ericsalomaki — eric@krtecek: ~ — ssh krtecek — 144×47

eric@krtecek:~$

Lab Introduction and an Introduction to Unix

Anna Karnkowska, Eric Salomaki

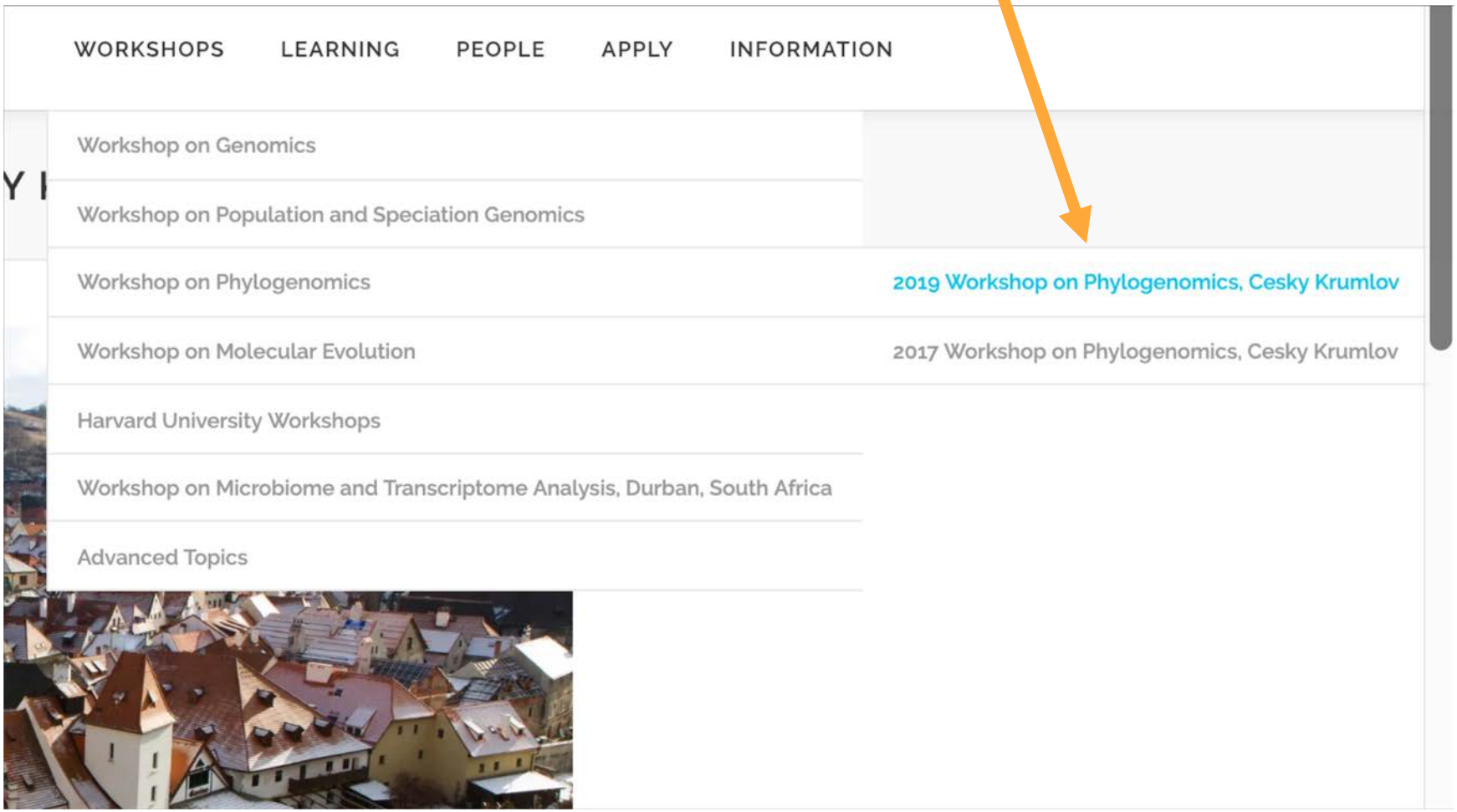
Many slides courtesy
Dr. Sophie Shaw

Overview

- Introduction
- Using the Amazon Machine Images (AMI)
- Introduction to Unix

These Slides!

