

Setting hardware/software baseline skills



Objectives

- Basic understanding of Virtual Machines and containers.
- Gain familiarity with basic Linux commands
- Learn to navigate the Linux file system
- Become familiar with Atmosphere and the Data Store at CyVerse



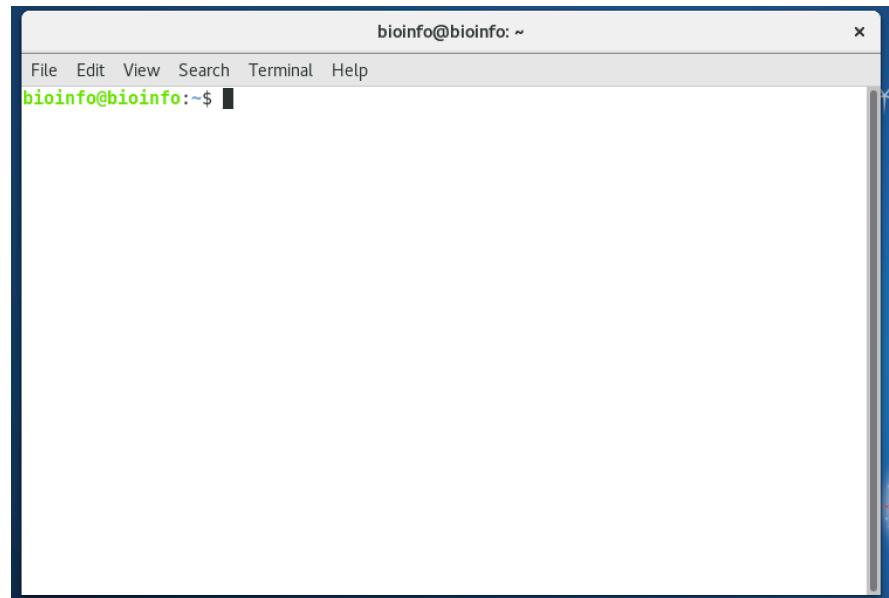
What is a Virtual Machine?

- 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 the CyVerse platform
today

About CyVerse

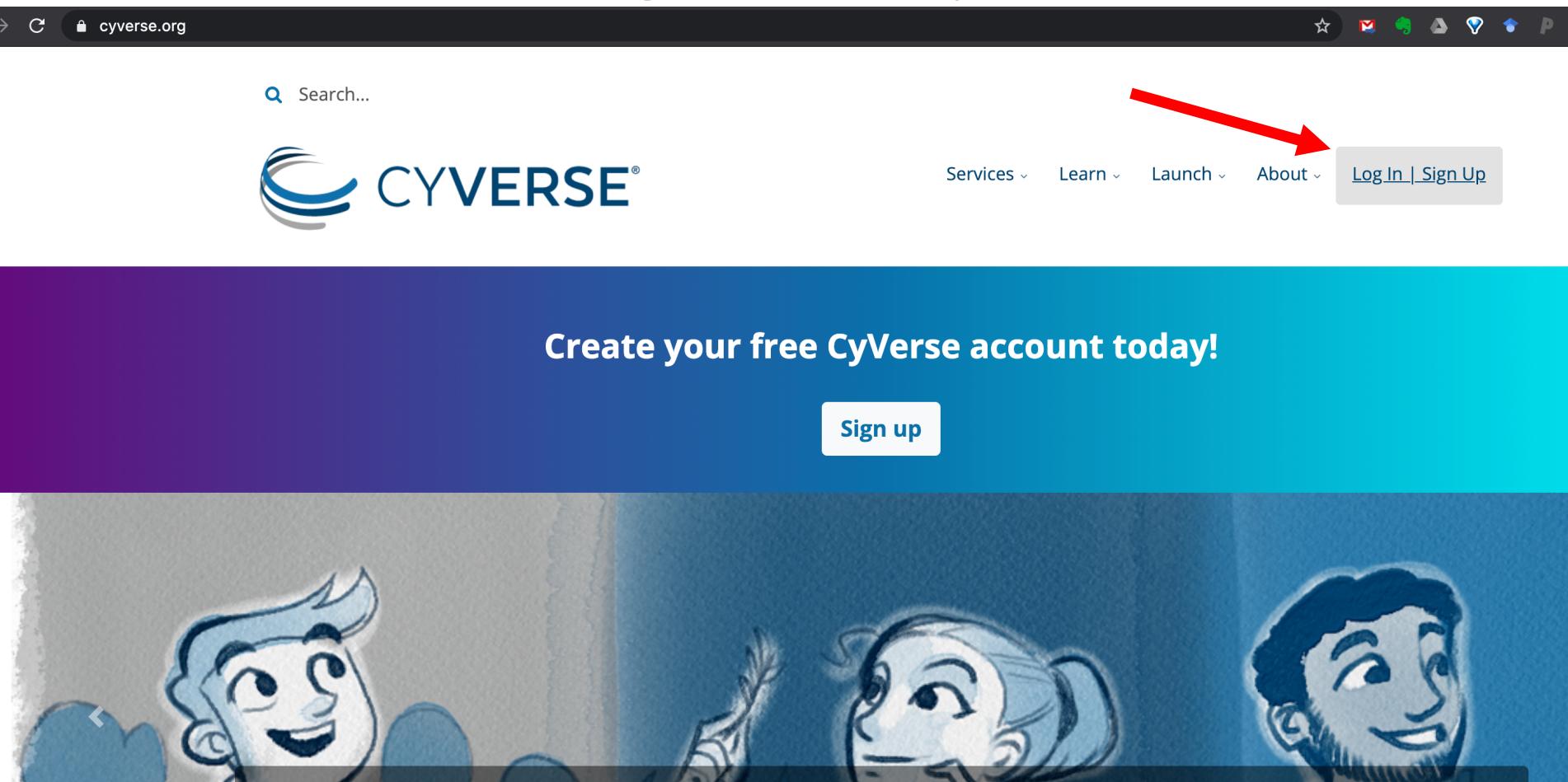
Vision: Transforming Science through Data-Driven Discovery

