Workshop on Genomics 2024





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What is UNIX?

powerful

Operating system

multi-user

multitasking



Why is it important for bioinformatics?

Facilitates sharing and reproducing analyses

Efficiency and speed

Access to powerful tools and applications

Handling large datasets and running analyses efficiently

Using scripts to automate repetitive tasks



The terminal



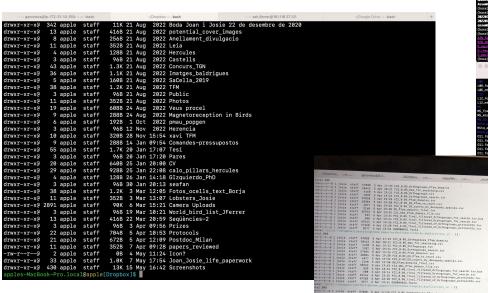
Make it comfortable to work in

- Resize the window
- Change the font size
- Open multiple terminal windows (or tabs)
- Make sure you have the right combination of colours that work for you.

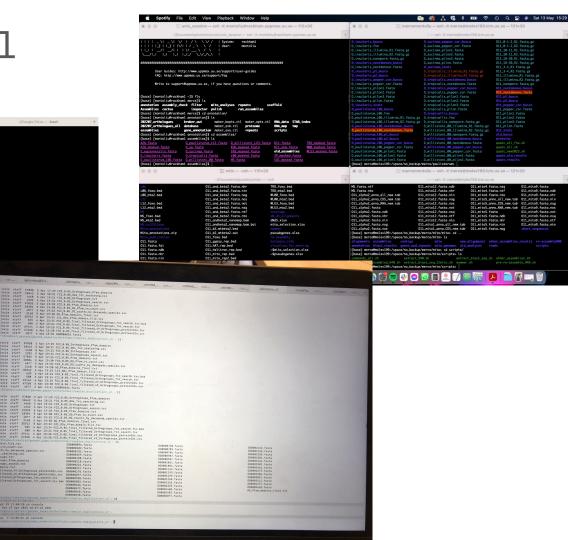




The terminal



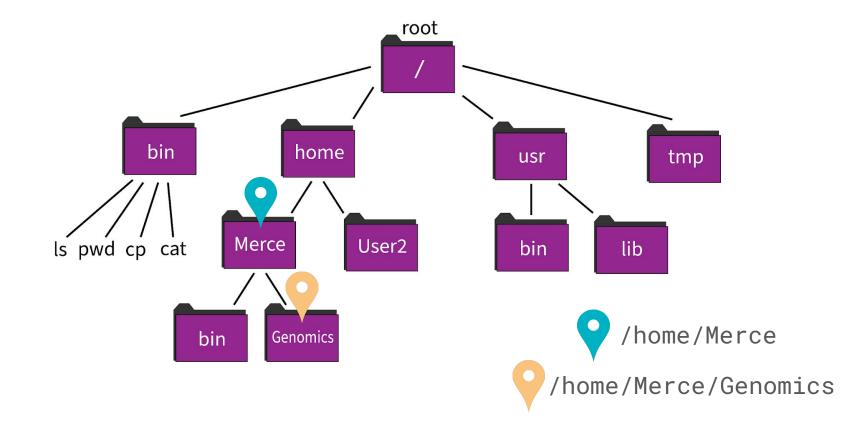
View | Not | 1928 | 1924 | 1927 | 1931 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 191



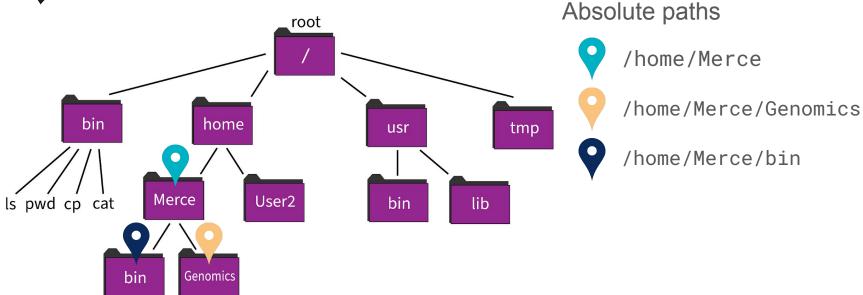
011_3-4_RZ.fastq.gz 011_illumina_R1.fastq.gz