http://evomics.org/workshops/2019-workshop-on-phylogenomics-cesky-krumlov/



What We're Going To Do

21 Jan	9a – 12p	Scott Handley & Toni Gabaldón	Introduction and Orientation	Theater
	2p – 5p	Workshop Team	Lab Introduction	House of Prelate
	7p – 10p	Everyone	Scientific Speed Networking	TBD
22 Jan	9a – 12p	Antonis Rokas	Introduction to Phylogenomics	Theater
	2p – 5p	Workshop Team	Alignment and Alignment Trimming	House of Prelate
	7p – 10p	Workshop Team	Tree Visualization	House of Prelate
23 Jan	9a – 12p	Toni Gabaldón	Introduction to Phylogenetics, and Orthology and Paralogy	Theater
	2p – 5p	Toni Gabaldón	Orthology and Paralogy Prediction lab	House of Prelate
	7p – 10p	Workshop Team	Partitioning and Concatentation Laboratory	House of Prelate

Background on Unix, Cloud computing, and in working in an instance
Introduction to Terminal and Unix

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How and why to build a multiple sequence alignment
Is your alignment correct?
How to trim your alignment for phylogenetics

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Important concepts for making your data accessible

Exploring tools for looking at your tree(s)

- Web Based
- Software
- Toolkits

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What is Partitioning and the why/when/how to do it
Tools for partitioning your data
How to concatenate your data

Good Workshop Practice

- PowerPoint interspersed with Challenges
- Ask us lots of questions!
- Work together
- Take breaks
- Use a cheat sheet, google, etc.
- Have Fun!

Unix/Linux Command Reference

FOSSwire.com

File Commands

ls – directory listing
ls -al – formatted listing with hidden files
cd *dir* - change directory to *dir*
cd – change to home
pwd – show current directory
mkdir *dir* – create a directory *dir*
rm *file* – delete *file*
rm -r *dir* – delete directory *dir*
rm -f *file* – force remove *file*
rm -rf *dir* – force remove directory *dir* *
cp *file1 file2* – copy *file1* to *file2*
cp -r *dir1 dir2* – copy *dir1* to *dir2*; create *dir2* if it doesn't exist
mv *file1 file2* – rename or move *file1* to *file2* if *file2* is an existing directory, moves *file1* into directory *file2*
ln -s *file link* – create symbolic link *link* to *file*
touch *file* – create or update *file*
cat > *file* – places standard input into *file*
more *file* – output the contents of *file*
head *file* – output the first 10 lines of *file*
tail *file* – output the last 10 lines of *file*
tail -f *file* – output the contents of *file* as it grows, starting with the last 10 lines

Process Management

ps – display your currently active processes
top – display all running processes
kill *pid* – kill process id *pid*
killall *proc* – kill all processes named *proc* *
bg – lists stopped or background jobs; resume a stopped job in the background
fg – brings the most recent job to foreground
fg *n* – brings job *n* to the foreground

File Permissions

chmod *octal file* – change the permissions of *file* to *octal*, which can be found separately for user, group, and world by adding:

- 4 – read (r)
- 2 – write (w)
- 1 – execute (x)

Examples:
chmod 777 – read, write, execute for all
chmod 755 – rwx for owner, rx for group and world
For more options, see **man chmod**.

SSH

ssh *user@host* – connect to *host* as *user*
ssh -p *port user@host* – connect to *host* on port *port* as *user*
ssh-copy-id *user@host* – add your key to *host* for *user* to enable a keyed or passwordless login

Searching

grep *pattern files* – search for *pattern* in *files*
grep -r *pattern dir* – search recursively for *pattern* in *dir*
command* | grep *pattern – search for *pattern* in the output of *command*
locate *file* – find all instances of *file*

System Info

date – show the current date and time
cal – show this month's calendar
uptime – show current uptime
w – display who is online
whoami – who you are logged in as
finger *user* – display information about *user*
uname -a – show kernel information
cat /proc/cpuinfo – cpu information
cat /proc/meminfo – memory information
man *command* – show the manual for *command*
df – show disk usage
du – show directory space usage
free – show memory and swap usage
whereis *app* – show possible locations of *app*
which *app* – show which *app* will be run by default

Compression

tar cf *file.tar files* – create a tar named *file.tar* containing *files*
tar xf *file.tar* – extract the files from *file.tar*
tar czf *file.tar.gz files* – create a tar with Gzip compression
tar xzf *file.tar.gz* – extract a tar using Gzip
tar cjf *file.tar.bz2* – create a tar with Bzip2 compression
tar xjf *file.tar.bz2* – extract a tar using Bzip2
gzip *file* – compresses *file* and renames it to *file.gz*
gzip -d *file.gz* – decompresses *file.gz* back to *file*

