

**UT Southwestern**  
Medical Center

BioHPC

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# The Linux Command Line & Shell Scripting

[web] [portal.biohpc.swmed.edu](http://portal.biohpc.swmed.edu)  
[email] [biohpc-help@utsouthwestern.edu](mailto:biohpc-help@utsouthwestern.edu)

The Linux command line is provided by a *shell*.

By far the most common shell on linux is *bash* (Bourne Again SHell)

The shell lets us run other programs or commands. It also has a lot of built-in commands, and is a programming language in itself (bash script).

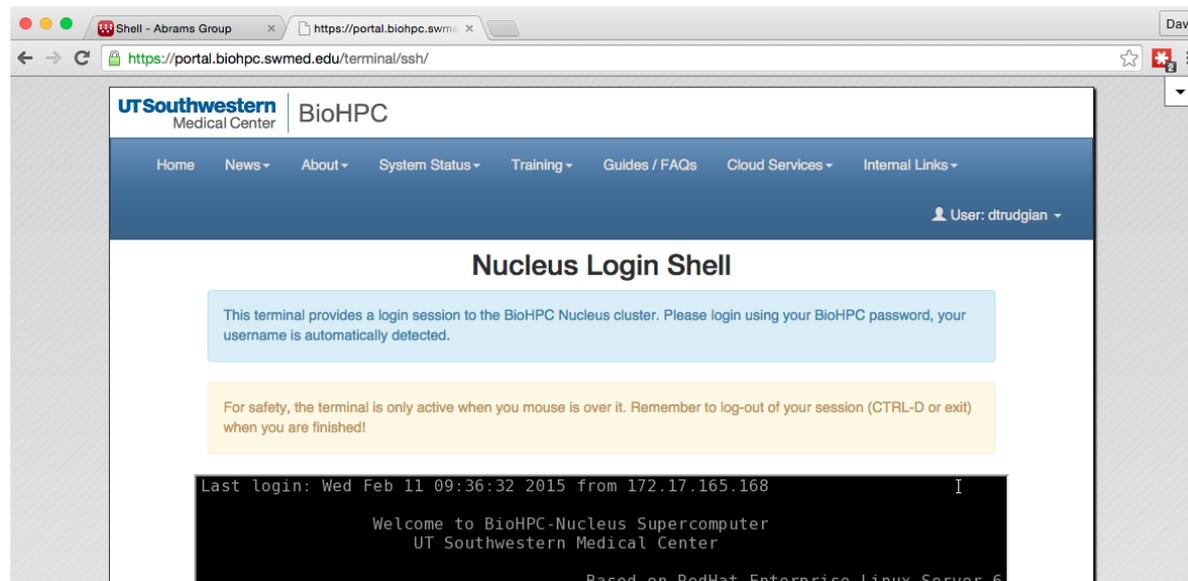
The shell is scary, but a little knowledge can make difficult things easy, and time-consuming things quick.

## Follow Along...

Today is mostly demos. Slides and cheat sheets for reference. Stop me with questions!

You can follow along using the Nucleus Web terminal on the BioHPC portal:

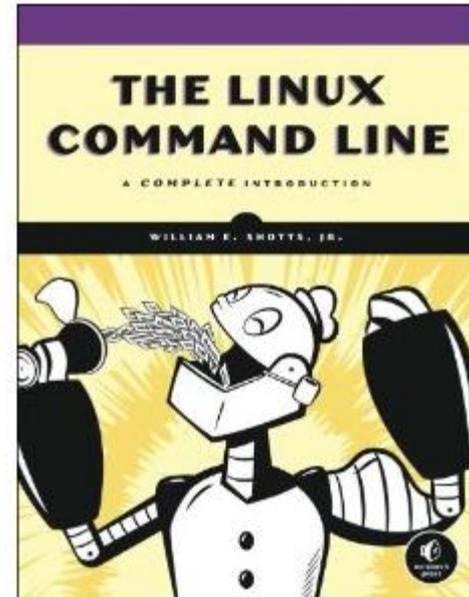
<https://portal.biohpc.swmed.edu/terminal/ssh/>



