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## Basics of Linux I

### The Linux Command Line Interface

[web] [portal.biohpc.swmed.edu](http://portal.biohpc.swmed.edu)

[email] [biohpc-help@utsouthwestern.edu](mailto:biohpc-help@utsouthwestern.edu)

*So, you wish to learn the art of Linux-Fu...*

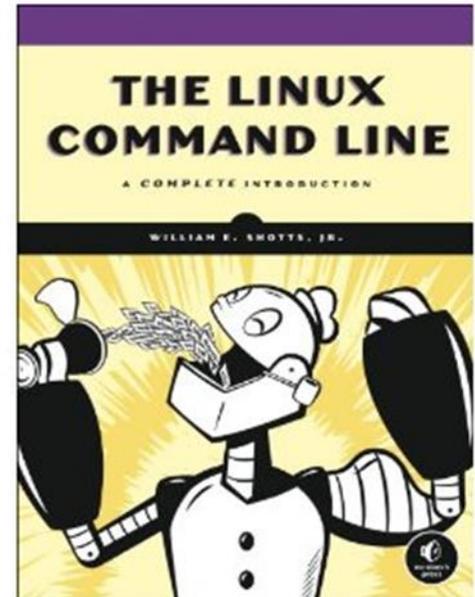


## Study Resources: A Free Book

Free, Creative-Commons PDF

On the portal  
Training -> Slides & Handouts

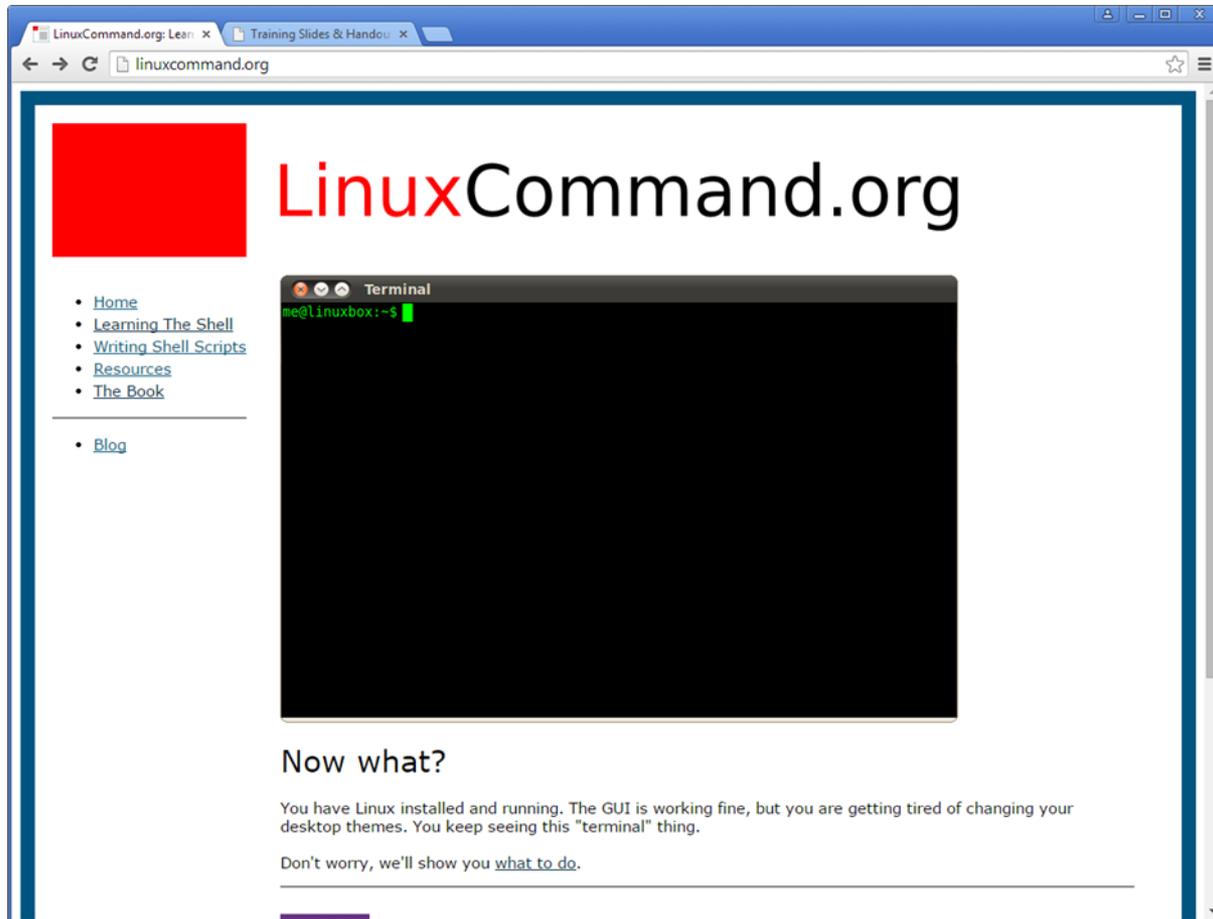
<http://linuxcommand.org/tlcl.php>



500+ pages

\*Some of the materials covered in today's training is from this book

# Study Resources: tutorial website



This is a good place to start...

