

Setting hardware/software baseline skills



Class Content

- Introduction to Virtual Machines, Containers
- Terminals & file system navigation
- Anatomy of a UNIX command
- Wildcards, shortcuts and special characters
- File permissions
- Compression UNIX commands
- Networking UNIX commands



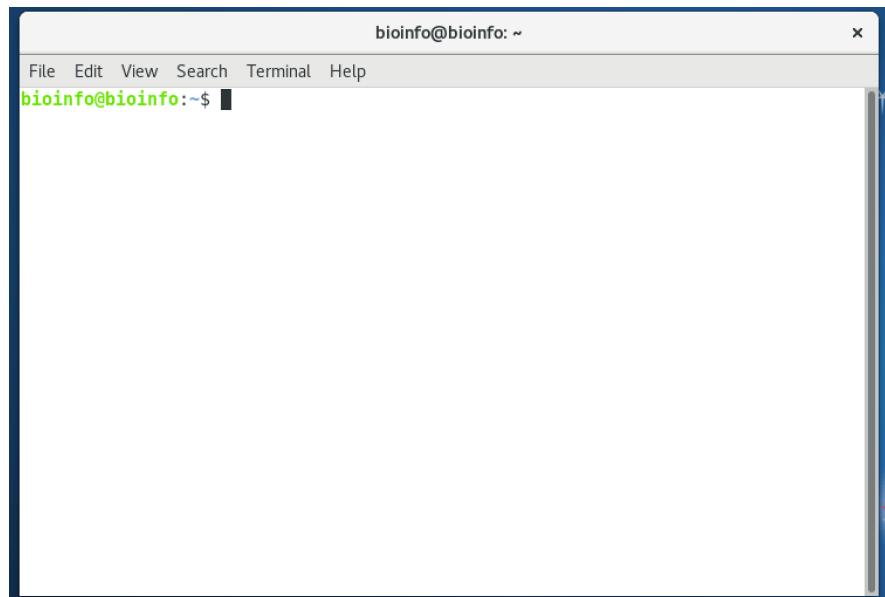
What is a Virtual Machine?

- A VM is an operating system which has been installed inside a simulated environment.
- Unlike emulators, virtual machines interface with real hardware.



What is a Terminal?

- A terminal is a textual interface for interacting with a computer.
- Using the terminal, one can issue powerful and concise command-line instructions for the computer to follow.



Why use the command-line (terminal)?

- Most software for biological data analysis is used through UNIX command-line operations.
- Most of the servers for biological data analysis use Linux/Unix as their operating system.
- Data analysis on calculation servers are much faster since we can use more CPUs and RAM than in a PC or laptop (*e.g.* BTI's "Boyce" server has 64 cores and 1TB RAM)
- Large NGS data files can not be opened or loaded in most graphical software and web sites.



We will use CyVerse tools today

About CyVerse

Vision: Transforming Science through Data-Driven Discovery

Mission: To design, deploy, and expand a national Cyberinfrastructure for Life Sciences research, and to train scientists in its use.

CyVerse provides life scientists with powerful computational infrastructure to handle huge datasets and complex analyses, thus enabling data-driven discovery. Our extensible platforms provide data storage, bioinformatics tools, data visualization, interactive analyses, cloud services, APIs, and more.

CyVerse is funded by the National Science Foundation's Directorate for Biological Sciences. We are a dynamic virtual organization, led by the University of Arizona in partnership with the Texas Advanced Computing Center and Cold Spring Harbor Laboratory, fulfilling a broad mission to enable data-driven, collaborative research.

Let's log in to CyVerse!

The screenshot shows the CyVerse User Portal homepage at user.cyverse.org/services/mine. The top navigation bar includes links for SERVICES, POWERED BY, HELP RESOURCES, FORMS, WORKSHOPS, and a user profile for 'srs57'. Below the navigation, there are two tabs: 'MY SERVICES' (which is selected) and 'AVAILABLE'. Four service cards are displayed:

- Atmosphere**: Cloud computing platform for CyVerse. [LAUNCH](#)
- CoGe**: Online system for quick and easy retrieval and comparison of genomic information and sequences. [LAUNCH](#)
- Data Commons**: A unified system for managing and sharing your data across CyVerse's tools and services. [LAUNCH](#)
- Discovery Environment**: Use hundreds of bioinformatics apps and manage data in the CyVerse Data Store from a simple web interface. [LAUNCH](#)



Your Atmosphere Instance is Available ➔ Inbox X

Atmosphere Admin atmo-notify@cyverse.org via cornellprod.onmicrosoft.com
to Susan, Atmosphere ▾

Hello Susan Strickler,

The CyVerse instance <Botany2020NMGWorkshop> is running and ready for use.

Your Instance Information:

- * Name: Botany2020NMGWorkshop
- * IP Address: 128.196.142.98
- * SSH Username: srs57
- * SSH Keys deployed for root:
- * UUID: 030b816e-5b25-4c9a-9fd2-232d9be4bb92
- * Cloud Provider: CyVerse Cloud - Marana
- * Launched at: Jul, 23 2020 00:52:16 UTC (Jul, 22 2020 17:52:16 Arizona time)

This e-mail notification was auto-generated after instance launch.

Helpful links:

Getting Started with a new Instance

- * <https://pods.iplantcollaborative.org/wiki/display/atmman/Using+Instances>

Atmosphere FAQs

- * <https://cyverse-learning-center-faq.readthedocs-hosted.com/en/latest/atmosphere-faq.html>

E-mail Support:

- * Atmosphere RT &[<intercom-atmo@cyverse.org>](mailto:intercom-atmo@cyverse.org);

CyVerse Atmosphere Team

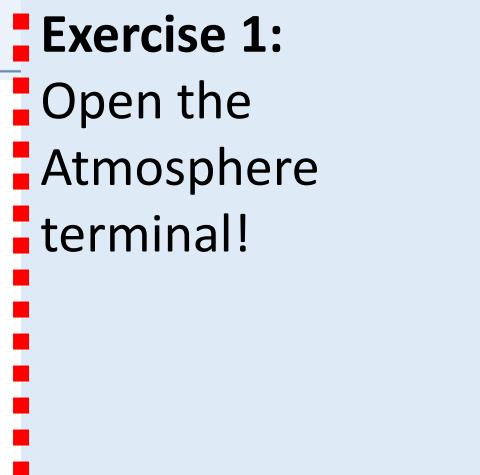


Search...

