
Linux Command Line Reference

Advanced Bioinformatics: Genome Analysis

Course code: MSIB 32500

Navigation in the terminal

UP arrow	Go the previous command in history	
DOWN arrow	Go to next command in history	
history	View the history of commands in the terminal	
!!	Re-execute last-used command	
exit	logout, leave the terminal	

Symbols used in command line

Tab	Autocomplete, completes words after only starting letters	
?	Wildcard in file names, refers to any character	
*	Wildcard in file names, refers to all characters e.g.: <code>rm*.fasta</code> remove all .fasta files in current directory	
	AND e.g.: <code>rm(seq1.txt seq2.txt)</code> remove seq1.txt and seq2.txt	
!	NOT e.g.: <code>rm !(sequence.fasta)</code> remove all files except sequence.fasta in current directory	
./	Current folder e.g.: <code>./bwa</code> execute bwa in current folder	
../	Parent folder e.g.: <code>find ../ -name sequence.fasta</code> find the file sequence.fasta in parent folder	
~	Represents your home folder e.g.: <code>cd ~</code> change to home directory	

Privileges

su	Become a superuser, you stay su until you exit	
sudo	Do as superuser e.g.: <code>sudo chmod 777 data.txt</code> change the 'mode' of file as a superuser	
chmod	Change permissions of file e.g.: <code>chmod 777 data.txt</code> allow everybody to read, write and execute	
chown	Change owner of file e.g.: <code>chown gregor seq1.txt</code> change owner of file seq1.txt to user gregor	

Downloading data from the internet

wget	Download a file from the provided url e.g.: <code>wget ftp://ftp-trace.ncbi.nih.gov/SRR001115/SRR001115.sra</code>	

Navigation on the file system

cd	Change directory e.g.: <code>cd ..</code> go one folder up; <code>cd ~</code> go to home; <code>cd /usr/bin/db</code> go folder db	
pwd	Show current folder (print working directory)	
ls	List of files in current directory	
ll	List detailed content of current directory including hidden files	

File compression

zip	Compress file e.g.: <code>zip text.zip text.txt</code>	
unzip	Decompress file e.g. <code>unzip text.zip</code>	
gzip	Compress file to .gz e.g.: <code>gzip data.txt</code>	

gunzip	Decompress a .gz file e.g.: <code>gunzip data.gz</code>
tar	Compress/Decompress (tape archive) a single file or entire directory(recursively) e.g.: <code>tar -czvf name-of-archive.tar.gz /path/to/directory-or-file</code> -c: create and archive -z: compress the archive with gzip -v: Display progress in terminal (verbose) -f: Allows you to specify the filename for the archive e.g.: <code>tar -xzvf name-of-archive.tar.gz</code> -x: specify you want to extract an archive instead of create one

File handling

mkdir	Create a folder/directory e.g.: <code>mkdir newfolder</code>
touch	Create a file e.g.: <code>touch newfile.txt</code> create an empty file called newfile.txt
rmdir	Remove directory (only if the folder is empty)
rm	Remove a file
cp	Copy a file from source to destination e.g.: <code>cp /YourData/data.txt /Mydata/</code>
mv	Rename or move file from source to destination e.g.: <code>mv /YourData/data.txt /Mydata/</code>
diff	Compares two files and prints how they differ e.g.: <code>diff -b file1 file2</code> (-b: ignore blanks)
find	Locate file or folder e.g.: <code>find / -name sequence.txt</code> search in the complete file system
cat	Concatenate files e.g.: <code>cat file1 file2</code>

Command output redirection

>	Writes the output of a command to a file e.g.: <code>sort file1.txt>file2.txt</code>
>>	Appends the output of command to an existing file e.g.: <code>sort file1.txt>>file2.txt</code>
 	Pipe the output of a command as the input of other command e.g.: <code>ls grep data</code>

Installing tools

apt-get install	easy installation from repository e.g.: <code>sudo apt-get install r-base</code>	
pip	Install python scripts e.g.: <code>pip install cutadapt</code>	
./configure	Installation from source make sure all dependencies are installed	
make	Compile the source code	

Text processing

head	Show the first 10 lines of a file e.g.: <code>head code.py</code> one can also use <code>head -nX file</code> (X is a #)	
tail	Show the last 10 lines of a file e.g.: <code>tail code.py</code> one can also use <code>tail -nX file</code> (X is a #)	
grep	Search for a pattern in file e.g.: <code>grep ">" data.fasta</code> search for > in data.fasta <code>grep -c ">" data.fasta</code> count the lines in file that contain pattern	
sort	Sort lines in text file e.g.: <code>sort -kX file</code> sorts the lines in text file according to column X <code>sort -k2 data.txt</code> sorts lines in data.txt according to second column <code>sort -n file</code> sorts numerically instead of alphabetically <code>sort -r file</code> sorts in reverse order	
cut	Cut out parts from a file e.g.: <code>cut -c3 file</code> returns the third character of each line <code>cut -c1-3 file</code> returns the first 3 character of each line <code>cut -fX file</code> cuts column X from file <code>cut -f1,3 data.txt</code> cut first and third column from data.txt	
wc	Line, word and character count e.g.: <code>wc genetic_code.py</code> will produce x= # of lines, y= # words, and z= # of characters	
tr	Translate characters i.e. <code>tr a-z A-Z</code> will convert the text you type from lower case to upper case <code>tr 1234 ACGT</code> will return GTCAA when you type 34211	