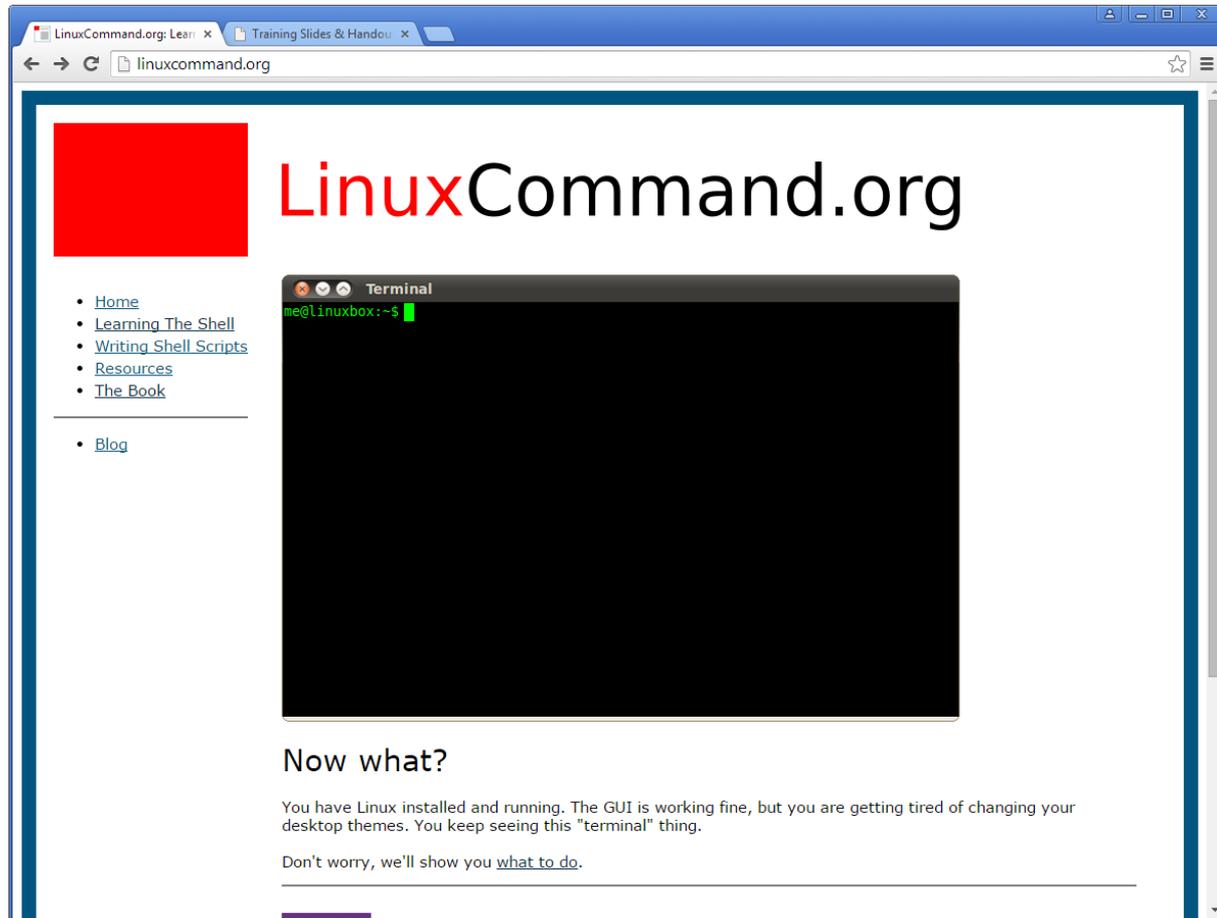
Free, Creative-Commons PDF

On the portal  
Training -> Slides & Handouts

<http://linuxcommand.org/tlcl.php>







Get a command's help page: `man <command>`

```
dtrudgian@biohpcws064:~/cli_scripts
10:41 AM $ man ls
```

```
LS(1)                                User Commands                                LS(1)

NAME
  ls - list directory contents

SYNOPSIS
  ls [OPTION]... [FILE]...

DESCRIPTION
  List information about the FILES (the current directory by default).
  Sort entries alphabetically if none of -cftuvSUX nor --sort.

  Mandatory arguments to long options are mandatory for short options
  foo
```