## Study Resources: websites

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<https://linuxide.com/>

An all-time favorite. Has all sorts of resources.

<https://itsfoss.com/>

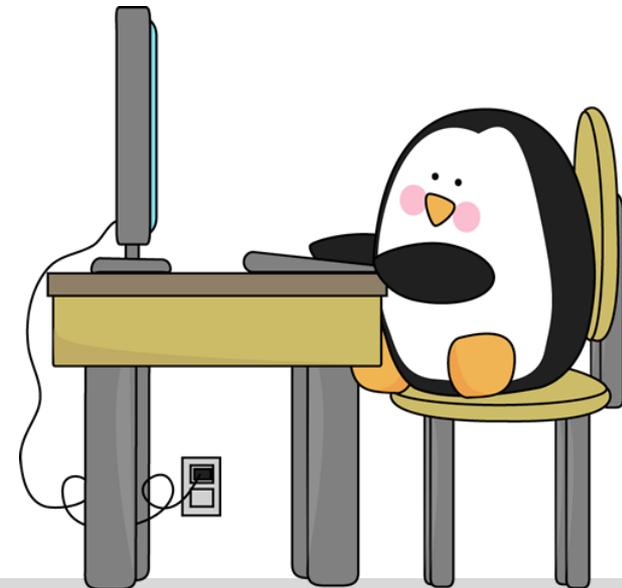
*"...an award-winning web-portal that focuses on Open Source in general and Linux in particular."*

<https://linuxjourney.com/>

Great for learning the basics of Linux!

<https://wizardzines.com/comics/>

Simply awesome!



## Study Resources: follow along...

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You can follow along using:

1. The Nucleus Web terminal on the BioHPC portal (VPN required):

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

2. PuTTY, WSL, MobaXterm or any other SSH client\* from your PC
3. Terminal from your MacBook

**ssh <username>@nucleus.biohpc.swmed.edu**

\*<https://www.smarthomebeginner.com/best-ssh-clients-windows-putty-alternatives/>

# The Terminal



Not too long ago (30+ years ago)...

Computers were primarily found in research centers, business, educational institutions, and libraries.

Access points to these computers were called **terminals**:

- Simple **keyboard** and **monitor** interface;
- Computer may be a small, single unit or part of a larger network;
- Many of these computers ran a licensed **UNIX** operating system developed by AT&T.

```
Terminal
-rwxr-xr-x 1 sys      52850 Jun  8  1979 hptmunix
drwxrwxr-x 2 bin      320 Sep 22 05:33 lib
drwxrwxr-x 2 root     96 Sep 22 05:46 mdec
-rwxr-xr-x 1 root    50990 Jun  8  1979 rkunix
-rwxr-xr-x 1 root    51982 Jun  8  1979 rl2unix
-rwxr-xr-x 1 sys     51790 Jun  8  1979 rpltunix
-rwxr-xr-x 1 sys     51274 Jun  8  1979 rptmunix
drwxrwxrwx 2 root     48 Sep 22 05:50 tmp
drwxrwxr-x12 root    192 Sep 22 05:48 usr
# ls -l /usr
total 11
drwxrwxr-x 3 bin      128 Sep 22 05:45 dict
drwxrwxrwx 2 dmr      32 Sep 22 05:48 dmr
drwxrwxr-x 5 bin      416 Sep 22 05:46 games
drwxrwxr-x 3 sys     496 Sep 22 05:42 include
drwxrwxr-x10 bin     528 Sep 22 05:43 lib
drwxrwxr-x11 bin     176 Sep 22 05:45 man
drwxrwxr-x 3 bin     208 Sep 22 05:46 mdec
drwxrwxr-x 2 bin      80 Sep 22 05:46 pub
drwxrwxr-x 6 root     96 Sep 22 05:45 spool
drwxrwxr-x13 root    208 Sep 22 05:42 src
# ls -l /usr/dmr
total 0
#
```

## Modern Unix Descendants



**GNU/Linux**

**Created by:**

Linus Torvalds  
and

community developers

1991-today

**macOS**

**macOS**

**Created by:**

Apple, Inc.

2001-today



**Android**

**Created by:**

Google

Forked from Linux

2008-today

# What operating system do BioHPC machines primarily run on?

- Red Hat Enterprise Linux (RHEL) 7.6
- GNU/Linux distribution
- Linux Kernel 3.10
- Gnome 3 Desktop Environment
- Bourne-Again Shell (bash)
- Modular environment
- Slurm Workload Manager

```
BASH(1)                                General Commands Manual                                BASH(1)
NAME
    bash - GNU Bourne-Again Shell
SYNOPSIS
    bash [options] [-file]
COPYRIGHT
    Bash is Copyright (C) 1989-2011 by the Free Software Founda-
    tion, Inc.
DESCRIPTION
    * GNU/Linux distribution
    Bash is an sh-compatible command language interpreter that
    executes commands read from the standard input or from a
    file. Bash also incorporates useful features from the Korn
    and C shells (ksh and csh).
    Bash is intended to be a conformant implementation of the
    Shell and Utilities portion of the IEEE POSIX specification
    (IEEE Standard 1003.1). Bash can be configured to be POSIX-
    Manual page bash(1) line 1 (press h for help or q to quit)
```



