

Animal Evolution and Diversity 23

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Worm-Laboratory

Linux I

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

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File compression/archiving

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

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Additional commands

Command	Function	Syntax
chmod	change permissions for files/directories	<code>chmod</code> [OPTIONS] RELATIONS[+/-]PERMISSIONS FILE
find	find a file/directory	<code>find . -name FILE</code>
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**
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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)