Press `q` or `Ctrl-C` to exit the man page

## The Basics – Listing files, changing, creating and removing directories

Command	What does it do?
<code>pwd</code>	Print Working Directory – where am I?
<code>ls</code>	List files in current directory
<code>ls -lah</code>	List files with detail (l = long format, a = all files including hidden, h = human readable file sizes)
<code>mkdir cli_training</code>	Make a directory called cli_training
<code>mkdir -p cli_training/ex1/oops</code>	Make a directory path structure, all directories necessary if they don't already exist.
<code>rmdir cli_training/ex1/oops</code>	Remove the cli_training/ex1/oops directory (if empty!)
<code>ls -lah cli_training</code>	List files inside the cli_training directory
<code>cd cli_training</code>	Change directory into cli_training
<code>cd ..</code>	Change directory to .. which is the parent directory – i.e. up one level.
<code>rm -r cli_training</code>	Remove recursively (-r) the cli_training directory (the directory and everything inside it).

## The Basics – Copying and Moving Files and Directories

Command	What does it do?
<code>mkdir cli_training</code>	Make the directory cli_training
<code>touch cli_training/file1</code>	Create an empty file called file1 inside cli_training
<code>mkdir new_training</code>	Make the directory new_training
<code>cp cli_training/file1 new_training/</code>	Copy file1 from cli_training into new_training
<code>cp -r new_training newer_training</code>	Copy new_training recursively (directory and everything inside) to a directory called newer_training)
<code>mv new_training old_training</code>	Move/rename new_training directory to old_training
<code>mkdir all_training</code>	Make a directory all_training
<code>mv newer_training old_training all_training/</code>	Move the newer_training and old_training directories inside all_training

- \* Match any number of characters

<code>ls *</code>	Any file
<code>ls notes*</code>	Any file beginning with notes
<code>ls *.txt</code>	Any file ending in .txt
<code>ls *2015*</code>	Any file with 2015 somewhere in its name

- ? Match a single character

<code>ls data_00?.txt</code>	Matches data_001, data002, data_00A etc.
------------------------------	--

- [] Match a set of characters

<code>ls data_00[0123456789].txt</code>	
<code>ls data_00[0-9].txt</code>	Matches data_001 – data_009, not data_00A

## File Permissions

ls -l

```
drwxr-xr-x  4 dtrudgian biohpc_admin   58 Feb 16 15:13 all_training
drwxr-xr-x  7 dtrudgian biohpc_admin  140 Feb 12 10:36 Apps
drwxr-xr-x  2 dtrudgian biohpc_admin   26 Feb 16 15:12 cli_training
drwxr-xr-x  8 dtrudgian biohpc_admin  4.0K Feb 16 14:25 Cluster_Installs
drwxr-xr-x  3 dtrudgian biohpc_admin  4.0K Feb 16 11:49 Desktop
drwxr-xr-x  2 dtrudgian biohpc_admin   10 Feb 16 14:10 Documents
drwxr-xr-x  9 dtrudgian biohpc_admin  135 Feb 16 14:32 Downloads
-rw-r--r--  1 dtrudgian biohpc_admin  336 Feb 16 15:16 error.txt
drwxr-xr-x 10 dtrudgian biohpc_admin  4.0K Feb  9 12:45 Git
drwxr-xr-x 17 dtrudgian biohpc_admin  4.0K Feb 16 15:17 ownCloud
drwxr-xr-x  2 dtrudgian biohpc_admin   10 Feb 16 14:18 Pictures
drwxr-xr-x  5 dtrudgian biohpc_admin  102 Feb  4 11:19 portal_jobs
```