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!

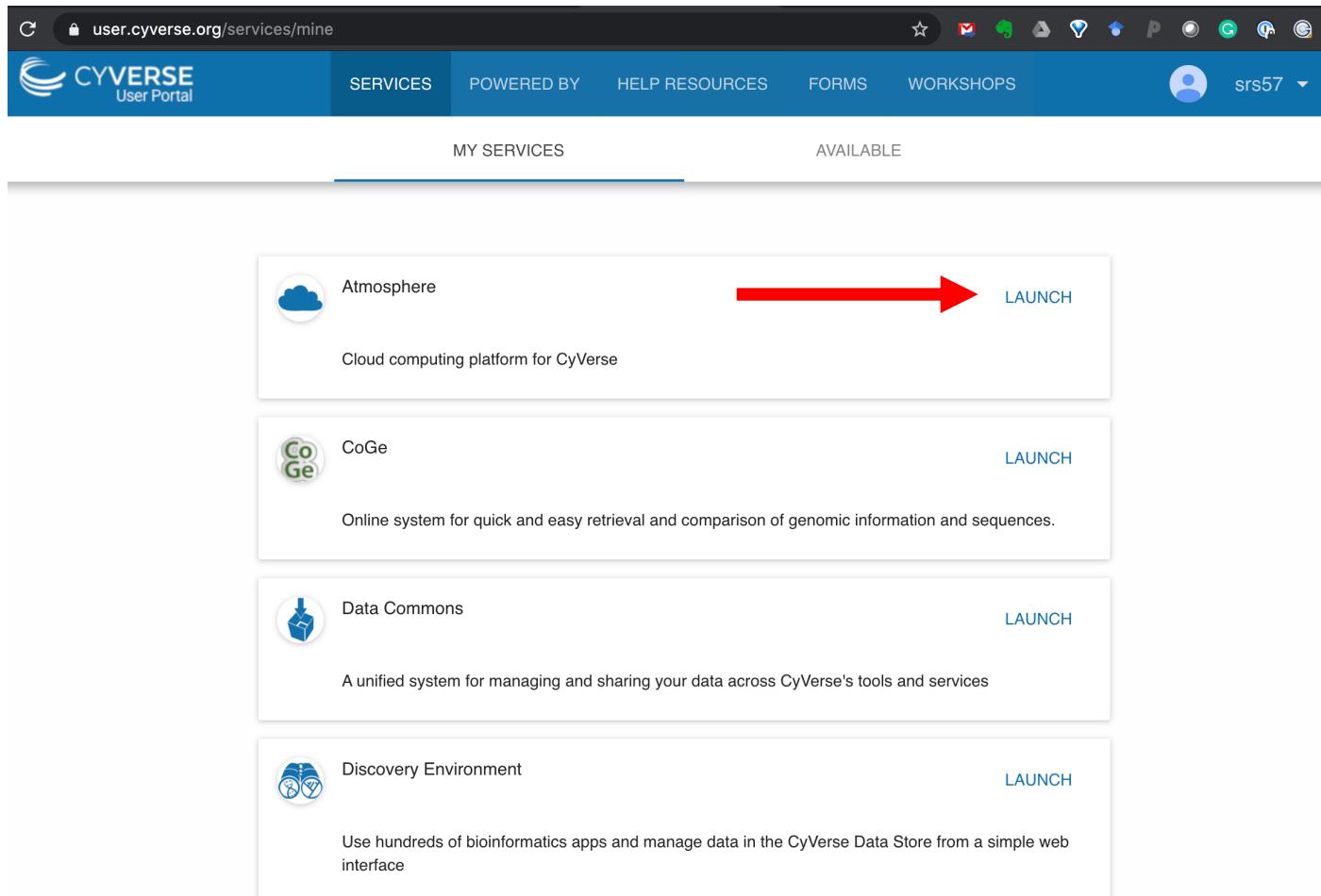


A screenshot of the CyVerse website login page. The header features the CyVerse logo and navigation links for Services, Learn, Launch, About, Log In | Sign Up. A red arrow points to the "Log In | Sign Up" button. The main section has a gradient background and a "Create your free CyVerse account today!" call-to-action with a "Sign up" button. Below the main image is a cartoon illustration of three diverse people looking at a computer screen.