[Services](#) [Learning](#) [Launch](#) [About](#) [Log In](#) | [Sign Up](#)

Atmosphere

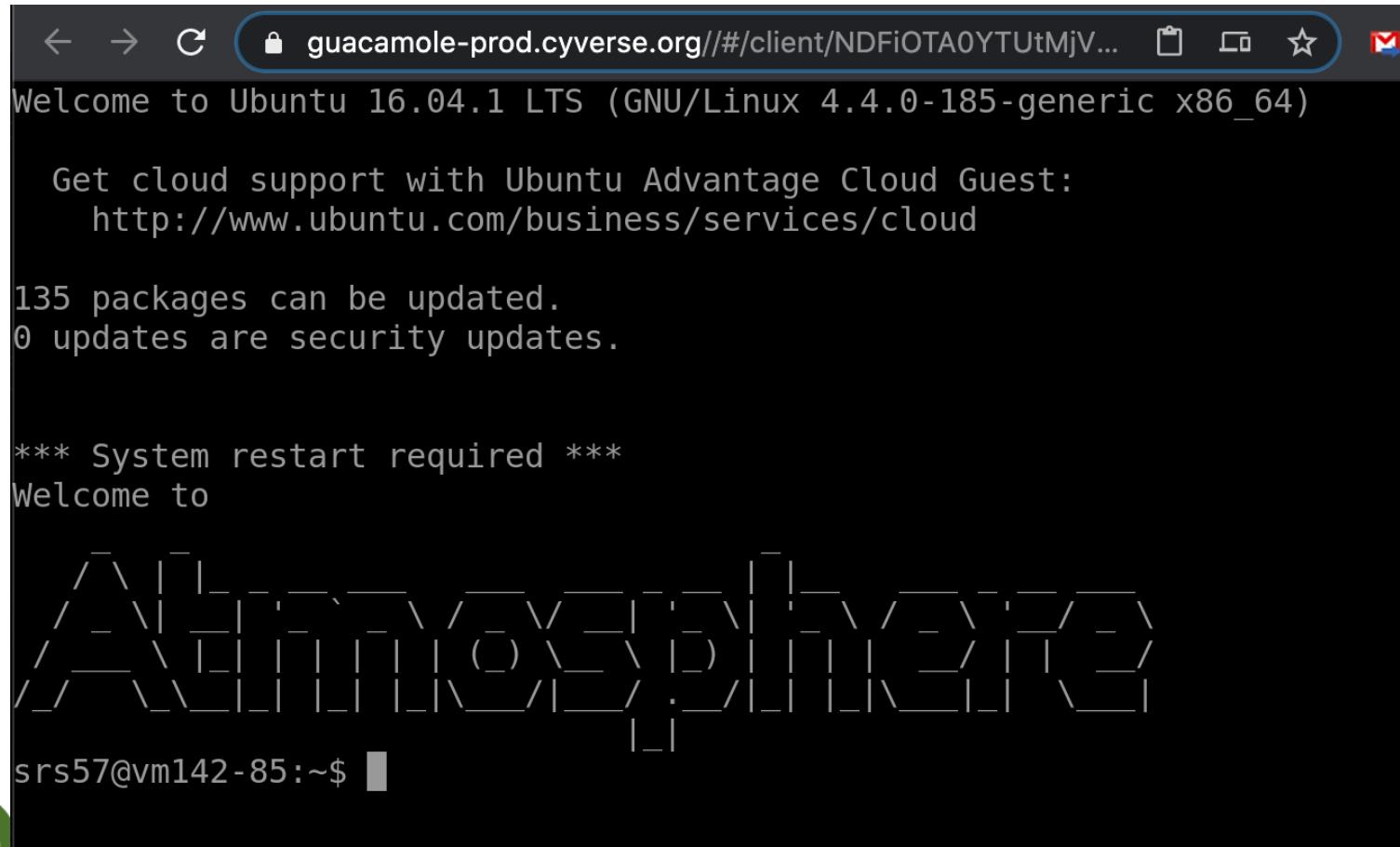
A cloud-based resource offering customizable virtual machine images for specific learning or analysis goals.

[Launch](#)[Manual](#)[Tutorials](#)**Exercise 1:**

Open the
Atmosphere
terminal!



Atmosphere terminal



← → C 🔒 guacamole-prod.cyverse.org//#/client/NDFiOTA0YTUtMjV... 🛍️ 🖥 ☆ 📧

Welcome to Ubuntu 16.04.1 LTS (GNU/Linux 4.4.0-185-generic x86_64)

Get cloud support with Ubuntu Advantage Cloud Guest:
<http://www.ubuntu.com/business/services/cloud>

135 packages can be updated.
0 updates are security updates.

