Linux I

BASIC BASH COMMANDS

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Navigation and file management commands

Command	Function	Syntax
ls	list contents	ls **OPTIONS DIRECTORY**
pwd	print working directory	pwd
cd	change directory	cd ~ or cd #home directory
		cd .. #previous directory

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Directory operations

Command	Function	Syntax
mkdir	make directory	**mkdir DIRECTORY**
cp	copy files/directory	**cp SOURCE DESTINATION**
man	manual page (help)	**man COMMAND**
mv	move files/directories	**mv SOURCE DESTINATION**
touch	create file	**touch FILE**
nano	edit file	**nano FILE**

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Directory operations

Command	Function	Syntax
less	view file (less display)	`less` **FILE**
more	view file (more display)	`more` **FILE**
cat	catalog file contents	**cat FILE**
head	show first few lines of a file	`head` **FILE**
tail	show last few lines of a file	`tail` **FILE**
rmdir	remove empty directory	**rmdir DIRECTORY**
rm	remove file(s)	**rm FILE**

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File manipulation

Command	Function	Syntax
grep	search a pattern	grep [OPTIONS] "PATTERN" FILENAME
sed	stream edit a file	`sed 's/search/replace/g'`FILENAME
awk	multi-purpose command	`awk 'PATTERN {ACTION}'`FILENAME
tr	translate or transliterate a file	`tr` [OPTIONS] "STRING1" "STRING2" < INFILE
sort	sort files	`sort` FILE1 > SORTED_FILE1
uniq	display unique lines	`uniq` [OPTIONS] INFILE > OUTFILE
diff	display difference	`diff` [OPTIONS] FILE1 FILE2

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File manipulation

Command	Function	Syntax
comm	display common lines among files	`comm` [OPTIONS] FILE1 FILE2
cut	break files vertically based on fields	`cut -d` "DELIMITER" `-f` NUMBER FILE
split	break files horizontally	split [OPTIONS] FILENAME
paste	combine files side by side	`paste` FILE1 FILE2 > FILE3
join	join files based on common field	`join -t` 'DELIMITER' `-1` N `-2` N FILE1 FILE2
wc	word count	`wc` FILENAME
scp	remotely copy	`scp` FILE user@host:/path/to/directory/

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File compression/archiving

Command	Function	Syntax
zip	zip compress	`zip` OUTFILE.zip INFILE.txt
		`zip -r` OUTDIR.zip DIRECTORY
unzip	decompress zipped file	`unzip` ANYTHING.zip
tar	archive and compress files/directories	`tar -czvf` OUTFILE.tar.gz DIRECTORY #compress
		`tar -xzvf` OUTFILE.tar.gz # extract
gzip	gzip files	`gzip` SOMEFILE
gunzip	decompress gzipped files	`gunzip` SOMEFILE.gz

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Additional commands

Command	Function	Syntax
chmod	change permissions for files/directories	`chmod` [OPTIONS] RELATIONS[+/-]PERMISSIONS FILE
find	find a file/directory	`find . –name FILE`
du –sh	DIR show directory size	
clear	clear screen	
top	current running processes	
ps	current running processes	
wget	URL download specified URL	

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Practical 1 working with directories

1. Display your **current working directory**
2. Change to **etc/** directory
3. Now change to your **home** directory
4. Go to the **parent directory** of the **current working directory**
5. Go to the **root** directory
6. List the contents of the **root** directory
7. List a long listing of the **root** directory
8. Stay where you are, and list the contents of **/etc**
9. Stay where you are, and list the contents of **/bin**
10. Stay where you are, and list the contents of **~**
11. Now go back to your **home** directory

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Practical 1 working with directories

1. Display your **current working directory**
2. Change to **etc/** directory
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4. Go to the **parent directory** of the **current working directory**
5. Go to the **root** directory
6. List the contents of the **root** directory
7. List a long listing of the **root** directory
8. Stay where you are, and list the contents of **/etc**
9. Stay where you are, and list the contents of **/bin**
10. Stay where you are, and list the contents of **~**
11. Now go back to your **home** directory
12. List all the files (including hidden files) in your **home** directory.

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Practical 1 working with directories

13. List all the files in human readable format in your **home** directory
14. Create a directory **testdir** in your home directory
15. Change to the **/etc** directory, stay here and create a directory **newdir** in your **home** directory.
16. Create in one command the directories in your **home** directory ~/dir1/dir2/dir3 (dir3 is a subdirectory from dir2,and dir2 is a subdirectory from dir1).
17. Remove the directory **testdir**
18. Create a directory **~/touched** and enter it
19. Create the files **seq1.txt** and **seq2.txt** in touched
20. Copy seq1.txt to copy.seq1.txt

Use the man page of bash to find information about these commands. **pushd and popd**

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Working with files

- Use **wget** to download proteomes of ***Acanthocheilonema viteae, Ancylostoma ceylanicum, Panagrolaimus ps1159*** from (https://parasite.wormbase.org/)
- Extract files with **gunzip**
- How many sequence lines begin with **>** (use **grep** command**)**
- Extract the sequence names and save them to **Acav.txt, Ancc.txt** and **Pan.txt** respectively (use **cut** command)