*Use Chrome or Firefox web browsers



Let's launch Atmosphere!



The screenshot shows the CyVerse User Portal interface. At the top, there is a navigation bar with links for SERVICES, POWERED BY, HELP RESOURCES, FORMS, and WORKSHOPS. On the right side of the bar, there is a user profile icon and the text "srs57". Below the navigation bar, there are two tabs: "MY SERVICES" (which is highlighted) and "AVAILABLE". The main content area displays four service cards:

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



Let's launch Atmosphere!

Your Atmosphere Instance is Available ➤ Inbox ×

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



Let's launch Atmosphere!



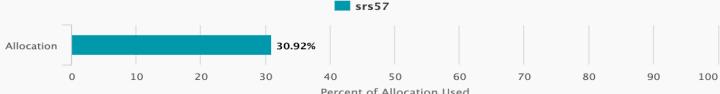
The screenshot shows the CyVerse Atmosphere interface. A red arrow points to the 'Projects' tab in the top navigation bar.

Getting Started

- Launch New Instance**: Browse Atmosphere's list of available images and select one to launch a new instance.
- Browse Help Resources**: View a video tutorial, read the how-to guides, or email the Atmosphere support team.
- Change Your Settings**: Modify your account settings, view your resource quota, or request more resources.

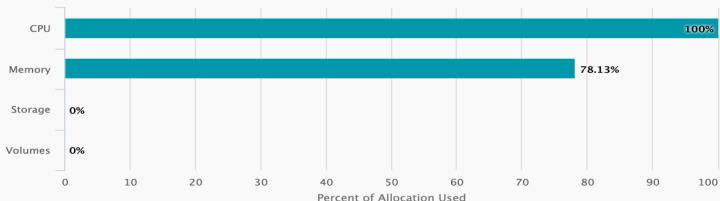
Resources Used [NEED MORE ?](#)

Allocation Source



Allocation	Percent of Allocation Used
srs57	30.92%

Provider Resources



Resource	Percent of Allocation Used
CPU	100%
Memory	78.13%
Storage	0%
Volumes	0%

Instances



Status	Count
suspended	0
active	5

Volumes

0 Volumes

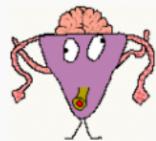
Instance History (12 instances launched)

Image	Name	Description	Updated
	Botany2020NMGWorkshop	Launched from Botany2020NMGWorkshop Ran: Jul 27, 2020 09:30 am - Present	Updated 2 minutes ago 0 days ago on CyVerse Cloud - Marana
	Botany2020NMGWorkshop	Launched from Botany2020NMGWorkshop Ran: Jul 26, 2020 09:16 am - Present	1 days ago on CyVerse Cloud - Marana
	Botany2020NMGWorkshop	Launched from Botany2020NMGWorkshop Ran: Jul 22, 2020 08:52 pm - Present	4 days ago on CyVerse Cloud - Marana



Botany2020Workshop

[Resources](#) > Botany2020NMGWorkshop



Botany2020NMGWorkshop

Allocation Source

srs57

Allocation Used

31% of 5000 AU from srs57

Instance Details

Status ● Active

Activity N/A

Size tiny1 (CPU: 1, Mem: 4 GB, Disk: 30 GB root)

IP Address 128.196.142.25 [Copy](#)

Launched Jul 27, 2020 (6 hours ago)

Based on [Botany2020NMGWorkshop v1.4](#)

Provider CyVerse Cloud - Marana

ID 46345

Alias 12bf1bba-5d48-4c9e-a426-c61ffeb1c7d0 [Copy](#)

Instance Status History

Status	Start Date	End Date
active	July 27th 2020, 10:07 am	Present
deploying	July 27th 2020, 9:47 am	July 27th 2020, 10:07 am
active	July 27th 2020, 9:45 am	July 27th 2020, 9:47 am
deploying	July 27th 2020, 9:41 am	July 27th 2020, 9:45 am

Actions

Report

Image

Suspend

Shelve

Stop

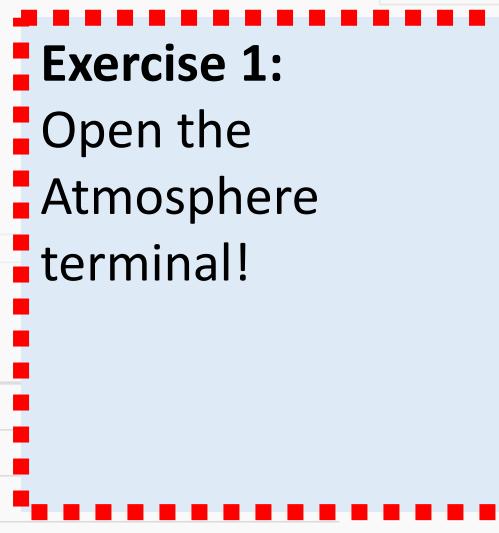
Reboot

Redeploy

Delete

Links

Open Web Shell [Copy](#)


Exercise 1:
Open the
Atmosphere
terminal!