*** System restart required ***

Welcome to

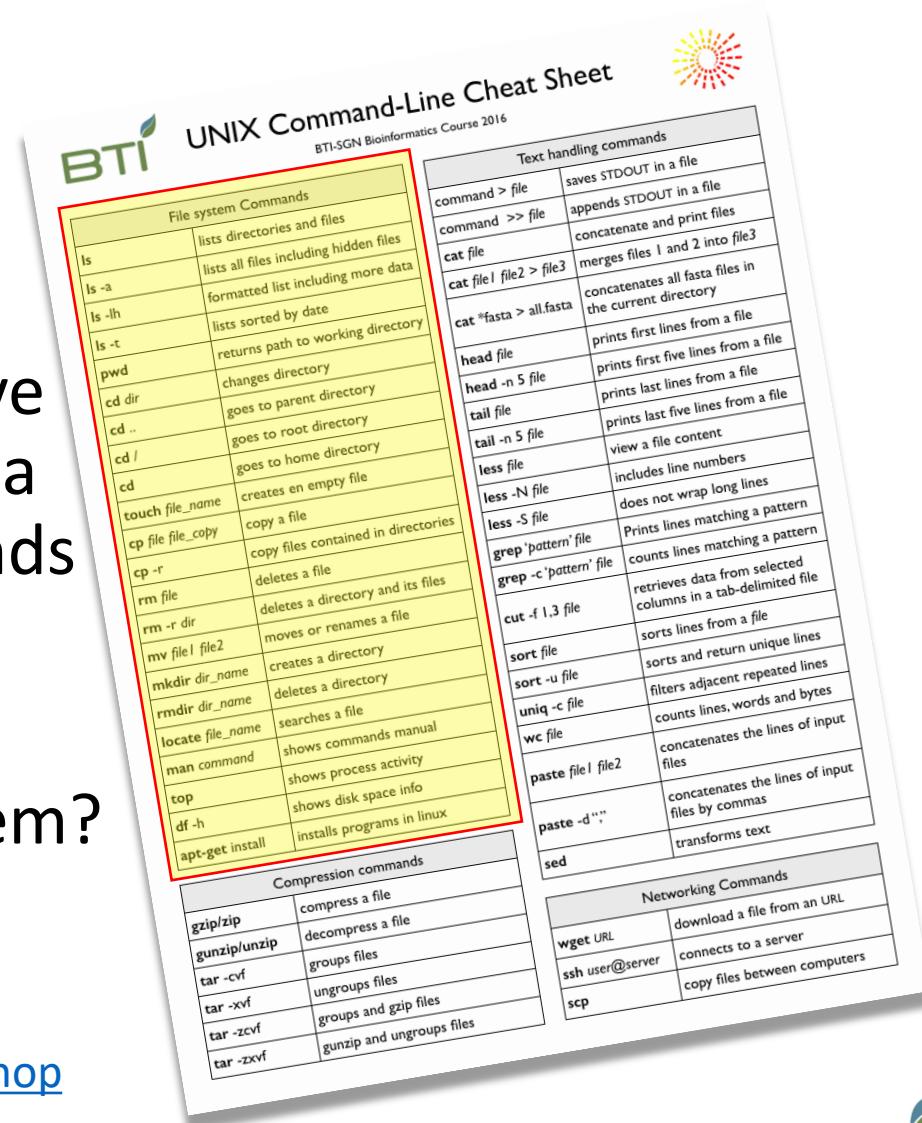
srs57@vm142-85:~\$ █



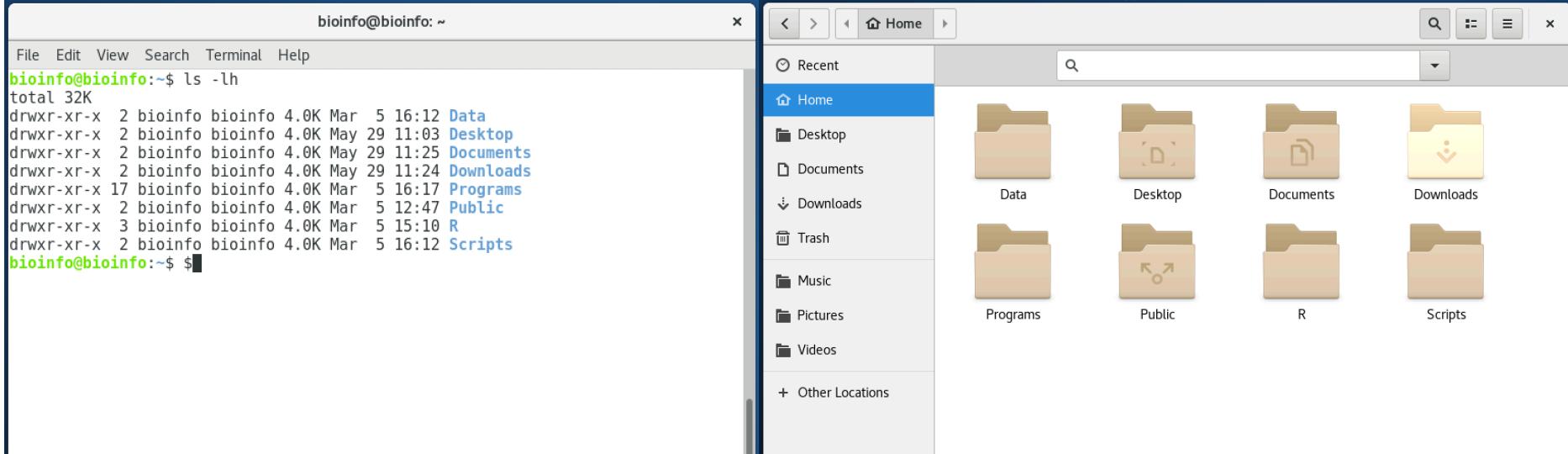
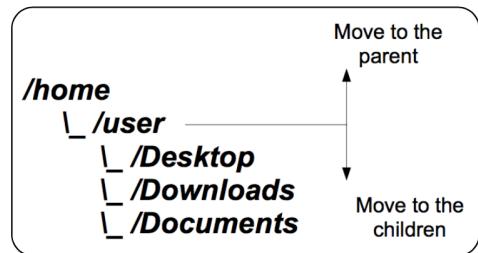
Command-line File System Navigation.

- The cheat sheet you have been provided contains a list of common commands for navigating the file system.
- But what *is* the file system?

<https://github.com/bcbc-group/Botany2020NMGWorkshop>



The File System



Exercise 2:

Type “ls -lh” into the terminal and press enter.



Home and Root Directories

```
Noes-MacBook-Pro:~ Noe$ ls -lht
total 0
drwx-----+ 29 Noe  staff  986B May 31 11:24 Desktop
drwx-----@  8 Noe  staff  272B May 31 08:26 Dropbox
drwx-----+ 54 Noe  staff  1.8K May 30 16:01 Downloads
drwx-----+  8 Noe  staff  272B May 28 21:06 Pictures
drwxr-xr-x  18 Noe  staff  612B May 17 11:12 BTI
drwxr-xr-x  5 Noe  staff  170B May  8 11:44 programs
drwx-----+ 15 Noe  staff  510B Apr 10 08:33 Documents
drwxr-xr-x  6 Noe  staff  204B Mar 18 09:22 VirtualBox VMs
drwxr-xr-x  8 Noe  staff  272B Mar 14 19:26 py_devel
drwx-----@ 51 Noe  staff  1.7K Mar 11 15:08 Library
```

Home directory

/home/bioinfo
/home/noe
/home/noe/Desktop

```
noe@debian-virtualbox:~$ ls -l /
total 108
drwxr-xr-x  2 root root  4096 Sep 26  2012 bin
drwxr-xr-x  3 root root  4096 Nov  9  2012 boot
drwxr-xr-x  15 root root  3140 May 31 12:46 dev
drwxr-xr-x 130 root root 12288 May 31 12:45 etc
drwxr-xr-x  5 root root  4096 Feb 28 13:54 export
drwxr-xr-x  4 root root  4096 Nov  7  2012 home
lrwxrwxrwx  1 root root   30 Sep 26  2012 initrd.img
drwxr-xr-x 12 root root 12288 Nov  9  2012 lib
drwxr-xr-x  2 root root 12288 Nov  9  2012 lib32
lrwxrwxrwx  1 root root   4 Sep 26  2012 lib64 -> /1
drwxr-xr-x  2 root root 16384 Sep 26  2012 lost+found
drwxr-xr-x  3 root root  4096 Sep 26  2012 media
drwxr-xr-x  2 root root  4096 May  1  2012 mnt
drwxr-xr-x  2 root root  4096 Sep 26  2012 opt
dr-xr-xr-x 134 root root     0 May 31 12:45 proc
drwxr-xr-x  10 root root  4096 Nov 15  2012 root
drwxr-xr-x  2 root root  4096 Nov  9  2012 sbin
drwxr-xr-x  2 root root  4096 Jul 21  2010 selinux
drwxr-xr-x  2 root root  4096 Sep 26  2012 srv
drwxr-xr-x  13 root root     0 May 31 12:45 sys
drwxrwxrwt  11 root root  4096 May 31 19:56 tmp
drwxr-xr-x  11 root root  4096 Sep 26  2012 usr
drwxr-xr-x  14 root root  4096 Sep 26  2012 var
```