**Red Hat**

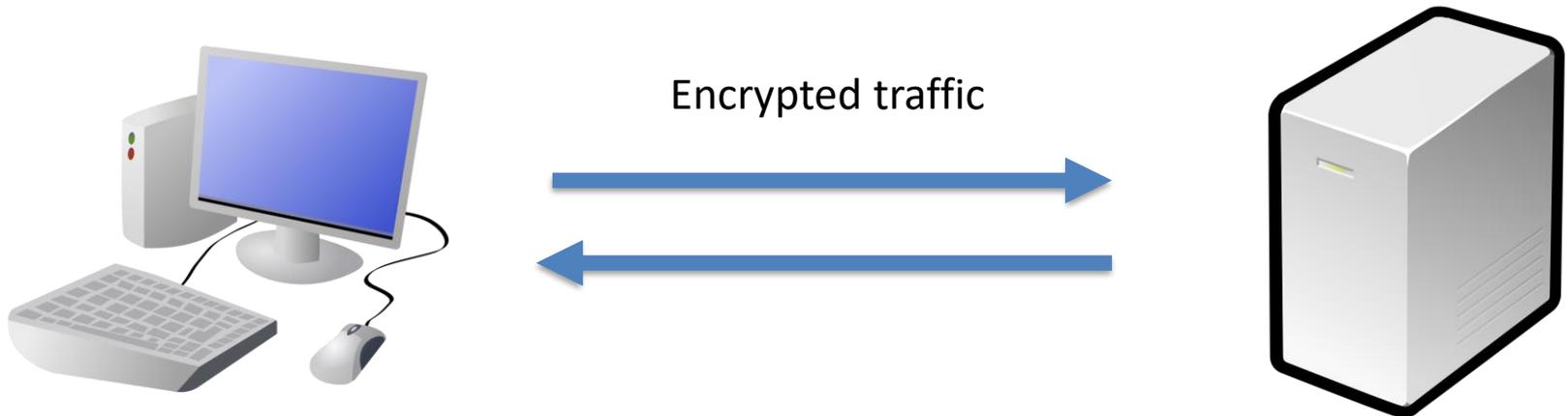
## SSH – Secure Shell

Most of your interactions with the **Nucleus** cluster will likely be through SSH.

Most modern GNU/Linux distributions have an **OpenSSH** client installed by default. Mac OS X also has SSH. **PuTTY** is recommended for MS Windows.

Another option on Windows: use **Windows Subsystem for Linux (WSL)**.

```
$ ssh s191529@nucleus.biohpc.swmed.edu
```



## The Text (Command-Line Interface) Shell

The interaction between user and the operating system is provided by a **shell**.

The shell accepts keyboard commands and hands them off to the operating system.

The BioHPC default shell is *bash* – the *Bourne-Again Shell*.

```
[s191529@Nucleus005 ~]$ echo -n Hello, world!
```

↓  
user

↓  
host name

↓  
working directory

↓  
name of the command

↓  
options/switches

↓  
arguments

# About the shell

JULIA EVANS  
@b0rk

# what's a shell?

a shell reads your commands and tells the OS to do things

ls -l

bash

run "ls", "-l"

Linux

example:  
\$ cd /tmp

bash

hey change my working directory to /tmp!

Linux

example:  
\$ sort file | grep foo

bash

give me a pipe!

bash

now start 2 processes + attach their I/O to the pipe!

now run sort and grep in those processes!

example:  
you press Ctrl+Z

bash

you stopped (SIGSTOP) that process! I'll remember which process and bring it back if you type "fg".

it has a  
\* programming language \*

variables!

for!

if!

while!

shellcheck is a great bash script linter

a few common shells

- bash + sh (always there!)
- zsh (more features!)
- fish (f is for ♥friendly♥) my favourite.

<https://twitter.com/b0rk/>

## Logging into Nucleus – Where Am I?

---

```
[s191529@Nucleus005 ~]$ pwd
```

**pwd** – print working directory

```
/home2/s191529
```

**ls** – list contents of a directory

```
[s191529@Nucleus005 ~]$ ls
```

```
[s191529@Nucleus005 ~]$ ls /home2/s191529
```

```
[s191529@Nucleus005 ~]$ ls ~
```

```
[s191529@Nucleus005 ~]$ ls .
```

## Study Resources: man pages

---

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

```
[s191529@rhel7vm ~]$ man ls
```

Press **q** to exit the man page

Filenames that start with **.** are hidden. You can view them however with the **ls** command and pass the **-a** flag to it (**a** for all).

