

Crib Sheet: Intro to Unix

Command	Translation	Examples
cd	change directory	<code>cd /absolute/path/of/the/directory/</code> Go to the home directory by typing simply <code>cd</code> or <code>cd ~</code> Go up (back) a directory by typing <code>cd ..</code>
pwd	print working directory	<code>pwd</code>
mkdir	make directory	<code>mkdir newDirectory</code> creates newDirectory in your current directory Make a directory one level up with <code>mkdir ../newDirectory</code>
cp	copy	<code>cp file.txt newfile.txt</code> (and file.txt will still exist!)
mv	move	<code>mv file.txt newfile.txt</code> (but file.txt will <i>no longer</i> exist!)
rm	remove	<code>rm file.txt</code> removes file.txt <code>rm -r directoryname/</code> removes the directory and all files within
ls	list	<code>ls *.txt</code> lists all .txt files in current directory <code>ls -a</code> lists all files including hidden ones in the current directory <code>ls -l</code> lists all files in current directory including file sizes and timestamps <code>ls -lh</code> does the same but changes file size format to be human-readable <code>ls ../</code> lists files in the directory above the current one
man	manual	<code>man ls</code> opens the manual for command <code>ls</code> (use <code>q</code> to escape page)
grep	global regular expression parser	<code>grep ">" seqs.fasta</code> pulls out all sequence names in a fasta file <code>grep -c ">" seqs.fasta</code> counts the number of those sequences
cat	concatenate	<code>cat seqs.fasta</code> prints the contents of seqs.fasta to the screen (ie stdout)
head	head	<code>head seqs.fasta</code> prints the first 10 lines of the file <code>head -n 3 seqs.fasta</code> prints first 3 lines
tail	tail	<code>tail seqs.fasta</code> prints the last 10 lines of the file <code>tail -n 3 seqs.fasta</code> prints last 3 lines
wc	word count	<code>wc filename.txt</code> shows the number of new lines, number of words, and number of characters <code>wc -l filename.txt</code> shows only the number of new lines <code>wc -c filename.txt</code> shows only the number of characters
sort	sort	<code>sort filename.txt</code> sorts file and prints output
uniq	unique	<code>uniq -u filename.txt</code> shows only unique elements of a list (must use sort command first to cluster repeats)

Shortcut

Use

Ctrl + C	kills current process
Ctrl + L	clears screen
Ctrl + A	Go to the beginning of the line
Ctrl + E	Go to the end of the line
Ctrl + U	Clears the line before the cursor position
Ctrl + K	Clear the line after the cursor

Shortcut	Use
*	wildcard character
tab	completes word
Up Arrow	call last command
.	current directory
..	one level up
~	home
>	redirects stdout to a file, <i>overwriting</i> file if it already exists
>>	redirects stdout to a file, <i>appending</i> to the end of file if it already exists
	redirects stdout to become stdin for next command