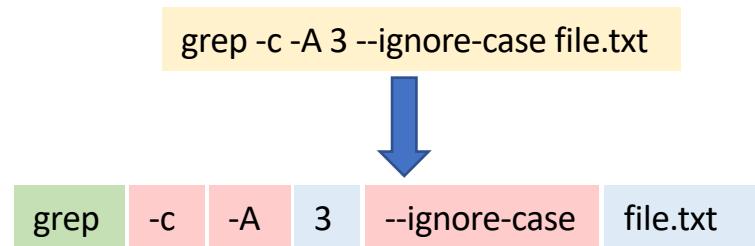
Root directory

/bin, /lib, /usr code and code libraries
/var logs and other data
/home user directories
/tmp temporary files
/etc configuration information
/proc special file system in Linux



Anatomy of a UNIX Command

- Every UNIX command is made up of a series of space-separated strings.
- The first of these strings is always the command you will run.
- The user can also provide options (shown in red) and arguments (shown in blue)
- A command can require arguments, as can an option.
- In this example, the “-A” option is being given the argument “3” and the command is being given the argument “file.txt”



- Options often have a short form (starting with “-”) and a long form (starting with “--”).
- If an option flag does not have any arguments, then can often be concatenated
(e.g. “`ls -h -l -a`” is equivalent to “`ls -hla`”)



`pwd`, `ls`, and `cd`

- **`pwd`** — where am I?
- **`ls`** — what is inside the current directory?
- **`cd`** — change my current directory.

Exercise 3:

Change into the “/opt/” directory and list the files found there.



ls lists files and directories

list directories and files in current directory

list all directories and files, including hidden files

```
ls
```

```
ls -a
```

```
ls -l -h
```

```
ls -l -h -t
```

```
ls -lhS
```

list in long format

human readable

time sorted

size sorted

```
Noe-MacBook-Pro:~ Noe$ ls -lht
total 0
drwx-----+ 29 Noe staff 986B May 31 11:24 Desktop
drwx-----@ 8 Noe staff 272B May 31 08:26 Dropbox
drwx-----+ 54 Noe staff 1.8K May 30 16:01 Downloads
drwx-----+ 8 Noe staff 272B May 28 21:06 Pictures
drwxr-xr-x 18 Noe staff 612B May 17 11:12 BTI
drwxr-xr-x 5 Noe staff 170B May 8 11:44 programs
drwx-----+ 15 Noe staff 510B Apr 10 08:33 Documents
drwxr-xr-x 6 Noe staff 204B Mar 18 09:22 VirtualBox VMs
drwxr-xr-x 8 Noe staff 272B Mar 14 19:26 py-devel
drwx-----@ 51 Noe staff 1.7K Mar 11 15:08 Library
drwxr-xr-x 6 Noe staff 204B Nov 28 2012 PTA
drwx-----+ 4 Noe staff 136B Sep 26 2012 Music
drwx-----+ 3 Noe staff 102B Sep 26 2012 Movies
drwxr-xr-x+ 4 Noe staff 136B Sep 26 2012 Public
```



The ls list output

permissions	links #	owner user	owner group	size	date	File name
drwx-----	29	Noe	staff	986B	May 31 11:24	Desktop
drwx-----	8	Noe	staff	272B	May 31 08:26	Dropbox
drwx-----	54	Noe	staff	1.8K	May 30 16:01	Downloads
drwx-----	8	Noe	staff	272B	May 28 21:06	Pictures
drwxr-xr-x	18	Noe	staff	612B	May 17 11:12	BTI
drwxr-xr-x	5	Noe	staff	170B	May 8 11:44	programs
drwx-----	15	Noe	staff	510B	Apr 10 08:33	Documents
drwxr-xr-x	6	Noe	staff	204B	Mar 18 09:22	VirtualBox VMs
drwxr-xr-x	8	Noe	staff	272B	Mar 14 19:26	py_devel
drwx-----	51	Noe	staff	1.7K	Mar 11 15:08	Library
drwxr-xr-x	6	Noe	staff	204B	Nov 28 2012	PTA
drwx-----	4	Noe	staff	136B	Sep 26 2012	Music
drwx-----	3	Noe	staff	102B	Sep 26 2012	Movies
drwxr-xr-x	4	Noe	staff	136B	Sep 26 2012	Public

group

user

other

drwx r-X r-X

d Directory
- Regular file

r readable

w writable

x executable or searchable

- not rwx



- Exercise 4:
- List ALL files present in
- the root directory
- (including hidden files)

```
bioinfo@bioinfo: ~
File Edit View Search Terminal Help
bioinfo@bioinfo:~$ ls -lh /
total 92K
drwxr-xr-x  2 root root 4.0K May 29 11:07 bin
drwxr-xr-x  3 root root 4.0K Mar  5 12:41 boot
drwxr-xr-x 18 root root 3.0K Jun 13 13:46 dev
drwxr-xr-x 132 root root 12K Jun 13 22:17 etc
drwxr-xr-x  3 root root 4.0K Mar  5 12:45 home
lrwxrwxrwx  1 root root  29 Mar  5 12:20 initrd.img -> boot/initrd.img-4.9.0-4
-amd64
lrwxrwxrwx  1 root root  29 Mar  5 12:20 initrd.img.old -> boot/initrd.img-4.9
.0-4-amd64
drwxr-xr-x 16 root root 4.0K Mar  5 12:40 lib
drwxr-xr-x  2 root root 4.0K Mar  5 12:20 lib64
drwx-----  2 root root 16K Mar  5 12:19 lost+found
drwxr-xr-x  3 root root 4.0K Mar  5 12:19 media
drwxr-xr-x  2 root root 4.0K Mar  5 12:20 mnt
drwxr-xr-x  3 root root 4.0K May 29 10:53 opt
dr-xr-xr-x 156 root root   0 Jun 13 13:46 proc
drwx-----  6 root root 4.0K May 29 10:49 root
drwxr-xr-x 22 root root  660 Jun 13 22:17 run
drwxr-xr-x  2 root root 12K May 29 11:07 sbin
drwxr-xr-x  2 root root 4.0K Mar  5 12:20 srv
dr-xr-xr-x 13 root root   0 Jun 13 16:19 sys
drwxrwxrwt 14 root root 4.0K Jun 13 22:45 tmp
```