Network

ping *host* – ping *host* and output results
whois *domain* – get whois information for *domain*
dig *domain* – get DNS information for *domain*
dig -x *host* – reverse lookup *host*
wget *file* – download *file*
wget -c *file* – continue a stopped download

Installation

Install from source:
./configure
make
make install
dpkg -i *pkg.deb* – install a package (Debian)
rpm -Uvh *pkg.rpm* – install a package (RPM)

Shortcuts

Ctrl+C – halts the current command
Ctrl+Z – stops the current command, resume with **fg** in the foreground or **bg** in the background
Ctrl+D – log out of current session, similar to **exit**
Ctrl+W – erases one word in the current line
Ctrl+U – erases the whole line
Ctrl+R – type to bring up a recent command
!! - repeats the last command
exit – log out of current session

* use with extreme caution.

https://files.fosswire.com/2007/08/fwunixref.pdf

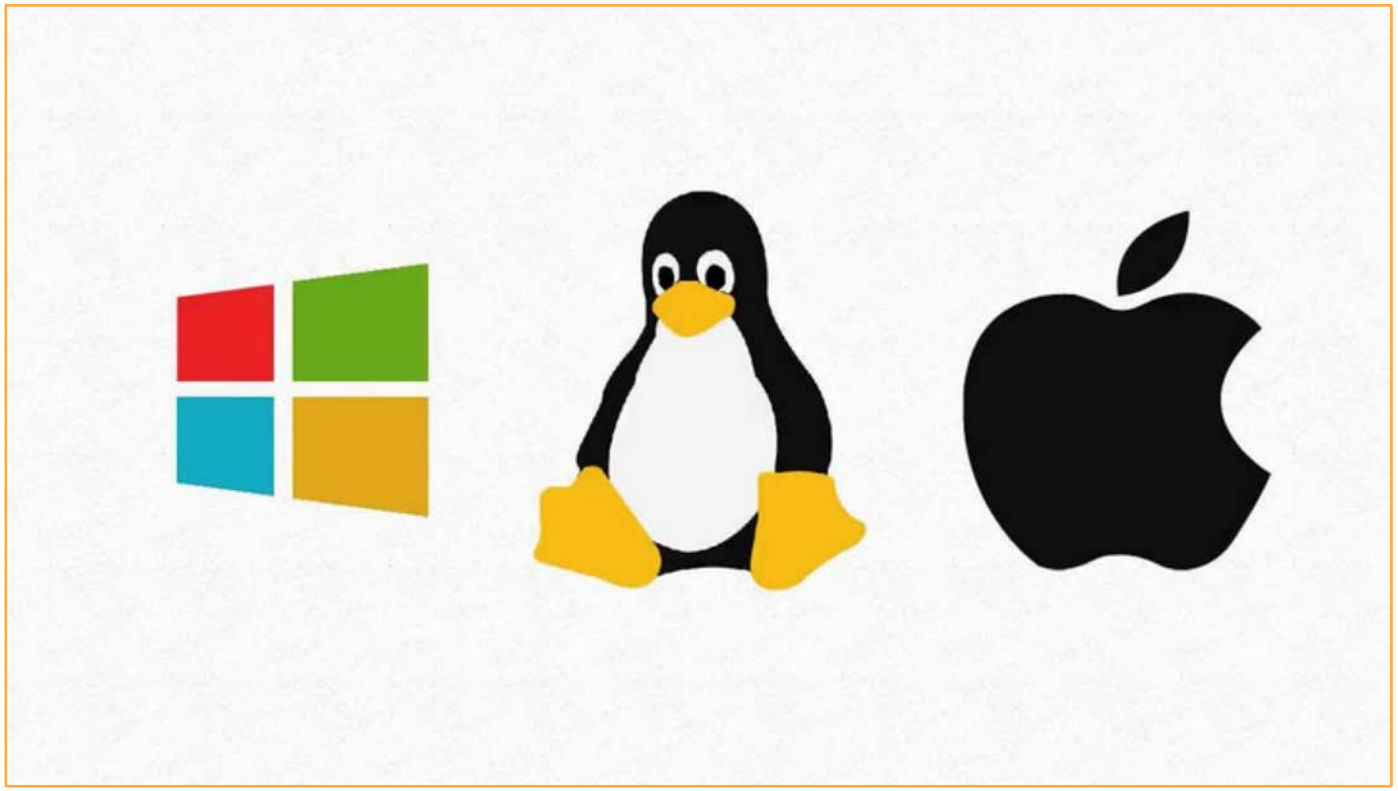
Watching vs Doing

Watch and Listen

Try it for yourself

What is Unix?

- Operating System



Why Unix?