Atmosphere terminal

A screenshot of an Atmosphere terminal window. The title bar shows the URL "guacamole-prod.cyverse.org//#/client/NDFiOTA0YTUtMjV..." and various icons. The main area displays a Linux login screen for "Ubuntu 16.04.1 LTS (GNU/Linux 4.4.0-185-generic x86_64)". It includes a welcome message, a link to Ubuntu Advantage Cloud Guest, package update information (135 packages can be updated, 0 are security updates), a system restart notice, and a welcome message. At the bottom, it shows the prompt "srs57@vm142-85:~\$".

```
← → 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

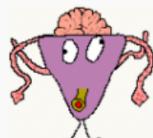
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   / / \ \ | | | | | | | | | | | | | | | | | | | | | | | |
  / / \ \ | | | | | | | | | | | | | | | | | | | | | | | |
 srs57@vm142-85:~$
```



Using terminal and ssh to access the Atmosphere instance

Botany2020Workshop

[Resources](#) > Botany2020NMGWorkshop



Botany2020NMGWorkshop

Allocation Source

srs57

Allocation Used

31% of 5000 AUs from srs57

Instance Details

Status ● Active

Activity N/A

Size tiny1 (CPU: 1, Mem: 4 GB, Disk: 30 GB root)

IP Address 128.196.142.25 [Copy](#)

Launched Jul 27, 2020 (6 hours ago)

Based on Botany2020NMGWorkshop v1.4

Provider CyVerse Cloud - Marana

ID 46345

Alias 128.196.142.25

The default interactive shell is now zsh.
To update your account to use zsh, please run `chsh -s /bin/zsh`.
For more details, please visit <https://support.apple.com/kb/HT208050>.
Susans-MacBook-Pro:~ srs57\$ ssh srs57@128.196.142.25
The authenticity of host '128.196.142.25 (128.196.142.25)' can't be established.
ECDSA key fingerprint is SHA256:C1ti/1rJ3kW6yUQGiW07d5551LMHRgJ3dTfaIb0RH7k.
Are you sure you want to continue connecting (yes/no/[fingerprint])? yes
Warning: Permanently added '128.196.142.25' (ECDSA) to the list of known hosts.
srs57@128.196.142.25's password:
Welcome to Ubuntu 16.04.1 LTS (GNU/Linux 4.4.0-186-generic x86_64)

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

151 packages can be updated.

0 updates are security updates.

New release '18.04.4 LTS' available.
Run 'do-release-upgrade' to upgrade to it.