Try some other Linux commands and see what they output:

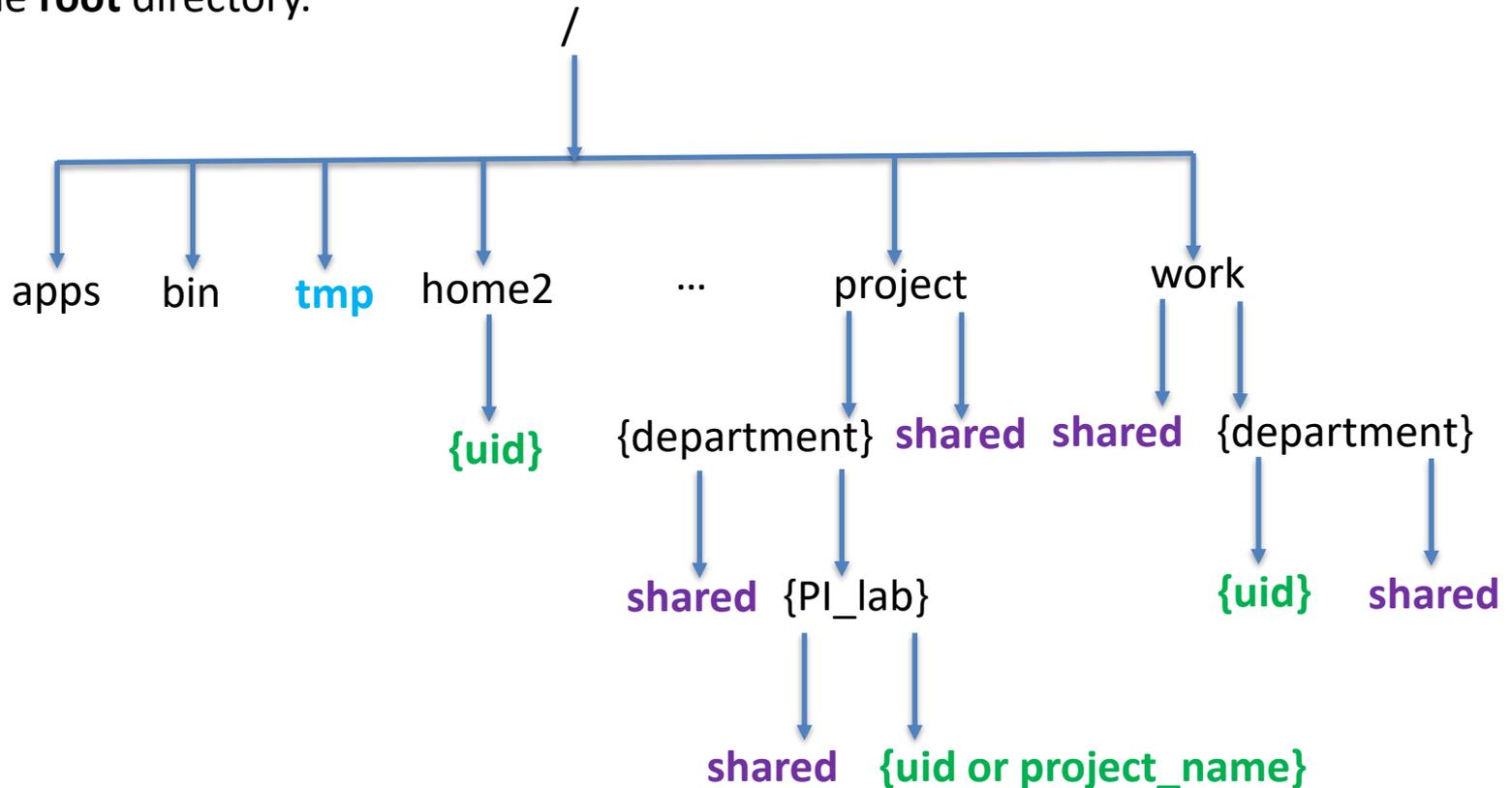
```
[s191529@rhel7vm ~]$ date
```

```
[s191529@rhel7vm ~]$ whoami
```

```
[s191529@rhel7vm ~]$ echo Hello World!
```

# Linux Basics: The File System

**Everything in Linux is a file.** Keep this in mind. Files on a Linux system are arranged in a **hierarchical directory structure**. The first directory in the filesystem is named the **root** directory.



## Navigating the file system

---

How does one change his/her working directory?

**cd** – change directory

```
[s191529@Nucleus005 ~]$ cd /work/biohpcadmin/s191529/
```

```
[s191529@Nucleus005 s191529]$ cd ..
```

```
[s191529@Nucleus005 biohpcadmin]$ cd s191529/
```

### Shortcuts to help you out:

- `.` This is the directory you are currently in.
- `..` Takes you to the directory above your current one.
- `~` This directory defaults to your home directory.
- `-` This will take you to the previous directory you were just at.
- Finally, the **Up Arrow** brings the last command you hit.

## Linux Command Line: Files and Directories

Files and directories may be referenced by an absolute or relative path

- **Absolute path**—specify the location of a file or directory from / (the root directory)

```
[s191529@Nucleus005 ~]$ cd /project/biohpcadmin
```

**Pros: you know exactly where you are going!**

**Cons: tedious if there are many nested folders.**

- **Relative path**— paths relative to your working directory.

```
[s191529@Nucleus005 biohpcadmin]$ cd s191529
```

```
[s191529@Nucleus005 s191529]$ cd ..
```

## Determining your storage quota

```
[s191529@Nucleus005 ~]$ quota -s
```

Disk quotas for user s191529 (uid 191529):

Filesystem	space	quota	limit	grace	files	quota	limit	grace
lysosomehome:/home2	21581M	51200M	71680M		153k	0	0	

```
[s191529@Nucleus005 ~]$ lfs quota -g 1001 /project -h
```

Disk quotas for grp 1001 (gid 1001):

Filesystem	used	quota	limit	grace	files	quota	limit	grace
/project	17.59T	0k	0k	-	12021829	0	0	-

How does one find the **gid**?

```
[s191529@Nucleus005 ~]$ id 191529
```

## How much storage is a directory occupying?

```
[s191529@Nucleus005 ~]$ ls -l Documents/misc/
```

How much space does this directory, and all its contents use?