- Bioinformatics software designed to run on Unix platforms.
- Large amounts of data.
- Much faster than Windows PC.

trimAl

A tool for automated alignment trimming

IQ-TREE

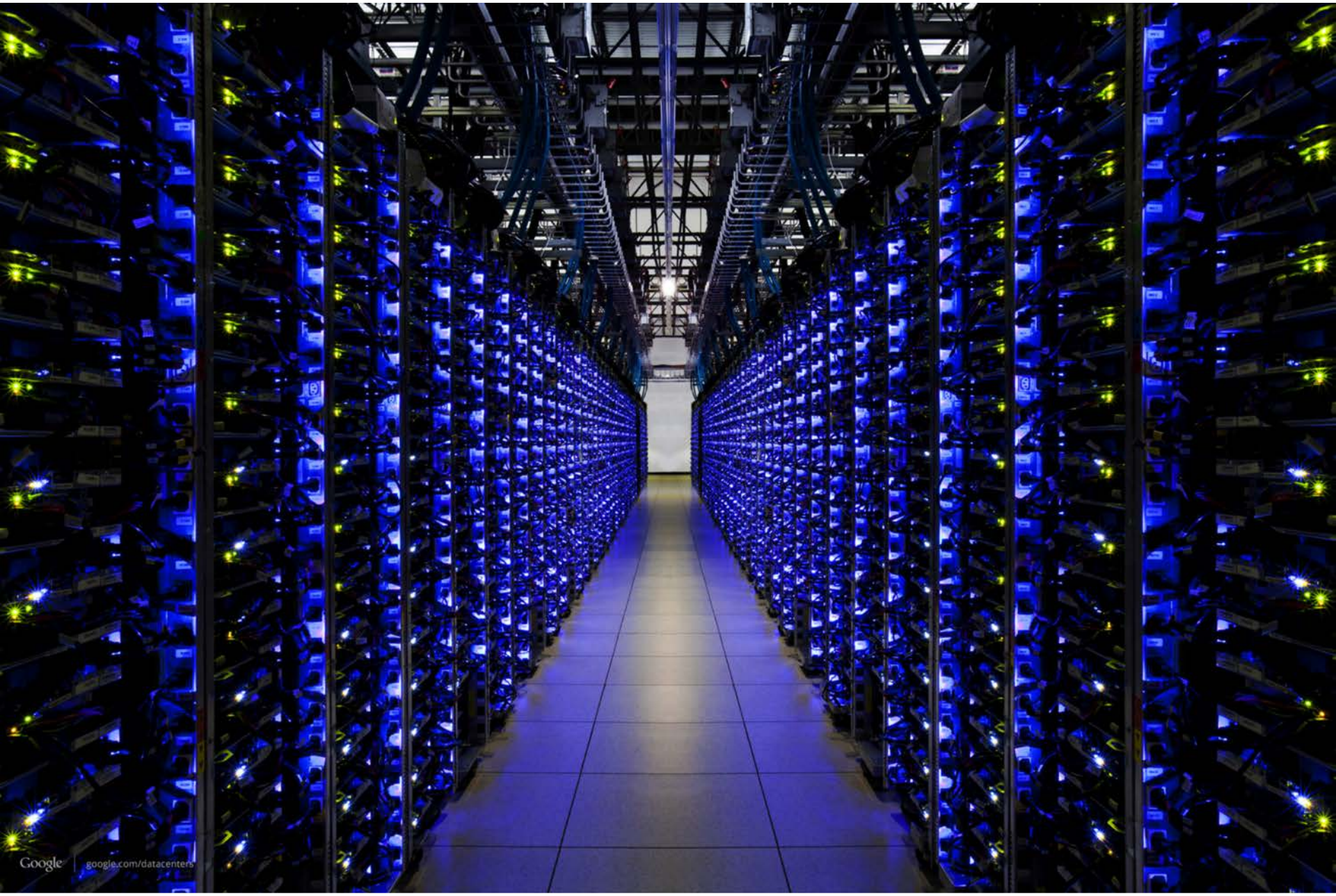
Efficient software for phylogenomic inference

Beast2

Bayesian evolutionary analysis by sampling trees

How Can We Use Unix?