Welcome to



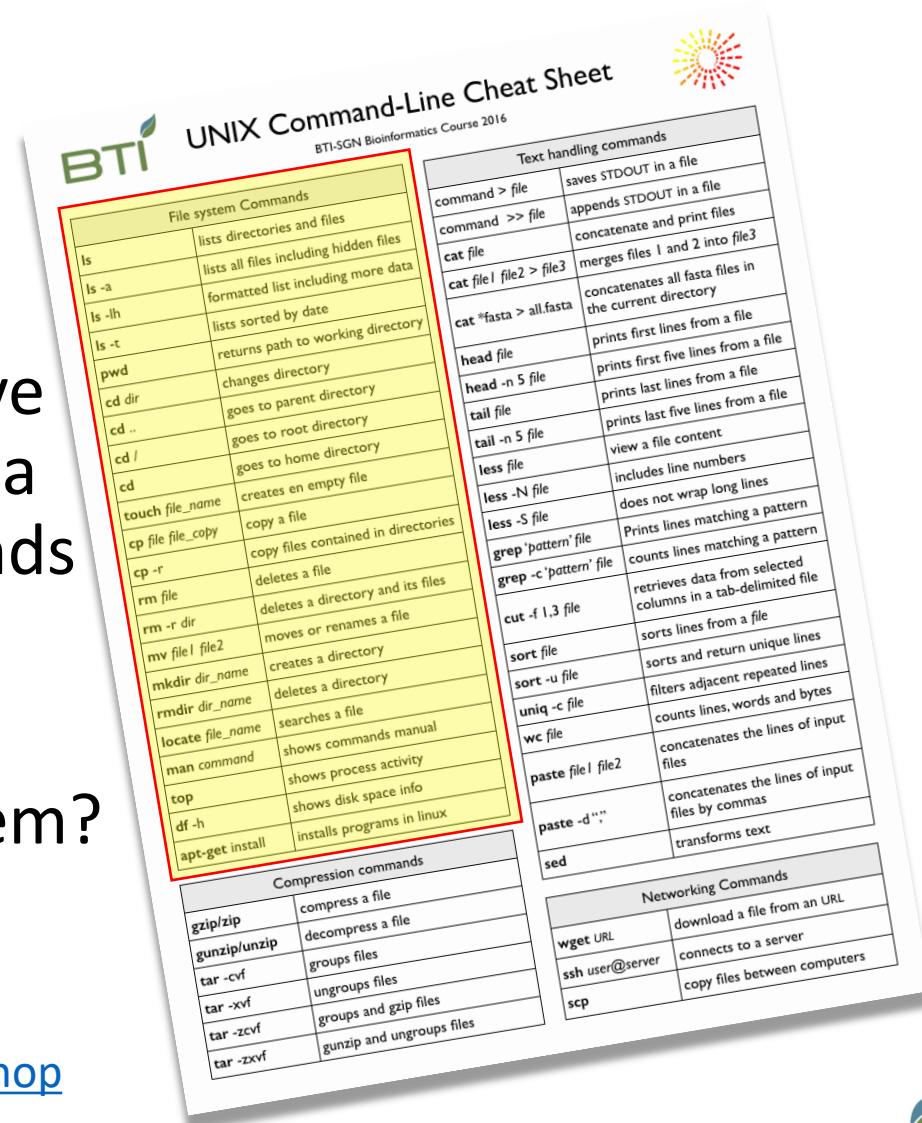
srs57@vm142-25:~\$



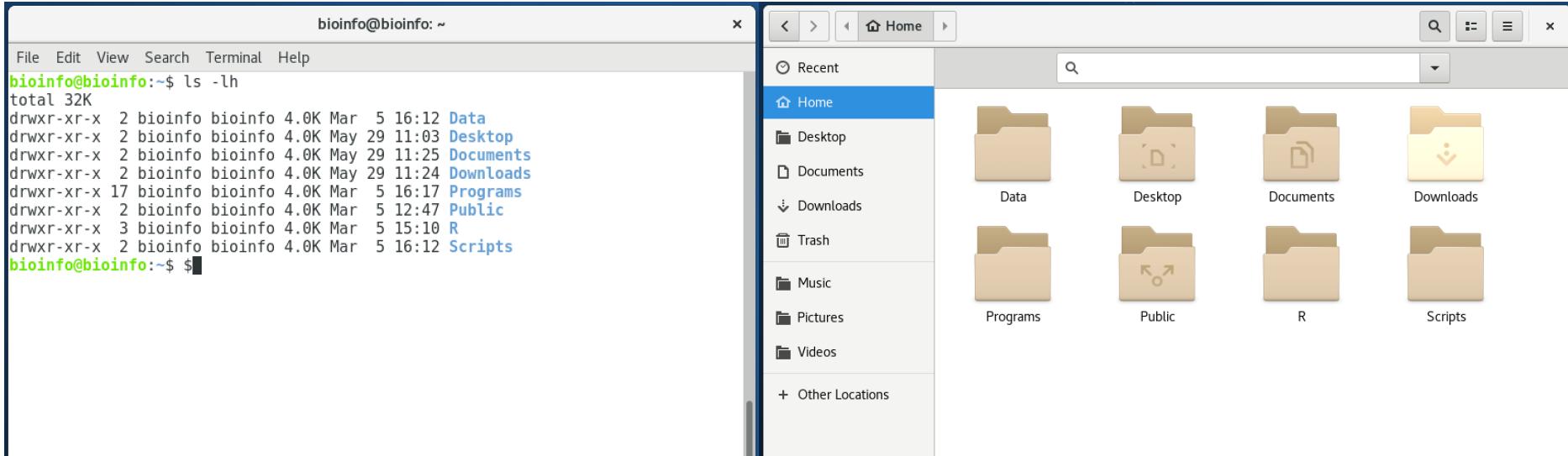
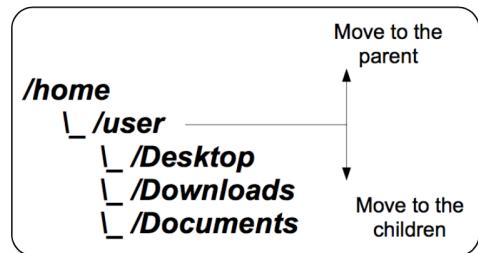
Command-line File System Navigation.