File system organization

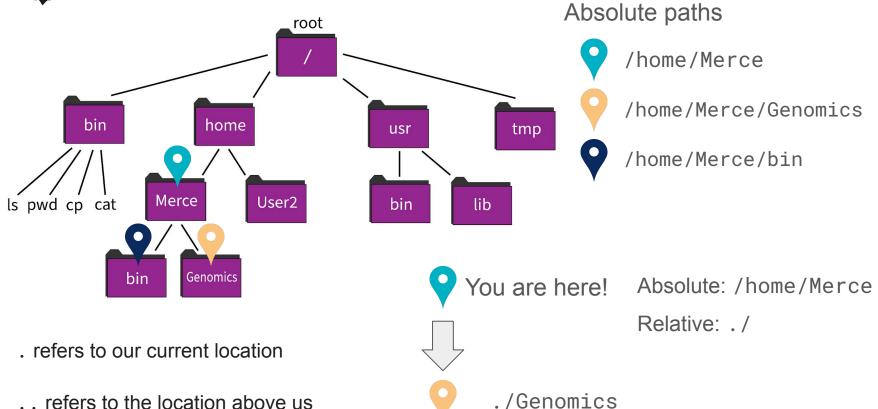




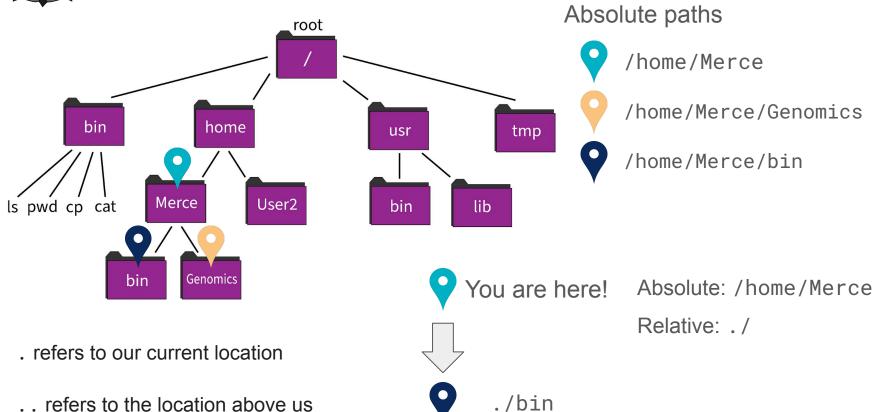


- . refers to our current location
- .. refers to the location above us

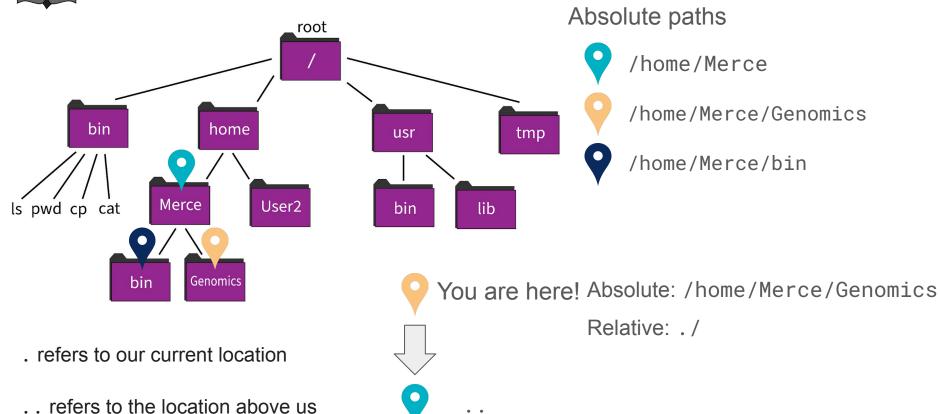




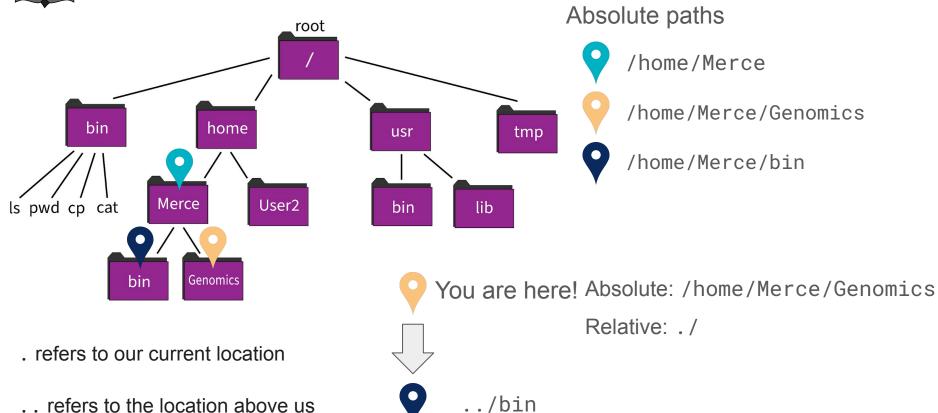








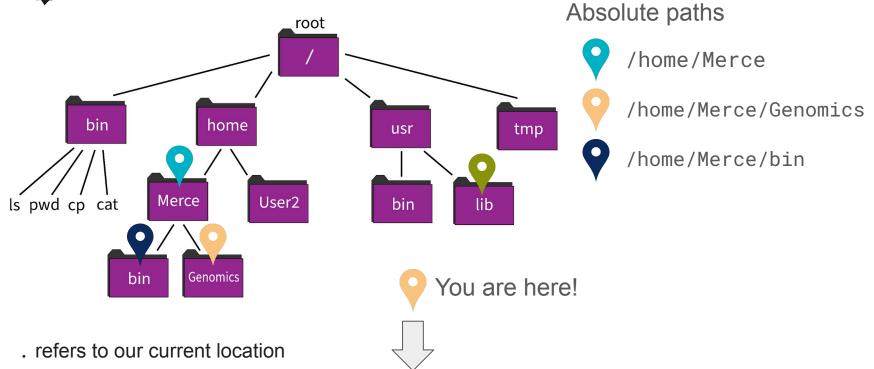






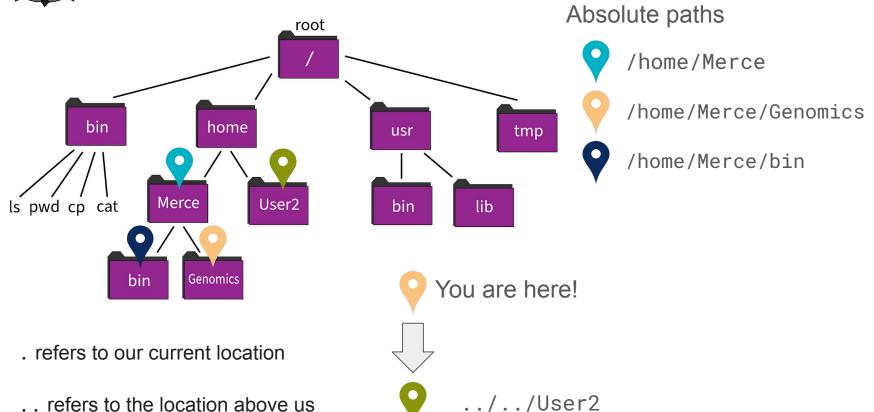
.. refers to the location above us

Paths - Absolute vs Relative



How do we refer to this directory?







File system navigation

pwd - where am I?