**du** – disk usage (**-h** – human readable; **-s** – summarize)

```
[s191529@Nucleus005 ~]$ du -hs Documents/misc/
```

How can I create a new (empty) file?

**touch**

```
[s191529@Nucleus005 misc]$ touch myfile.txt
```

The command **touch** can also be used to change timestamps.

What kind of file a file is?

**file**

```
[s191529@Nucleus005 misc]$ file myfile.txt
```

In Linux, file extensions aren't required.

## Exploring the file system

---

```
[s191529@Nucleus005 ~]$ cd /project/shared/biohpc_training
```

Let's concatenate the contents of a file to the standard output of the terminal.  
In other words, let's print to the terminal:

```
[s191529@Nucleus005 biohpc_training]$ cat c475_r0ck_4m_1_r16h7.txt
```

**Notice:** not all files have an extension:

```
[s191529@Nucleus005 biohpc_training]$ file RJ_WS
```

Wish to clear the terminal?

```
[s191529@Nucleus005 biohpc_training]$ clear
```

```
[s191529@Nucleus005 biohpc_training]$ reset
```



Bash has a very useful auto-completion shortcut for typing commands more quickly.

Give it a try!

Type:

```
cd /project/shared/biohpc_training  
cat c475_r0ck_4m_1_r16h7.txt
```

## Viewing large text files

A file does not have to be very large before concatenating them to the standard output becomes unhelpful. The file extension has a **.fastq.gz** file extension, but what does **file** produce?

```
[s191529@Nucleus005 biohpc_training]$ file HD728.R1.fastq.gz
```

The file is a compressed file – its contents are unreadable to us. Let's decompress the file first using **gzip**.

```
[s191529@Nucleus005 biohpc_training]$ file HD728.R1.fastq.gz
```

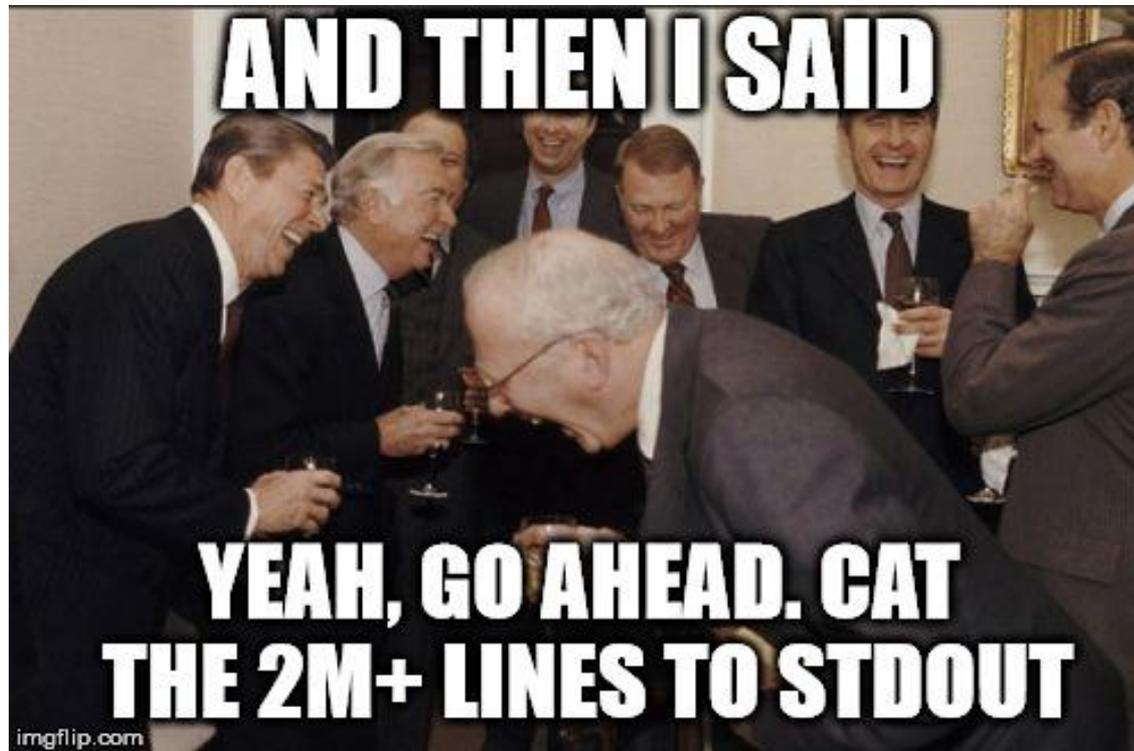
```
[s191529@Nucleus005 biohpc_training]$ gzip -cd HD728.R1.fastq.gz >  
HD728.R1.fastq
```

### Exercise

Using the program **wc**, count how many lines of text are inside **HD728.R1.fastq**?  
How would one access information on how to use this program?