- 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
```

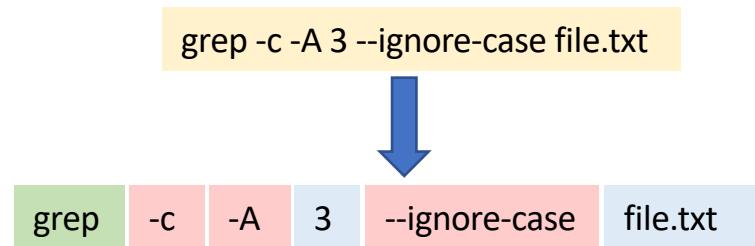
Root directory

/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.



Wildcards, Shortcuts, and Command History

```
ls *txt
```

list all txt files in current directory

```
ls P*s
```

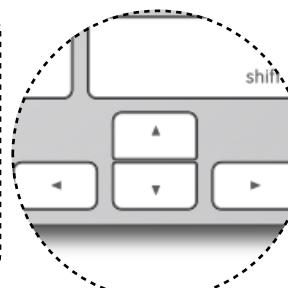
list files starting with P and ending with s,
e.g.: Pictures, Photos, Programs ...

ctrl-c stop process

ctrl-a go to begin of line

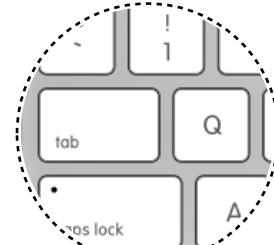
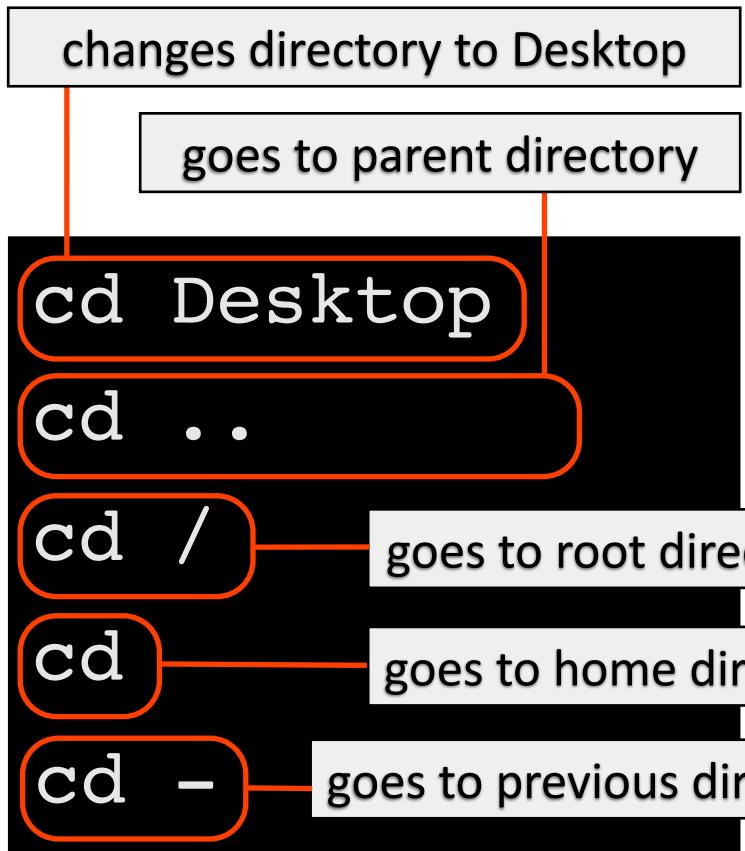
ctrl-e go to end of line

ctrl-r search in command history

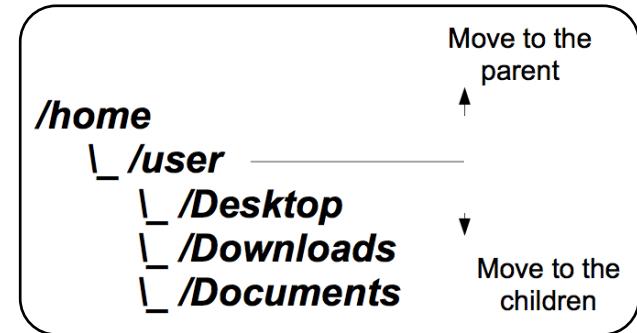


Use up and down
arrows to navigate
the command
history

`cd` changes directory



Use tab key to autocomplete names



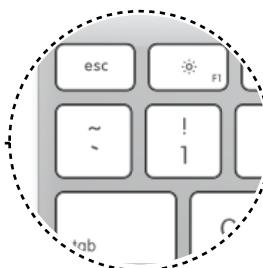
Absolute and relative paths

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/

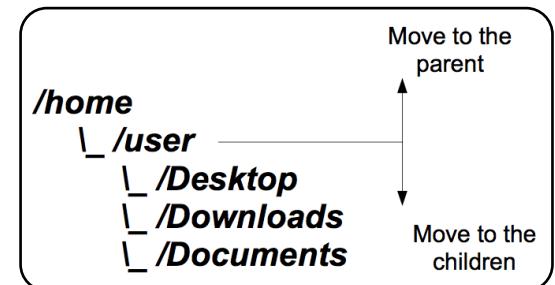
Absolute and relative paths

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 4:

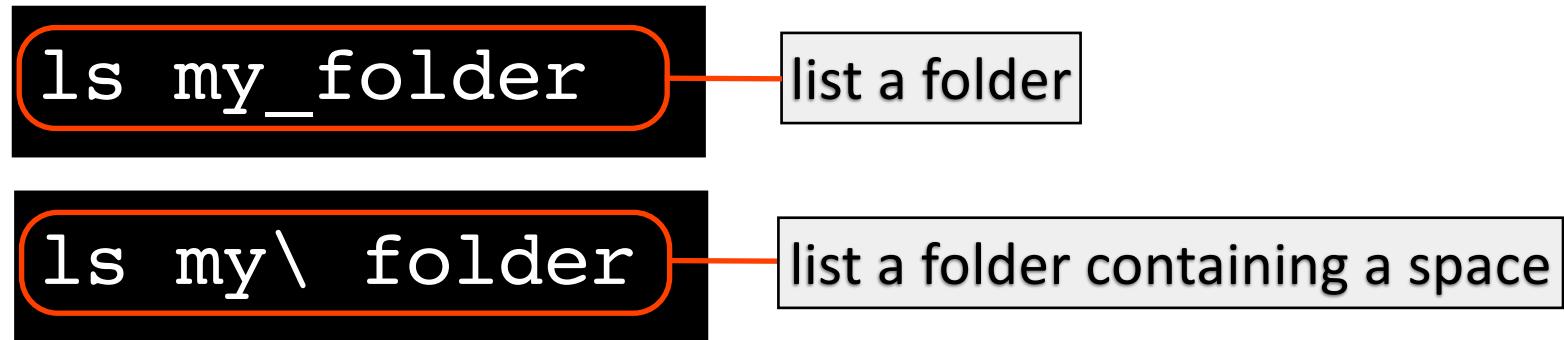
- List ALL files in the “/bin” directory that start
- with “ntfs” (do this once *without* changing your working directory, and once *with* changing your working directory)