cd - change directory





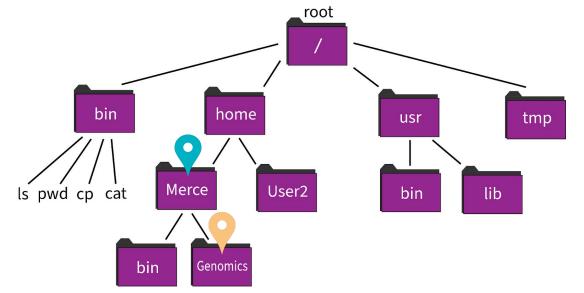
File system navigation

pwd - where am I?



/home/Merce

cd - change directory





> cd /home/Merce/Genomics

> cd ./Genomics



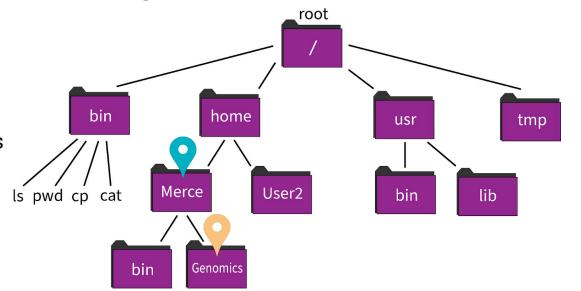
File system navigation

pwd - where am I?



/home/Merce/Genomics

cd - change directory





> cd /home/Merce

> cd ../



File system visualization

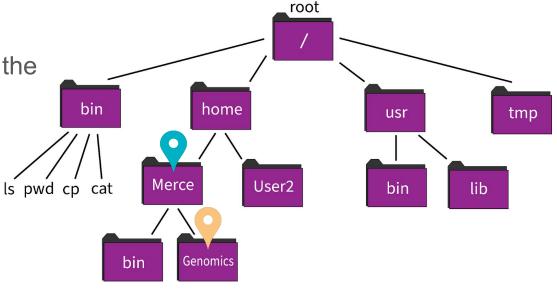
Is - shows you the contents the

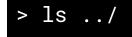
directory you are in

> 1s

> 1s .

