Introduction of Bioinformatics: Command line examples

Unix command line interface

Windows user:	**macOS/Linux** user:
• Scan the QR code below to download **Git Bash** • Download the "**Windows Portable**" one for installation	• Open the built-in **Terminal** app in your laptop

Navigating

Command	Explanation	Example usage
pwd	**Print** working directory	pwd
cd	Change the **working directory** to the target directory	cd /path/of/directory
cd ~	Chagne the **working directory** to user's home directory	cd ~
cd ..	Chagne to **parent directory of the current directory**	cd ..
ls	**List** the contents of a directory	ls
ls -a	**List all contents** in a directory	ls -a
ls -l	**List** the contents in a directory in **long format**	ls -l

Changing the file system

Command	Explanation	Example usage
mkdir	**Create a directory** with a specific name	mkdir name_of_folder
rmdir	**Remove a directory** with a specific name	rmdir name_of_folder
cp	**Copy** a file (to a directory or to another file)	cp output_1.txt /path/of/directory
mv	**Move** a file to the target directory	mv output_1.txt /path/of/directory
nano	Text editor to create text file	nano workshop_script.txt
rm	**Remove** a target file **(once delete, no restore)**	rm workshop_script.txt

Viewing

Command	Explanation	Example usage
less	**View** the contents of a file on one page at a time Press "Q" to exit	less workshop_script.txt
cat	**Concatenate** and **display** the content of a file	cat output_1.txt
head	Print the **first 10** lines of each file	head workshop_script.txt
tail	Print the **last 10** lines of each file	tail output_1.txt

Others

Command	Explanation	Example usage
cp file_1 file_2	**Copy** file_1 to file_2	cp output_1.txt output_2.txt
mv file_1 file_2	**Rename** file_1 to file_2	mv output_1.txt output_2.txt
sort	**Sort** or merge records (lines) of text files	sort output_1.txt
uniq	Filter out **repeated** lines in a file	uniq output_1.txt
>	**Output redirection** symbol, save the output of a command into a file.	uniq output_1.txt > output_2.txt

Manual and help

Command	Explanation	Example usage
<command> --help	Display **help** information for the usage of a command	less --help
man <command>	Open a **manual** page for a command	man less

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mv file_1 file_2	**Rename** file_1 to file_2	mv output_1.txt output_2.txt
sort -n	**Sort** or merge records (lines) of text files with numeric data	sort output_1.txt
sort -u	Sort or merge records and print the **unique** keys in a file	uniq output_1.txt
>	**Output redirection** symbol, save the output of a command into a file.	uniq output_1.txt > output_2.txt

Manual and help

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<command> --help	Display **help** information for the usage of a command	less --help
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