```
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$
```

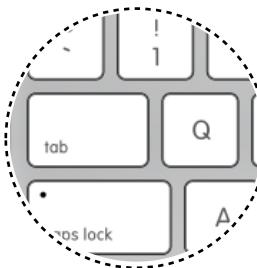


Escaping special characters

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



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	
<code>ls</code>	lists directories and files
<code>ls -a</code>	lists all files including hidden files
<code>ls -lh</code>	formatted list including more data
<code>ls -t</code>	lists sorted by date
<code>pwd</code>	returns path to working directory
<code>cd dir</code>	changes directory
<code>cd ..</code>	goes to parent directory
<code>cd /</code>	goes to root directory
<code>cd</code>	goes to home directory
<code>touch file_name</code>	creates an empty file
<code>cp file_file_copy</code>	copy a file
<code>cp -r</code>	copy files contained in directories
<code>rm file</code>	deletes a file
<code>rm -r dir</code>	deletes a directory and its files
<code>mv file1 file2</code>	moves or renames a file
<code>mkdir dir_name</code>	creates a directory
<code>rmdir dir_name</code>	deletes a directory
<code>locate file_name</code>	searches a file
<code>man command</code>	shows commands manual
<code>top</code>	shows process activity
<code>df -h</code>	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	
<code>wget URL</code>	download a file from an URL
<code>ssh user@server</code>	connects to a server
<code>scp</code>	copy files between computers
<code>apt-get install</code>	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
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
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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



Networking Commands: iCommands

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

Exercise 5: 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. The main content area displays four service cards:

- 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](#)

A large red arrow points to the [LAUNCH](#) button for the Discovery Environment service.



CyVerse Discovery Environment



Data: Botany2020NMGWorkshop

Upload ▾ File ▾ Edit ▾ Download ▾ Share ▾ Metadata ▾ Refresh

Navigation

- Community Data
 - Astrolabe
 - BioViz
 - Botany2020NMGWorkshop**
 - Brassica_dwarf
 - CAP_TCN
 - EuPathDB-Data
 - G-OnRamp_hubs
 - GoreLab
 - KBase_staging
 - Legume_Federation
 - NAM
 - NASA_GeneLab_data
 - NEON_Pilot
 - NEON_data_institute_20
 - SEPA_microbiome_2016
 - TCIA
 - Trinity_transdecoder_trin
 - UNI_PlantVision

Viewing: /iplant/home/shared/Botany2020NMGWorkshop

Name	Last Modified	Size	⋮
Genome_assembly	2020 Jul 26 10:35:57		⋮
Presentations	2020 Jul 26 10:35:59		⋮
Scripts	2020 Jul 26 10:35:52		⋮
annotation	2020 Jul 27 13:45:07		⋮
assemblies	2020 Jul 23 10:11:20		⋮
embryophyta_odb9	2020 Jul 26 10:36:02		⋮
raw_data	2020 Jul 26 15:04:01		⋮
README	2020 Jul 23 16:04:31	3.06 KB	⋮

Displaying 1 - 8 of 8 0 item(s)

Details
Select a file or folder to view its details



iCommands

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

- **Exercise 6:**
- Download the “Botany2020NMGWorkshop”
- folder on the DE
- (/iplant/home/shared/Botany2020NMG
- Workshop/) to /scratch on your Atmo instance.