## Interrupting a Running Program



What happens if I need to kill a program that is running?  
Pressing **CTRL + C** will send an interruption signal (SIGINT) to the program which usually kills it. If not...

```
[s191529@Nucleus005 biohpc_training]$ man kill
```

## Head, Tail, More, Less

Not always practical to print an entire file to the shell. Use these commands:

**head** – print the first 10 lines of each file to the standard output

**tail** – print the last 10 lines of each file to the standard output

```
[s191529@Nucleus005 biohpc_training]$ head HD728.R1.fastq
```

### Exercise

Print the first 50 lines of **HD728.R1.fastq**! Hint: **man head**

You can navigate through a text file page by page with **less**:

```
[s191529@Nucleus005 biohpc_training]$ less HD728.R1.fastq
```

To navigate through **less**:

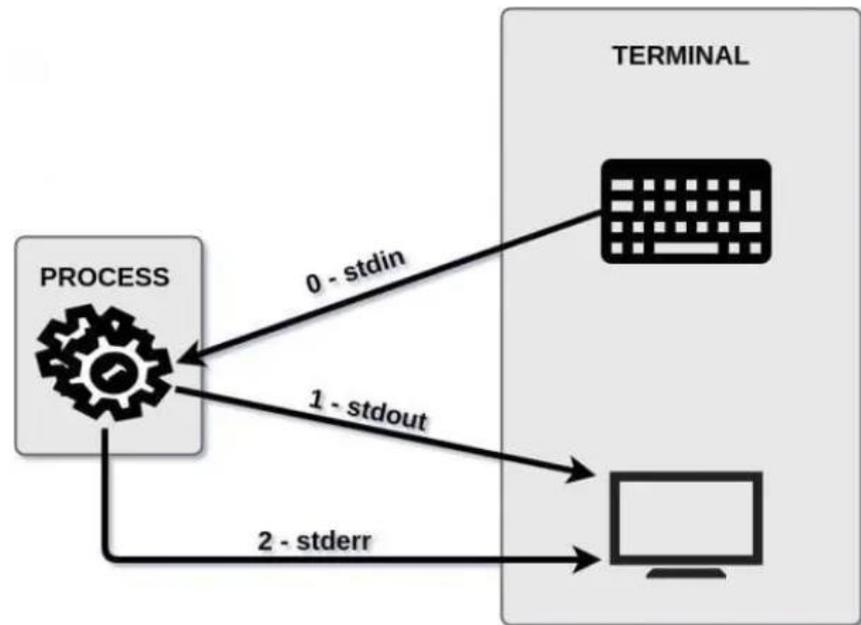
- **q** – to quit out of less
- **Page up/down, Up/Down** – to navigate
- **g/G** - moves to the beginning/end of the text file
- **/text** - search for specific **text**
- **h** – If you need a little help about how to use less while you're in less, use help.

## Standard Streams

**Streams** are usually connected to the terminal in which they are executed, but that can be changed using **redirection operators** and/or **pipes**.

**Redirection operators** are a subset of control operators. They allow you to direct the input or output (stream) of your command.

The **pipe** operator is used to pass the output of a command to the input of another command. The vertical bar ( | ) represents this operator.



## Redirection Operators

A simple example of a program that uses **standard input** is the **cat** command. Standard input can also come from an input file:

```
[s191529@Nucleus005 biohpc_training]$ cat ~/.bashrc
```

You can use **input redirection** (represented by **<**) to achieve the same results as above:

```
[s191529@Nucleus005 biohpc_training]$ cat < ~/.bashrc
```

You can redirect **standard output** to a file (represented by **>**). This is useful if you want to save the output for later use, or as a log of a script:

```
[s191529@Nucleus005 biohpc_training]$ cat ~/.bashrc > bashrc.txt
```

Use the **output append operator** (represented by **>>**) if you want to append to an existing file:

```
[s191529@Nucleus005 biohpc_training]$ stat ~/.bashrc >> bashrc.txt
```

## File Descriptors

Linux often represents the three standard streams as file descriptors:

File Descriptor	Name	Standard Stream
0	Standard Input	stdin
1	Standard Output	stdout
2	Standard Error	stderr

Let's try the **standard error**:

```
[s191529@Nucleus005 biohpc_training]$ ls -l /bin/usr
```

We can redirect the **standard error** to a file:

```
[s191529@Nucleus005 biohpc_training]$ ls -l /bin/usr 2> error.txt
```

You can redirect **stderr** and **stdout** to a single file (two ways):

```
[s191529@Nucleus005 biohpc_training]$ ls -l /bin/usr > error.txt 2>&1
```

```
[s191529@Nucleus005 biohpc_training]$ ls -l /bin/usr &> error.txt
```