Wildcards, Shortcuts, and Command History

```
ls *txt
```

list all txt files in current directory

```
ls P*s
```

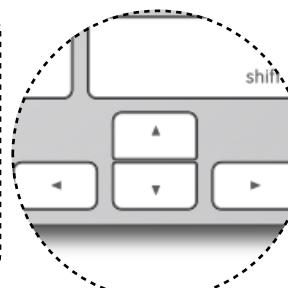
list files starting with P and ending with s,
e.g.: Pictures, Photos, Programs ...

ctrl-c stop process

ctrl-a go to begin of line

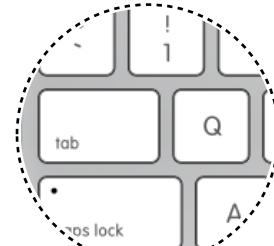
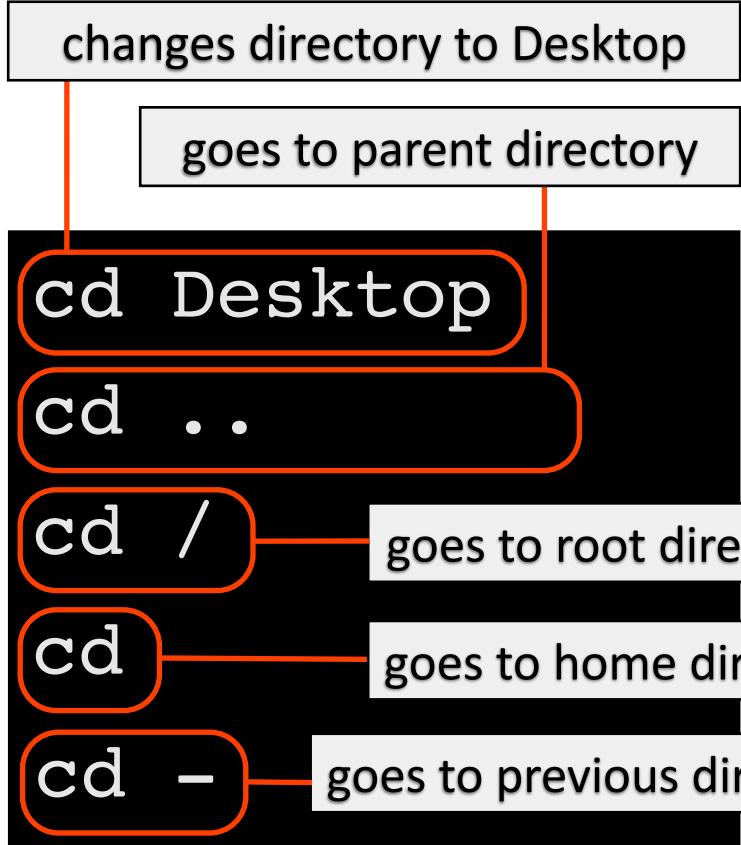
ctrl-e go to end of line

ctrl-r search in command history

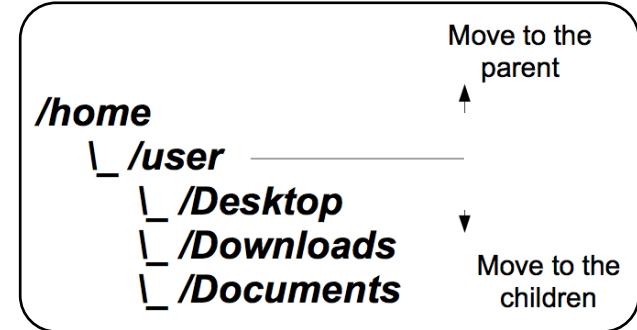


Use up and down
arrows to navigate
the command
history

`cd` changes directory



Use tab key to autocomplete names



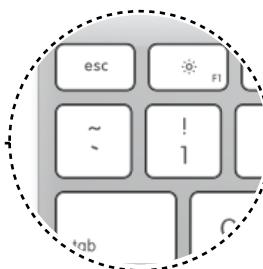
Absolute and relative paths

list files in Desktop using an absolute path

```
ls /home/user/Desktop
```

```
ls Desktop/
```

```
ls ~/Desktop
```



list files in Desktop using your home as a reference

list files in Documents using a relative path (from your home: /home/bioinfo)



Absolute and relative paths

Absolute paths do not depend on where you are

```
ls /home/bioinfo/Desktop  
ls ~/Desktop
```

~/ is equivalent to /home/bioinfo/



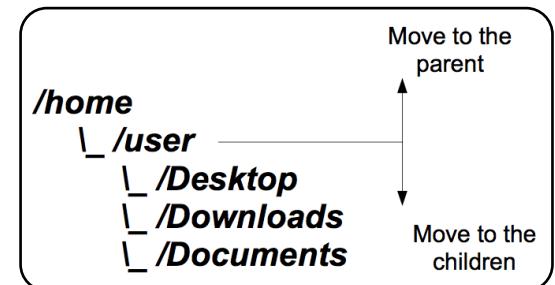
Absolute and relative paths

goes to *Desktop* from when you are in your home (/home/bioinfo)

```
cd Desktop/
```

```
ls .. /Documents
```

list files from *Documents* when you are in *Desktop*



Exercise 5:

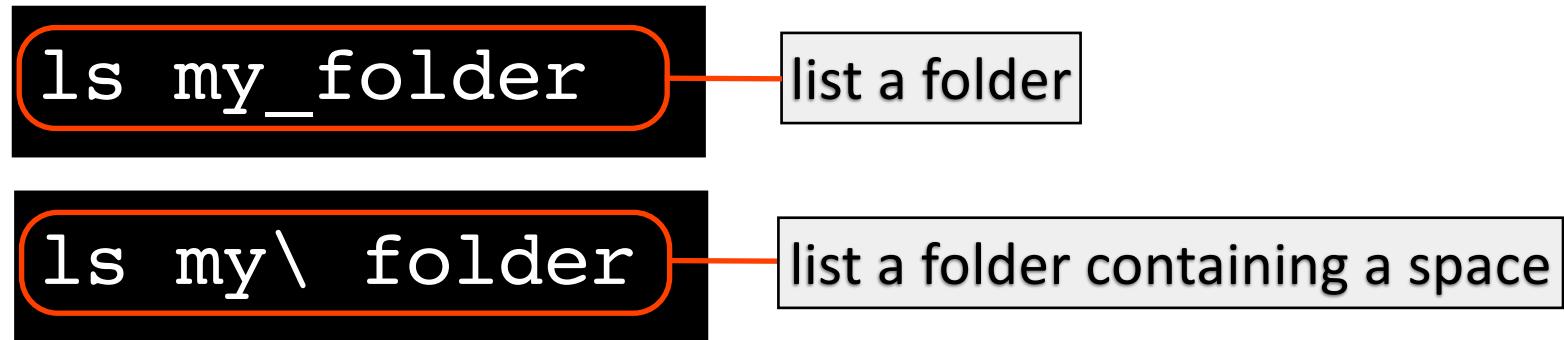
- List ALL files in the “/bin” directory that start
- with “ntfs” (do this once *without* changing your working directory, and once *with* changing your working directory)

```
bioinfo@bioinfo: /bin
File Edit View Search Terminal Help
bioinfo@bioinfo:/$ ls /bin/ntfs*
/bin/ntfs-3g      /bin/ntfscmp     /bin/ntfscls      /bin/ntfstruncate
/bin/ntfs-3g.probe /bin/ntfsfallocate /bin/ntfsmove    /bin/ntfsusermap
/bin/ntfscat       /bin/ntfsfix      /bin/ntfsrecover   /bin/ntfswipe
/bin/ntfscluster   /bin/ntfsinfo     /bin/ntfssecaudit
bioinfo@bioinfo:/$ cd /bin
bioinfo@bioinfo:/bin$ ls ntfs*
ntfs-3g          ntfscluster     ntfsfix      ntfsmove      ntfstruncate
ntfs-3g.probe    ntfscmp        ntfsinfo     ntfsrecover   ntfsusermap
ntfscat          ntfsfallocate  ntfscls     ntfssecaudit  ntfswipe
bioinfo@bioinfo:/bin$
```

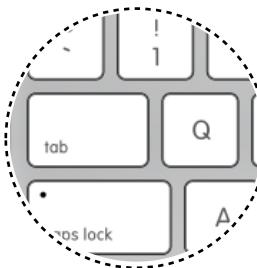


Escaping special characters

! @ \$ ^ & * ~ ? . | / [] < > \ ` " ; # ()



Tip: file names in lower case and with underscores instead of spaces



Use tab key to autocomplete names

Create, copy, move and delete files

creates an empty file called tmp_file.txt

copies tmp_file.txt in file_copy.txt

Tip: name files in lower case and with underscores instead of using spaces

```
touch tmp_file.txt
```

```
cp tmp_file.txt file_copy.txt
```

```
mv file1.txt file2.txt
```

moves or rename a file

```
rm file.txt
```

deletes file.txt



Locate a file

Locate the path for the file `augustus`

```
locate augustus
```



Create, copy and delete directories

creates an empty directory called *dir_name*

deletes *dir_name* directory if it is empty

`mkdir dir_name`

`rmdir dir_name`

`rm -r dir_name`

`cp -r dir_name dir_copy`



Music



Pictures



programs

delete *dir_name* and its files

copy *dir_name* and its files in a new folder

Compression commands

Compression commands	
gzip/zip	compress a file
gunzip/unzip	decompress a file
tar -cvf	groups files
tar -xvf	ungroups files
tar -zcvf	groups and gzip files
tar -zxvf	gunzip and ungroups files

groups and compress files

```
tar -zcvf file.tar.gz f1 f2
```

```
tar -zxvf file.tar.gz
```

decompress and ungroup a tar.gz file

UNIX Command-Line Cheat Sheet

BTI-SGN Bioinformatics Course 2014



File system Commands	
ls	lists directories and files
ls -a	lists all files including hidden files
ls -lh	formatted list including more data
ls -t	lists sorted by date
pwd	returns path to working directory
cd dir	changes directory
cd ..	goes to parent directory
cd /	goes to root directory
cd	goes to home directory
touch file_name	creates an empty file
cp file_file_copy	copy a file
cp -r	copy files contained in directories
rm file	deletes a file
rm -r dir	deletes a directory and its files
mv file1 file2	moves or renames a file
mkdir dir_name	creates a directory
rmdir dir_name	deletes a directory
locate file_name	searches a file
man command	shows commands manual
top	shows process activity
df -h	shows disk space info

Compression commands	
gzip/zip	compress a file
gunzip/unzip	decompress a file
tar -cvf	groups files
tar -xvf	ungroups files
tar -zcvf	groups and gzip files
tar -zxvf	gunzip and ungroups files

Networking Commands	
wget URL	download a file from an URL
ssh user@server	connects to a server
scp	copy files between computers
apt-get install	installs applications in linux

files, directories or wildcards



Compression commands

compress file f1.txt in f1.txt.gz

compress files f1 and f2 in file.zip

gzip f1.txt

zip file.zip f1 f2

unzip file.zip

gunzip file.gz

decompress file.zip

decompress file.gz



Networking Commands

● Networking commands

File system Commands	
ls	lists directories and files
ls -a	lists all files including hidden files
ls -lh	formatted list including more data
ls -t	lists sorted by date
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Compression commands	
gzip/zip	compress a file
gunzip/unzip	decompress a file
tar -cvf	groups files
tar -xvf	ungroups files
tar -zcvf	groups and gzip files
tar -zxf	gunzip and ungroups files
Text handling commands	
command > file	saves STDOUT in a file
command >> file	appends STDOUT in a file
cat file	concatenate and print files
cat file1 file2 > file3	merges files 1 and 2 into file3
cat *fasta > all.fasta	concatenates all fasta files in the current directory
head file	prints first lines from a file
head -n 5 file	prints first five lines from a file
tail file	prints last lines from a file
tail -n 5 file	prints last five lines from a file
less file	view a file
less -N file	includes line numbers
less -S file	wraps long lines
grep 'pattern' file	Prints lines matching a pattern
grep -c 'pattern' file	counts lines matching a pattern
cut -f 1,3 file	retrieves data from selected columns in a tab-delimited file
sort file	sorts lines from a file
sort -u file	sorts and return unique lines
uniq -c file	filters adjacent repeated lines
wc file	counts lines, words and bytes
paste file1 file2	concatenates the lines of input files
paste -d ","	concatenates the lines of input files by commas
sed	transforms text
Networking Commands	
wget URL	download a file from an URL
ssh user@server	connects to a server
scp	copy files between computers
apt-get install	installs applications in linux



Networking Commands

connects your terminal to your account in a server

```
ssh user_name@server_adress
```

```
wget https://btiscience.org/wp-content/uploads/BCBClogo.png
```

```
scp noe@boyce.sgn.cornell.edu:/home/noe/file.txt .
```

copy file.txt from your home in the server to the current directory in your computer

Tip: use the command pwd to get the path for cp and scp



iCommands

https://learning.cyverse.org/projects/data_store_guide/en/latest/step2.html

Exercise 6: Set up iCommands on your VM

```
$ iinit
One or more fields in your iRODS environment file (.irodsEnv) are
missing; please enter them.
Enter the host name (DNS) of the server to connect to: data.cyverse.org
Enter the port number: 1247
Enter your irods user name: #your_cyverse_username
Enter your irods zone: iplant
Those values will be added to your environment file (for use by
other i-commands) if the login succeeds.

Enter your current iRODS password: #your_cyverse_password
```



CyVerse Discovery Environment

The screenshot shows the CyVerse User Portal interface at user.cyverse.org/services/mine. The top navigation bar includes links for SERVICES, POWERED BY, HELP RESOURCES, FORMS, and WORKSHOPS. Below this, two tabs are visible: MY SERVICES (selected) and AVAILABLE.

