| sed  | sed '(script)' (in_file) > (out_file)<br>for example<br>sed 's/KJ908899/Thamnophis_sirtalis/'<br>T_sir_scn4a.fasta ><br>T_sir_scn4a.fasta_mod | stream editor | Find and replace/insert and delete patterns            | Use sed 's/(find)/(replace)/' to find and replace in the whole file; 's/(find)/(replace)/' is an example of a script! |
| tail | tail (file)<br>for example<br>tail T_sir_scn4a.fasta_mod  | Tail          | Enables you to see the bottom of a file                | Use tail -n # to define the number of lines to show; ex: tail -n (#) (file)   |
| vi   | vi (file)   | VIM           | VIM text editor  | Press "i" to write, :wq to quit and save, :q! to quit and NOT save  |
| wc   | wc (file)<br>for example<br>wc Lab_02/T_sir_scn4a.fasta   | Word count    | Count number of lines, word count, and character count | Use wc -l to count only lines   |

#### Fun facts and tips:

- 1) Use “Tab” to automatically complete words. e.g: If the name of your file is “Pokemon.csv”, write P, then press Tab to autocomplete. Be aware that coding differentiates between lowercase letters vs. capital letters.
- 2) We can use pipes, the long straight line ( | ), to link commands together. It takes the output from one command and feeds it directly to the next command. It helps make our command line work more efficient.

- 3) We use “>” to denote our output. Look at the example for using cat above.
- 4) Dots are used to signal a location in your computer. One dot (.) means “this present location”, (..) one folder back, (../..) two folders back. e.g: If you were  
>fall2024>Lab\_01 to go one folder back to >fall2024 you will need to use “cd ..”
- 5) Use the up arrow to go to a previous command you have written to edit it and run it again.