Permissions

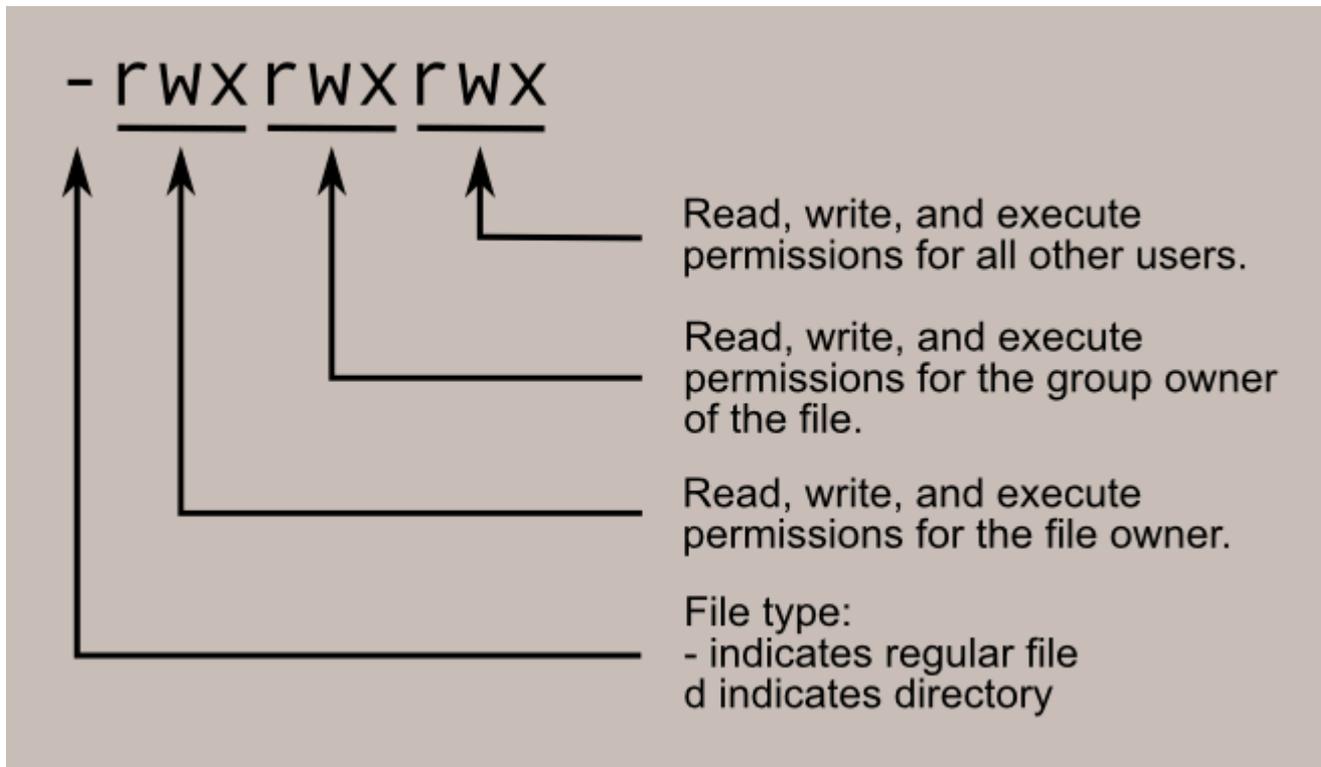


Owner



Group

## File Permissions



## Octal Permissions

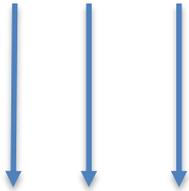
r = 4  
w = 2  
x = 1



Add up the permissions you need for each class, e.g.

rx = 5  
rw = 6  
rwx = 7

```
-rw-r--r-- 1 dtrudgian biohpc_admin 336 Feb 16 15:16 error.txt
```