Atmosphere
Cloud computing platform for CyVerse [LAUNCH](#)

CoGe
Online system for quick and easy retrieval and comparison of genomic information and sequences. [LAUNCH](#)

Data Commons
A unified system for managing and sharing your data across CyVerse's tools and services [LAUNCH](#)

Discovery Environment
Use hundreds of bioinformatics apps and manage data in the CyVerse Data Store from a simple web interface [LAUNCH](#)

BCBC logo

BTI logo

CyVerse Discovery Environment

The screenshot shows the CyVerse Discovery Environment (DE) web interface. The URL in the address bar is de.cyverse.org/de/. The page title is "CyVerse Discovery Environment".

The main area displays a file browser for the dataset "Botany2020NMGWorkshop". The left sidebar shows a navigation tree with categories like "srs57", "Community Data", and "Botany2020NMGWorkshop". The "Botany2020NMGWorkshop" category is expanded, showing sub-folders such as "Annotation", "Genome_assembly", "Presentations", "Scripts", "assemblies", "embryophyta_odb9", "raw_data", and "uniprot_sprot_plants.fasta".

The central panel lists files and folders under "Viewing: /iplant/home/shared/Botany2020NMGWorkshop". The table includes columns for Name, Last Modified, and Size. The "Details" pane on the right is empty, indicating no file is selected.

Name	Last Modified	Size	Actions
Annotation	2020 Jul 23 07:31:13		⋮
Genome_assembly	2020 Jul 22 10:10:05		⋮
Presentations	2020 Jul 20 11:38:05		⋮
Scripts	2020 Jul 17 16:31:08		⋮
assemblies	2020 Jul 17 16:14:26		⋮
embryophyta_odb9	2020 Jul 22 17:16:44		⋮
raw_data	2020 Jul 17 16:41:32		⋮
uniprot_sprot_plants.fasta	2020 Jul 22 17:24:18	17.62 MB	⋮
uniprot_sprot_plants.fasta.fai	2020 Jul 22 17:24:20	1.43 MB	⋮
uniprot_sprot_plants.fasta.phr	2020 Jul 22 17:24:23	5.9 MB	⋮
uniprot_sprot_plants.fasta.pin	2020 Jul 22 17:24:26	295.81 KB	⋮
uniprot_sprot_plants.fasta.psq	2020 Jul 22 17:24:27	13.75 MB	⋮

Details
Select a file or folder to view its details

Displaying 1 - 12 of 12

0 item(s)

iCommands

https://learning.cyverse.org/projects/data_store_guide/en/latest/step2.html

Exercise 7:

- Download the Annotation folder on DE
(/iplant/home/shared/Botany2020NMGWorkshop/Annotation) to /scratch.

```
cd scratch
```

```
iget -rPT /iplant/home/shared/Botany2020NMGWorkshop/Annotation
```



Useful commands in the server

`df -h`

shows disk space information

`top`

display and update sorted information about processes

Also:

`cat /proc/cpuinfo`
`free -m`



Processes

- Every running program is treated as a process
- Every process has a process ID and an “environment”
- Processes are created only from other processes through a *fork*. (parent ID)
- First process is init, with process ID 1
- Viewing processes: ps , jobs , top, pstree
- Terminating processes: kill



“Man” pages

Man pages are the documentation for UNIX commands

- \$ man <command>
- \$ man ls

Searching man pages

- Use the apropos command
- \$ apropos “text editor”



Controlling processes

- Interrupting, terminating execution
- control-Z , control-C
- Viewing running jobs (jobs)
- Background/foreground jobs (bg , fg, &)
- screen
- Use sleep 100 to test