> ls ./









Key shortcuts

Ctrl + Shift + V

Ctrl + E

Ctrl + C halts current command

Ctrl + Shift + C copy (linux) - Cmd + C (mac)

Ctrl + W erases one word in current line

Ctrl + U erases whole line

Ctrl + A go to begining of line

go to end of line

paste (linux) - Cmd + V (mac)

Type exit log out of current session



Create, copy, move, and remove files and folders

mkdir - create new directory

cp - copy file

mv - move file or directory

rm - remove file

"Unix was not designed to stop its users from doing stupid things, as that would also stop them from doing clever things." - Doug Gwyn



Symbolic links

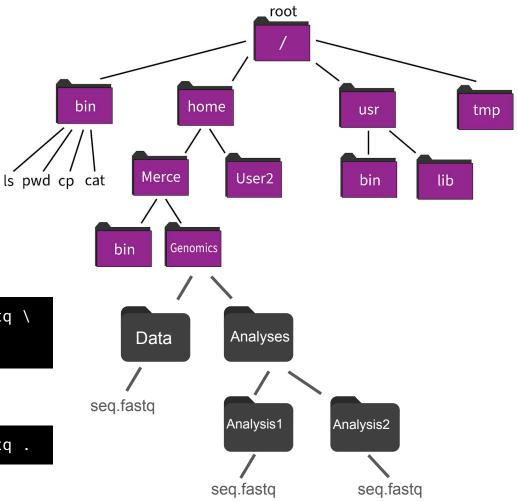
In -s /path/to/file link

create a symlink of file

> ln -s /home/Merce/Genomics/Data/seq.fastq \
/home/Merce/Genomics/Analyses/Analysis1/

If we are already inside the folder Analysis1:

> ln -s /home/Merce/Genomics/Data/seq.fastq .





man command - manual of the command

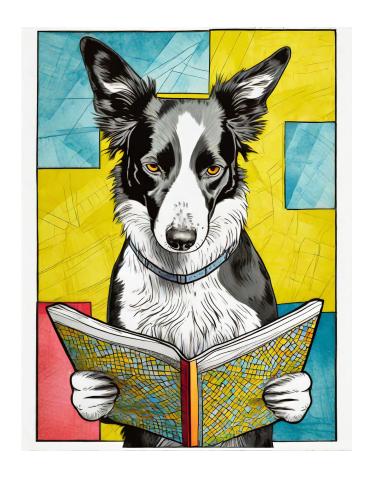
> man ls



Is -I formatted list

Is -h "human" formatted list

Is -Ih combination of flags



Inputs and outputs

stdin

It stands for standard input, and is used for taking text as an input.

stdout It stands for standard output, and is used to text output of any command you type in the terminal, and then that output is stored in the stdout stream.

stderr It stands for standard error. It is invoked whenever a command faces an error, then that error message gets stored in this data stream.



stdin, stdout, stderr

com	man	d st	d	in
COLL	HILALI	$\mathbf{u} \mathbf{v}_{\mathbf{i}}$	· W	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,

if it works: prints in our terminal the *stdout* if it fails: prints in our terminal the *stderr*

command *stdin* > *stdout*

if it works: *stdout* is redirected to a file if it fails: prints in our terminal the *stderr*

command2 *stdin2* > *stdout*

stdout is redirected to a file and rewrites its contents

command2 stdin2 >> stdout

stdout is redirected to a file and appended after its contents



stdin, stdout, stderr

command stdin

if it works: prints in our terminal the *stdout* if it fails: prints in our terminal the *stderr*

command file1 > output.txt stdin stdout

if it works: *stdout* is redirected to a file if it fails: prints in our terminal the *stderr*

command2 file2 > output.txt stdin stdout stdout is redirected to a file and rewrites its contents

command2 file2 >> output.txt stdin stdout stdout is redirected to a file and appended after its contents



stdin, stdout, stderr

command file1 2> errors.txt stdin stderr

if it works: prints in our terminal the *stdout* if it fails: *stderr* is redirected to a file

command file1 &> output.txt stdin stdout&stderr redirects both stdout and stderr to a file

command file1 > output.txt 2> errors.txt stdin stdout stderr redirects both *stdout* and *stderr* to a separate file each.