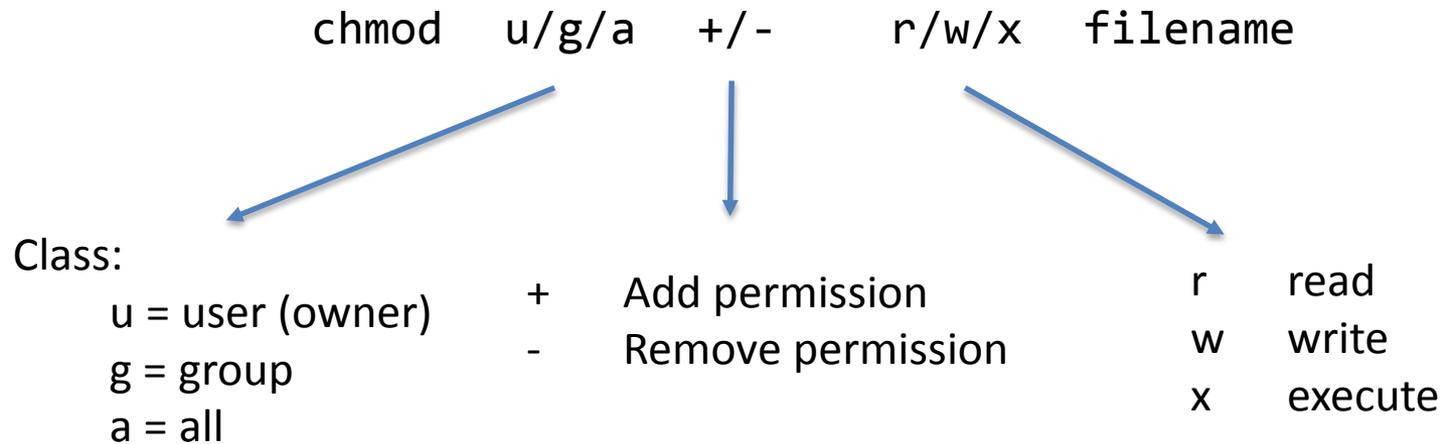
6 4 4

Owner can read+write  
Group can read  
Others can read

## Changing Permissions

Command	What does it do?
<code>chown dtrudgian error.txt</code>	Change the owner of error.txt to dtrudgian
<code>chgrp CellBiology error.txt</code>	Change the group owner of error.txt to danuser
<code>chmod 660 error.txt</code>	Set permissions 660 for error.txt Owner read/write, Group read/write, Others no access.
<code>chown dtrudgian.biohpcadmin cli_training</code>	Change ownership of the cli-training directory to dtrudgian, and group to biohpcadmin (in one step!)
<code>chown -R biohpcadmin cli_training</code>	Change the group of cli-training to biohpcadmin <i>recursively (directory and everything inside it)</i> .
<code>chmod -R 755 cli_training</code>	Change permissions of cli-training and everything inside it to 755 Owner read/write/execute, group read/execute, others read/execute

## Easier chmod!



```
chmod g+rw test.txt  
chmod a+x script.sh  
chmod g-x script.sh
```

Add read/write permissions for the group  
Add execute permission for everyone  
Remove execute permission for the group

vi / vim

Cryptic commands! Cheat sheet on the portal.

Quick tutorial: <http://www.washington.edu/computing/unix/vi.html>

nano

Easier to use.

Quick tutorial: <http://mintaka.sdsu.edu/reu/nano.html>

## Manipulating text files 1

Command	What does it do?
<code>cat story.txt</code>	Show the content of story.txt in the terminal
<code>less story.txt</code>	Show the content of story.txt in a pager that allows scrolling & searching
<code>head -n 15 story.txt</code>	Show the first 15 lines of story.txt
<code>tail -n 5 story.txt</code>	Show the last 5 lines of story.txt
<code>head -n 15 story.txt   tail -n 5</code>	Shows lines 11-15 of story.txt. We take the first 15 lines from story.txt using head, and extract the bottom of that selection by piping it through tail.
<code>grep "elephant" story.txt</code>	Find all lines in story.txt that contain "elephant" <i>case-sensitive</i> .
<code>grep -i "mouse" story.txt</code>	Find all lines in story.txt that contain "cat" <i>non-case sensitive</i> .
<code>grep -c "at" story.txt</code>	Count the number of lines in story.txt that contain "at".
<code>grep "^The" story.txt</code>	Find lines beginning with "In"
<code>grep "water\.\$" story.txt</code>	Find lines ending with "water". Note that "." is a special character so we have to <i>escape</i> it.

grep searches for patterns using *regular expressions* - <http://www.robelle.com/smugbook/regexpr.html>

