

Unix cheat sheet

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Being familiar with the Unix commandline is essential for bioinformatics data analysis but it might seem complex or tedious at the beginning. However, you will get already quite far with only a few commands. Here, I provide a cheat sheet that gives a quick overview of the most essential commands which will increase your efficiency in data analysis and file handling drastically - promised! You will find more details on most of these commands in my previous blog posts that were marked with the '[Commandline](#)' tag.

1 FILE system

<code>cd DIR</code>	change directory to DIR
<code>cd ..</code>	go up one directory
<code>cd ~</code>	to to your home directory
<code>pwd</code>	show present working directory
<code>ls</code>	list items in current directory
<code>ls -a</code>	list all items, including hidden ones
<code>ls -lhcr</code>	list all items in long, human-readable format and sort in reverse order by modification time
<code>ls -F</code>	list all items in current directory and show directories with a slash and executables with a star
<code>tree -C</code>	print hierarchical structure of your FILES and directories (color-coded)
<code>tree -d</code>	print hierarchical structure of all subdirectories
<code>tree -sh</code>	print hierarchical structure of FILES and directories with sizes (-s) in a human-readable format (-h)
<code>mkdir directoryname</code>	make new directory named directoryname
<code>mv FILE1 FILE2</code>	Rename FILE1 to FILE2
<code>mv FILE1 ../FILE2</code>	Move FILE1 one directory up
<code>cp FILE1 FILE2</code>	copy FILE1 and save it as FILE2
<code>rm FILE</code>	remove FILE
<code>rm -r DIRECTORY</code>	remove directory and all of its contents

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2 Opening FILES and extracting information

<code>less FILE</code>	open FILE and scroll through it line by line
<code>wc -l -w -m FILE</code>	Counting lines, words, and characters in FILE
<code>grep "pattern" FILE</code>	Print lines from FILE that contain "pattern"
<code>grep -v "pattern" FILE</code>	Print lines from FILE that do not contain "pattern"
<code>cat FILE > FILE2</code>	Write the content of FILE to FILE2
<code>cat FILE >> FILE2</code>	Append the content of FILE to FILE2
<code>sed -n 11,12p FILE</code>	Extract lines 11 to 12 from FILE
<code>awk -F "\t" '{if (\$1 > 20) print \$0}' FILE</code>	Print all columns of a line (\$0) in FILE if the value in column 1 (\$1) is bigger than 20
<code>unzip FILE.zip</code>	unzip the zip-compressed FILE
<code>gunzip FILE.gz</code>	unzip the gz-compressed FILE
<code>sort -n NUMBERS</code>	sort a row of NUMBERS numerically
<code>uniq -c FILE</code>	count unique lines in FILE
<code>nano FILE</code>	open FILE on the command-line
<code>xdg-open FILE</code>	open FILE with the standard program for its file type
<code>eog FILE</code>	open FILE (which is a figure) with the Eye of Gnome graphics viewer program

3 Data transfer

<code>rsync --progress -avz SRC DEST</code>	transfer from SRC to DEST, show the progress while FILES are compressed during the transfer in archive mode (including recursing into directories)
<code>rsync FILE user@host://home/usr/</code>	transfer FILE to the folder /home/usr on the remote server user@host
<code>rsync -avz directory/ DEST</code>	transfer all FILES saved in directory to DEST
<code>rsync -avz directory DEST</code>	create the folder directory in DEST and transfer all FILES in this directory
<code>scp -r SRC DEST</code>	transfer all FILES in SRC to DEST
<code>scp FILE DEST</code>	transfer FILE to DEST

4 Executing scripts and programs

<code>nohup ... &</code>	execute ... in the background
<code>nohup ... > FILE.txt &</code>	execute ... in the background and redirect output to FILE.txt
<code>ps -p ID</code>	print the status of a process with the specified process-ID
<code>kill ID</code>	stop the process with the specified process-ID
<code>pkill NAME</code>	stop all processes with NAME (NAME could be for example 'R' or 'python')
<code>top</code>	provides an ongoing look at processor activity in real time

5 Networking

<code>ssh user@host</code>	connect to host as user
<code>ssh -X user@host</code>	connect to host as user with X11 forwarding enabled (you can open programs with graphical user interface)

6 Help

<code>command --help</code>	Lists the options for command
<code>man command</code>	opens the manual page for command (exit with 'q')

7 Tricks

Pipe output from one command with `|` as input to another command.

<code>TAB key</code>	auto-completion of commands, FILE names etc.
<code>UP or DOWN arrows</code>	move through the history of your commands
<code>history</code>	Get overview of the commands you have used
<code>*</code>	Allows to generalize file names. For example, <code>*fasta</code> refers to all fasta files in a directory

Emacs 24.3.1 (Org mode 8.3beta)