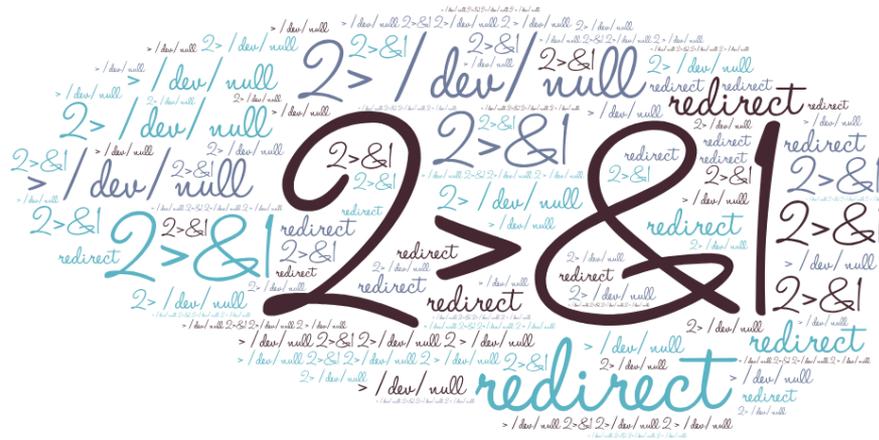
## Redirecting to /dev/null

What if I **don't care at all** about the **stdout** and **stderr**?

```
[s191529@Nucleus005 biohpc_training]$ ls -l /bin/usr > /dev/null 2>&1
```

```
[s191529@Nucleus005 biohpc_training]$ ls -l /bin/usr &> /dev/null
```

*“To begin, **/dev/null** is a special file called the null device in Unix systems. Colloquially it is also called the **bit-bucket** or the **blackhole** because it immediately discards anything written to it and only returns an end-of-file (EOF) when read.”*



# Text Editors



## Vim

Cryptic commands! Cheat sheet on the portal.

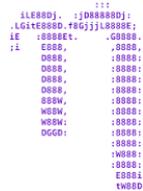
Quick tutorial: <http://www.washington.edu/computing/unix/vi.html>



## Emacs

An extensible, customizable text editor.

Quick tutorial: <http://www.gnu.org/software/emacs/tour/>



## nano

Easier to use.

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

## Any text editor from your PC or Mac.

Mount your directories as network drives:

<https://portal.biohpc.swmed.edu/content/guides/biohpc-cloud-storage/>

# Permissions

JULIA EVANS  
@bork

## unix permissions

4

There are 3 things you can do to a file

↓ read ↓ write ↓ execute

ls -l file.txt shows you permissions. Here's how to interpret the output:

```
rw- rw- r-- bork staff
  ↑   ↑   ↑
  bork (user) staff (group) ANYONE
  can can can
  read & write read & write read
```

File permissions are 12 bits

```
setuid setgid
  ↓   ↓
000 user group all
  ↑   ↓   ↓   ↓
sticky rwx rwx rwx
```

For files:

- r = can read
- w = can write
- x = can execute

For directories, it's approximately:

- r = can list files
- w = can create files
- x = can cd into & access files

110 in binary is 6

```
So rw- r-- r--
= 110 100 100
= 6 4 4
```

chmod 644 file.txt  
means change the permissions to:

```
rw- r-- r--
simple!
```

setuid affects executables

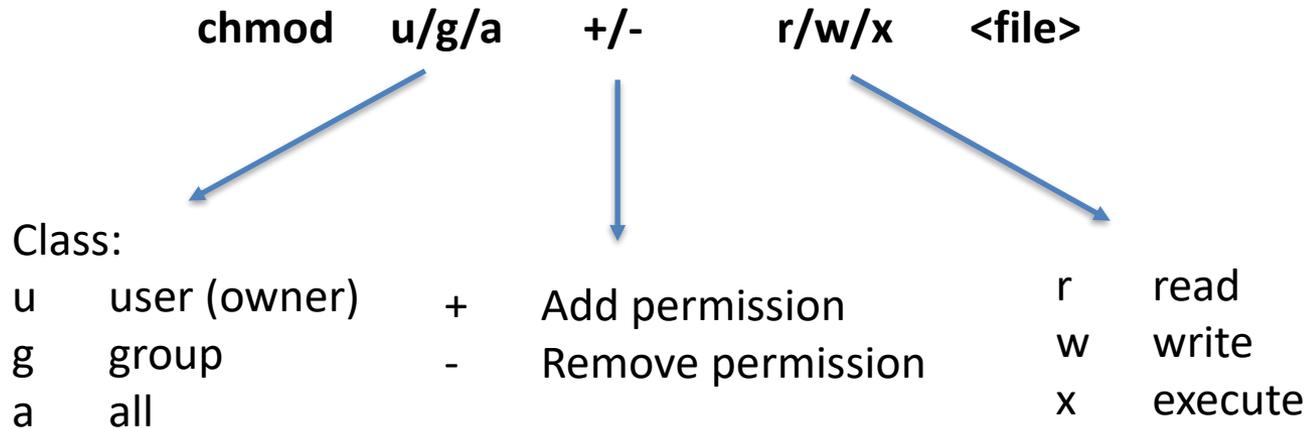
```
$ls -l /bin/ping
-rws r-x r-x root root
  ↑
this means ping always runs as root
```

setgid does 3 different unrelated things for executables, directories, and regular files.