```
cd /scratch
```

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



“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



Resource monitoring

top or **htop** display and update sorted information about processes

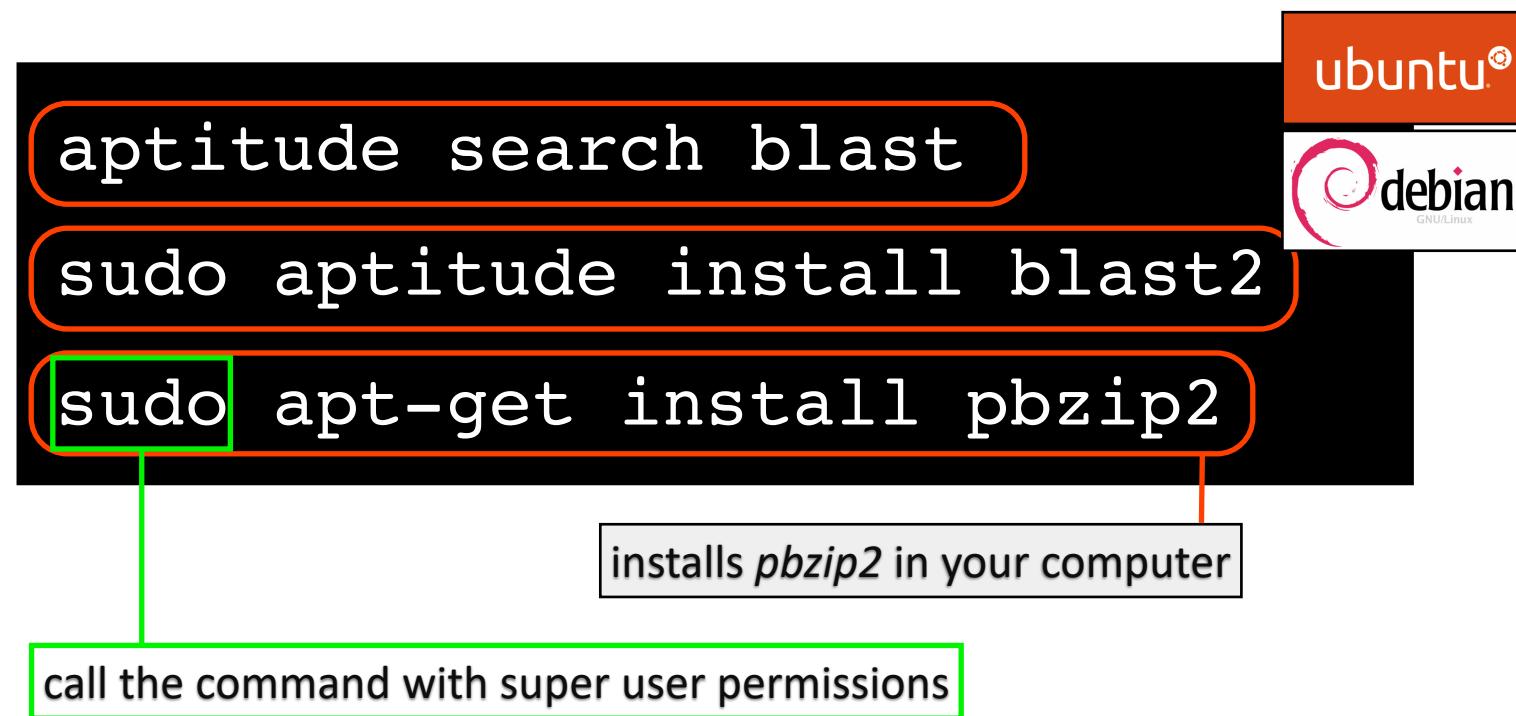
```
bioinfo@biodebian: ~
File Edit View Terminal Help
top - 15:07:10 up 3:50, 2 users, load average: 0.00, 0.00, 0.00
Tasks: 116 total, 1 running, 115 sleeping, 0 stopped, 0 zombie
Cpu(s): 0.3%us, 0.0%sy, 0.0%ni, 99.7%id, 0.0%wa, 0.0%hi, 0.0%si, 0.0%st
Mem: 1026940k total, 518232k used, 508708k free,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

Also:
free -m
cat /proc/cpuinfo
free -df
du -lh

Commands to install software



Also: CPAN, pip, conda



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.](#)

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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 
 bcbcgroup
[View All Orgs](#)

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