## Manipulating text files 2

Command	What does it do?
<code>sort gifts.txt</code>	Sort the lines in a file alphabetically
<code>sort -r gifts.txt</code>	Sort the lines in a file in reverse alphabetical order
<code>sort -nr numbers.txt</code>	Sort the lines in a file in reverse numerical order
<code>uniq repeats.txt</code>	Find all of the unique lines in a file
<code>sed "s/dog/cat/g" story.txt</code>	Change all instances of cat to dog, printing the result  s(substitute)/old/new/g(global)

sed can do a lot - <http://www.grymoire.com/Unix/sed.html>

awk can do even more - <http://www.grymoire.com/Unix/Awk.html>

## Redirection & Pipes

Command	What does it do?
<code>date &gt; date.txt</code>	Send the output of the date command into date.txt <b>overwriting</b> existing content.
<code>date &gt;&gt; date.txt</code>	Send the output of the date command into date.txt, <b>appending</b> to the end of the file.
<code>which nonsense 2&gt; error.txt</code>	Send the error output of the command 'which nonsense' into error.txt
<code>which nonsense 2&gt; /dev/null</code>	Discard the error output of the command 'which nonsense'
<code>which nonsense 2&gt;&amp;1 &gt; output.txt</code>	Combine the error output into the standard output, and direct into the file output.txt
<code>matlab &lt; hello.m</code>	Send the text in hello.m to the matlab command as input
<code>last   less</code>	<i>Pipe</i> the output of the last command to the less command as input

## Archives

Command	What does it do?
<code>gunzip mydata.txt.gz</code>	Extract a .gz gzipped file
<code>gzip mydata.txt</code>	Compress a file using gzip – becomes a .gz file
<code>tar xvf archive.tar</code>	Extract (x) everything from a tar archive file (f). Show verbose output (v).
<code>tar cvf new.tar file1 file2 folder1</code>	Create (c) a tar archive file (f) adding files and folders to it.
<code>tar zxvf archive.tar.gz</code>	Extract a compressed gzipped tar archive in one step
<code>tar jxvf archive.tar.bz2</code>	Extract a compressed bzipped tar archive in one step
<code>unzip archive.zip</code>	Extract a compressed ZIP archive.



A variable holds information to be used later

Set them using:

`name=value`

Get their value using:

`$name`

Make them available to other programs:

`export name`

```
#!/bin/bash
```

```
MY_NAME=dave
```



Set the variable MY\_NAME

```
echo Hello $MY_NAME
```



Run echo using the value in MY\_NAME

```
export MY_NAME
```



Put MY\_NAME into our *environment*

```
printenv | sort
```



Show our *environment variables*

We can assign the output of programs/commands into variables:

```
#!/bin/bash
```

```
NOW=$(date +%Y-%m-%d) ← Put the date (YY-MM-DD) into NOW
```

```
DATA_DIR="data_$(date +%Y-%m-%d)" ← Create a directory with a name  
mkdir $DATA_DIR incorporating the date
```

```
module load matlab  
matlab -nodisplay -nosplash < hello.m > $DATA_DIR/output.txt
```

Run matlab with input hello.m, and send the output into our data directory

```
#!/bin/bash
```

```
echo "This scripts checks for the dummy file."
```

```
echo "Checking..."
```

```
if [ -f "dummy" ]; then  
    echo "dummy exists."  
else  
    echo "Couldn't find it!"  
fi
```

file exists test is -f



Read about the available tests here



[http://tldp.org/LDP/Bash-Beginners-Guide/html/sect\\_07\\_01.html](http://tldp.org/LDP/Bash-Beginners-Guide/html/sect_07_01.html)

*This script lists all of the files in the current directory using a for loop:*

```
#!/bin/bash          Set variable i to each value in the output of the ls command
for i in $( ls ); do
    echo "item: $i"  ← Echo the current value of $i
done
```

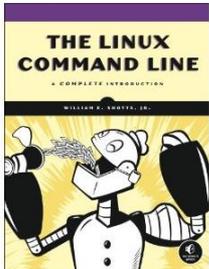
Read about the other loops here

<http://tldp.org/HOWTO/Bash-Prog-Intro-HOWTO-7.html>

## Learning Shell Scripting

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- Try to automate the next repetitive manual task you have to do.
- Invest some time in learning the shell to save a lot of time in future.
- Email [biohpc-help@utsouthwestern.edu](mailto:biohpc-help@utsouthwestern.edu) for advice if you're stuck.



Reminder – this book is a free PDF available from the portal website.