<https://wizardzines.com/comics/permissions/>

# Permissions



## Examples:

```
chmod g+rw script.sh # Add read/write permissions for the group
chmod a+x script.sh # Add execute permission for everyone
chmod g-x script.sh # Remove execute permission for the group

chmod 700 script.sh # ?
chmod 640 script.sh # ?
```

## Copying data

First, let's create an empty directory with **mkdir**:

```
[s191529@Nucleus005 biohpc_training]$ mkdir -p  
/project/biohpcadmin/shared/cuda_samples
```

Copy everything recursively (**-r**) from **source** to **destination**:

```
[s191529@Nucleus005 biohpc_training]$ cp -r ~/cuda_samples/*  
/project/biohpcadmin/shared/cuda_samples/
```

We can copy the entire folder recursively:

```
[s191529@Nucleus005 biohpc_training]$ cp -r ~/cuda_samples  
/project/biohpcadmin/shared/cuda_samples
```

If you copy a file over to a directory that has the same filename, the file will be overwritten with whatever you are copying over. You can use the **-i** flag (interactive) to prompt you before overwriting a file. By default, **cp** will apply your ownership and primary group to files.

## Moving data

---

Very similar to the copy command. You can rename a file (or a directory) with **mv**:

```
[s191529@Nucleus005 biohpc_training]$ mv foo.txt blah.txt
```

And of course, we can move things from **source** to **destination**:

```
[s191529@Nucleus005 biohpc_training]$ mv blah.txt foo.bar /somedir
```

If you don't want to overwrite anything:

```
[s191529@Nucleus005 biohpc_training]$ mv -i foo.txt blah.txt
```

Note that **mv** will attempt to preserve original permissions. You can also make a backup of that file and it will just rename the old version with a **~**:

```
[s191529@Nucleus005 biohpc_training]$ mv -b /somedir /newdir
```

## Deleting Files

- Be very cautious of your ability to destroy files!
- There is **no Recycling Bin** to restore your files.
- Once files are deleted by the CLI, it is generally very difficult to recover them.
- Make sure important data is backed up! The command to remove things is **rm**, and it's very similar to **cp** and **mv**.



To delete everything in a folder:

```
[s191529@Nucleus005 biohpc_training]$ rm somedir/*
```

To delete a folder recursively:

```
[s191529@Nucleus005 biohpc_training]$ rm -r somedir
```

Try deleting things interactively (recommended):

```
[s191529@Nucleus005 biohpc_training]$ rm -i somedir/*
```

## Wildcards

---

\* 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 *2019*</code>	Any file with 2015 somewhere in its name

? Match a single character:

<code>ls data_00?.txt</code>	Matches <code>data_001</code> , <code>data_002</code> , <code>data_00A</code> , etc.
------------------------------	--

[] Match a set of characters (bracket expression):

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

## History

---

There is a history of the commands that you previously entered. This is useful as you can look through these commands:

```
[s191529@Nucleus005 biohpc_training]$ history
```

To run the previous command without typing it again, hit **!!**. Another history shortcut is **Ctrl-R**, this is the reverse search command, if you hit **Ctrl-R** and you start typing parts of the command you want it will show you matches and you can just navigate through them by hitting the **Ctrl-R** key again. Once you found the command you want to use again, just hit the **Enter** key.

To find out what a command does, try using **whatis**:

```
[s191529@Nucleus005 biohpc_training]$ whatis cat
```

## Environmental Variables – Controlling the behavior of the Shell

Several variables control the behavior of the shell. You can print all these variables with:

```
$ env
```

Or print them individually:

```
$ echo $SHELL  
/bin/bash
```

```
$ echo $HOME  
/home2/s191529
```

```
$ echo $USER  
s191529
```

**\$PATH** variable is one of the most important and tells the shell where your programs are:

```
$ echo $PATH  
/home2/s191529/.local/bin:/cm/shared/apps/slurm/16.05.8/sbin:/cm/shared/apps/slurm/16.05.8/bin:/usr/local/bin
```

The module system on BioHPC modifies this **\$PATH** so that programs are made available to the user. One can also manually edit their **\$PATH**

```
$ export  
PATH=/home2/s191529/bin:$PATH
```

## Overview of commands used

Command	Full Name	Description
man	manual	man <command> opens manual for a command
ssh	secure shell	opens a remote shell on a server
echo	echo	prints statement to standard output
pwd	print working directory	prints current working directory
cd	change directory	change to specified directory
ls	list	list contents of a directory
file	file	determines type of file
cat	concatenate	concatenates files to standard output
head	head	prints the top n-lines of a text file
tail	tail	prints the bottom n-lines of a text file
history	command history	outputs previously hit commands
less	less	like more, but allows backwards traversal of a file
du	disk usage	calculate disk usage of a file or folder
vi	vi text editor	simple text editor
cp	copy	copy a file or directory from a source to a destination
mv	move	moves a file from a directory from a source to a destination
rm	remove	deletes a file or a directory
chmod	change mode	modifies permissions of a file or directory



KEEP  
CALM  
AND  
LEARN  
LINUX