wc - word count (-I lines, -c characters, -w words)

less - visualize file contents in your terminal screen (press q to exit)

cat - prints contents of your file as standard output in your terminal

head - visualize the first 10 lines of a file

tail - visualize the last 10 lines of a file

The character | (pipe) is used to concatenate commands, so that we can run one command after the other, avoiding the creation of intermediate files.

command1 input | command2 > output

Instead of:

command1 input > output1
command2 output1 > output2

Using pipe, the output of running *command1* on a given input gets directly piped into *command2*, and we obtain an output of these two consecutive commands, generating only one output.



cat - prints contents of your file as standard output in your terminal

redirect to a command

cat fileA | command > output.txt

concatenate files

cat fileA fileB >> fileC

cat fileA > fileC

cat fileB >> fileC



sort - puts in certain order a series of lines in our file

sort -r fileA sorts in reverse order

sort -n fileA sorts lines in fileA numerically

sort -k 2 fileA sort fileA by column 2

sort -k 2nr fileA sort fileA by column 2, numerically and in reverse order

sort -V fileA sort lines in fileA numerically natural.

sort -u fileA sort lines and removes duplicates -> sort fileA | uniq



Are these two files different?

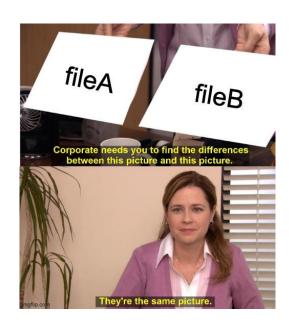
diff - can tell us if there are differences between two files

diff -q fileA fileB

"Files fileA and fileC differ"

diff fileA fileB

prints differences





Splitting a file

split - split a given file into multiple files (default 1000)

split -l 20 fileA

produce x number of files from fileA, each containing 20 lines.

cut - extract specific parts of a file

cut -c 2 fileA

extract specific columns from a file



Nano - The simpler option of text editor. All commands within the nano text editor are given by pressing the Control-key, usually represented as ^

^S save current file

^O save to (a different file)

^X exit from nano



Vim - a highly configurable text editor built to make creating and changing any kind of text very efficient

i start insert mode (you can start typing after where your cursor is)

ESC exits insert mode (also Ctrl + C)

:w save file without exiting

exit file (if there are unsaved changes, it fails)

:wq save and exit

:q! exit without saving changes



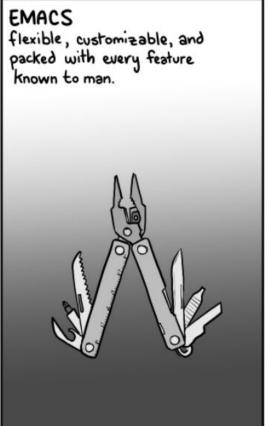
emacs - a text editor characterized by its extensibility and configurability. Some essential commands commands get activated by typing Control + X, then the command (while holding the control key), but there is a wide range of key combinations to be used to move and edit the text

Ctrl + x + s save file

Ctrl + x + s save file

Ctrl + x + c exit editor (if not saved, it ask if you want to save, then type "yes")







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What my family and friends think I do



What my supervisor thinks I do



What I actually do









Cheat-sheet

Workshop on Genomics 2024

bwd show current path / directory

list directory ls

cd dir change to directory dir

change to home cd cd ~ change to home

change to previous working directory cd -

current directory parent directory

mkdir dir create directory dir cp file1 file2 copy file1 to file2

mv file1 file2 move file1 to file2 or rename

file1 to file2

rm file1 delete file1

In -s file link create symbolic link

count (-I lines, -w words, -c characters) wc

tail file output last 10 lines of file head file output first 10 lines of file

less file / more file visualize contents of file cat file output file to standard output

sort sort rows diff fileA fileB differences? uniq keep unique rows cut -c 2 cut column 2

unix cheatsheet

man command manual for command makes file executable chmod +x file

command1 | command2 runs command2 on output

of command1

download file into current dir wget web-address-to-file ssh user@server

connect to cluster

tar -xzf archive.tar.gz uncompress tar.gz

tar -czf archive.tar.gz archive compress archive to .tar.qz gzip compress .gz gunzip uncompress .gz

Ctrl + C halts current command Tab autocomplete current line

Arrow up previous commands

Ctrl + Shift + C copy (linux) Cmd + C (mac) Ctrl + Shift + V paste (linux) Cmd + V (mac)

Ctrl + W erases one word in current line

Ctrl + U erases whole line Ctrl + A go to begining of line Ctrl + E go to end of line

log out of current session exit

#evomics2024



Cheat-sheet





Rubber duck







Now it is your turn to practice! And become each other's ducks!