Top displays and update sorted information about processes

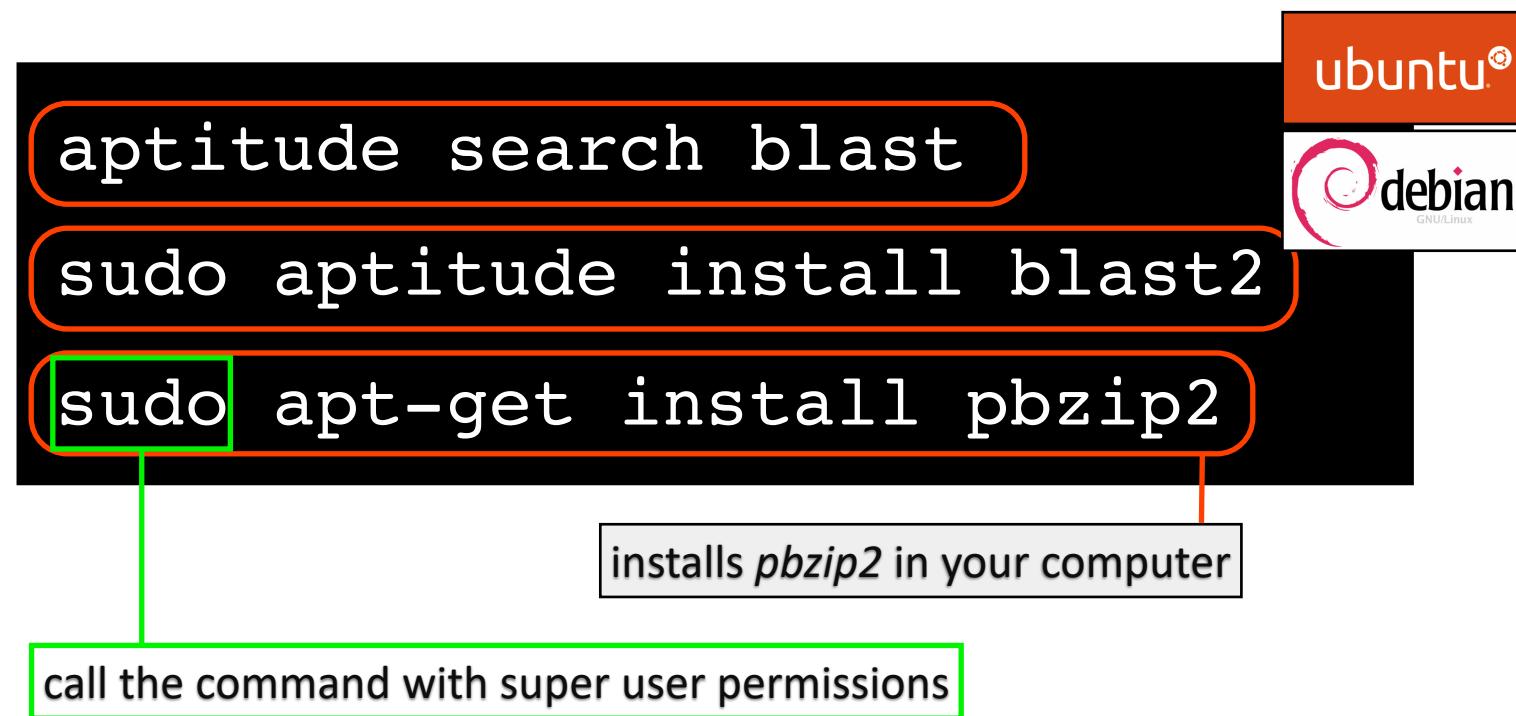
```
bioinfo@biodebian: ~
File Edit View Terminal Help
top - 15:07:10 up 3:50, 2 users, load average: 0.00, 0.00, 0.00
Tasks: 116 total, 1 running, 115 sleeping, 0 stopped, 0 zombie
Cpu(s): 0.3%us, 0.0%sy, 0.0%ni, 99.7%id, 0.0%wa, 0.0%hi, 0.0%si, 0.0%st
Mem: 1026940k total, 518232k used, 508708k free, 51872k buffers
Swap: 1134584k total, 0k used, 1134584k free, 221056k cached

PID USER      PR  NI    VIRT   RES   SHR S %CPU %MEM     TIME+ COMMAND
132 root      20   0      0     0   0 S  0.3  0.0  0:07.05 ata/0
1861 bioinfo  20   0  40744 1700 1088 S  0.3  0.2  0:28.12 VBoxClient
2234 bioinfo  20   0  220m 12m 9792 S  0.3  1.3  0:00.61 gnome-terminal
2304 bioinfo  20   0 19072 1352 1012 R  0.3  0.1  0:00.03 top
  1 root      20   0  8356  804  672 S  0.0  0.1  0:00.93 init
  2 root      20   0      0     0   0 S  0.0  0.0  0:00.00 kthreadd
  3 root      RT  0      0     0   0 S  0.0  0.0  0:00.00 migration/0
  4 root      20   0      0     0   0 S  0.0  0.0  0:00.04 ksftirqd/0
  5 root      RT  0      0     0   0 S  0.0  0.0  0:00.00 watchdog/0
  6 root      20   0      0     0   0 S  0.0  0.0  0:00.15 events/0
  7 root      20   0      0     0   0 S  0.0  0.0  0:00.00 cpuset
  8 root      20   0      0     0   0 S  0.0  0.0  0:00.00 khelper
  9 root      20   0      0     0   0 S  0.0  0.0  0:00.00 netns
 10 root     20   0      0     0   0 S  0.0  0.0  0:00.00 async/mgr
 11 root     20   0      0     0   0 S  0.0  0.0  0:00.00 pm
 12 root     20   0      0     0   0 S  0.0  0.0  0:00.02 sync_supers
 13 root     20   0      0     0   0 S  0.0  0.0  0:00.02 bdi-default
 14 root     20   0      0     0   0 S  0.0  0.0  0:00.00 kintegrityd/0
 15 root     20   0      0     0   0 S  0.0  0.0  0:00.06 kblockd/0
 16 root     20   0      0     0   0 S  0.0  0.0  0:00.00 kacpid
 17 root     20   0      0     0   0 S  0.0  0.0  0:00.00 kacpi_notify
 18 root     20   0      0     0   0 S  0.0  0.0  0:00.00 kacpi_hotplug
 19 root     20   0      0     0   0 S  0.0  0.0  0:00.00 kseriod
 21 root     20   0      0     0   0 S  0.0  0.0  0:00.00 kondemand/0
 22 root     20   0      0     0   0 S  0.0  0.0  0:00.00 khungtaskd
 23 root     20   0      0     0   0 S  0.0  0.0  0:00.00 kswapd0
 24 root     25   5      0     0   0 S  0.0  0.0  0:00.00 ksmd
 25 root     20   0      0     0   0 S  0.0  0.0  0:00.00 aio/0
 26 root     20   0      0     0   0 S  0.0  0.0  0:00.00 crypto/0
130 root     20   0      0     0   0 S  0.0  0.0  0:00.00 ksuspend_usbd
131 root     20   0      0     0   0 S  0.0  0.0  0:00.00 khubd
```

q quit
u user (top -u user)
M sort by memory usage



Commands to install software



Also: CPAN, pip, conda



Installing software - compiling

Exercise 8:

- Install gffread
- (<https://github.com/gpertea/gffread>) in
- the /opt/ dir

```
cd /some/build/dir  
git clone https://github.com/gpertea/gffread  
cd gffread  
make release
```



Resources

- Finding and use remote resources (cloud, XSEDE, HPC)
- Resource monitoring (e.g., is your machine about to blow up)
- Benchmarking -- figuring out what you need



Containers

Developing with Docker

Developing apps today requires so much more than writing code. Multiple languages, frameworks, architectures, and discontinuous interfaces between tools for each lifecycle stage creates enormous complexity. Docker simplifies and accelerates your workflow, while giving developers the freedom to innovate with their choice of tools, application stacks, and deployment environments for each project.



dockerhub

Thank you for attending DockerCon 2020! [Watch the recordings.](#)

 Explore Repositories Organizations Get Help srs57 

srs57 [Create Repository](#)

srs57 / snpbinner
Updated 4 months ago  0  5  Public

srs57 / pi-estimator
Updated 4 months ago  0  6  Public

srs57 / jupyter-scipy
Updated 4 months ago  0  14  Public

srs57 / lolcow
Updated 4 months ago  0  4  Public

 Tip: Not finding your repository? Try switching namespace via the top left dropdown.

Organizations 
 bcgcgroup
[View All Orgs](#)

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Practice Exercises

- a) Go to your scratch directory using the command cd
- b) Use the command touch to create a file called:
Do not Use “special characters” in file names!.txt
- c) Use the command rm to delete that file
- d) Use ige to copy the `Genome_assembly` dir to your scratch folder