- Linux computers or servers
- Computer clusters
- The cloud
  - What we're going to use this week


Google
google.com/datacenters

Cloud Computing Solutions

amazon web services™

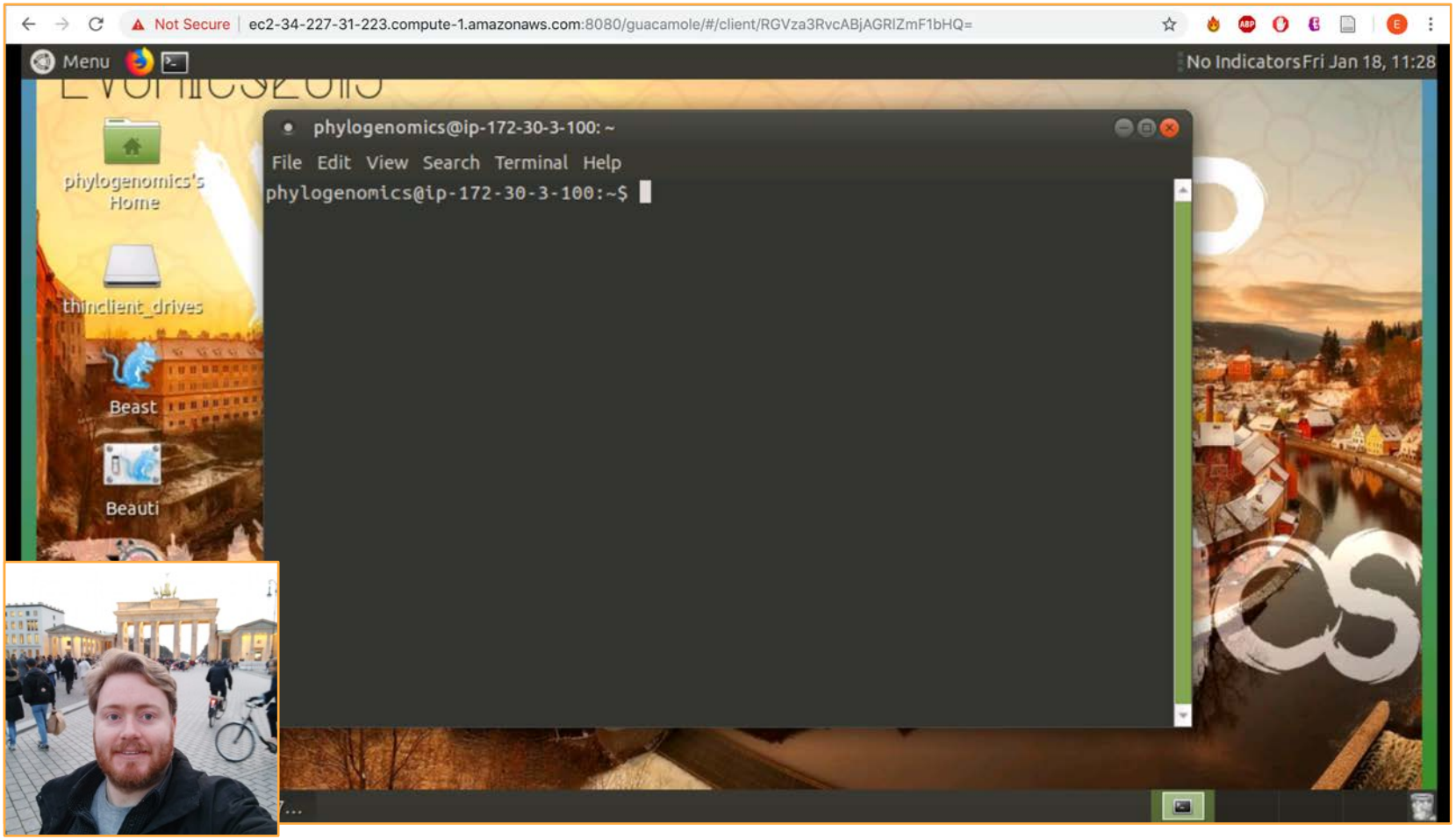
Google Cloud Platform

Microsoft Azure

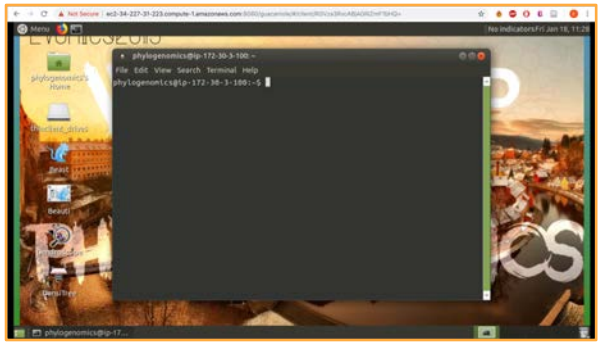
AWS “Availability Zones” and Data Centres

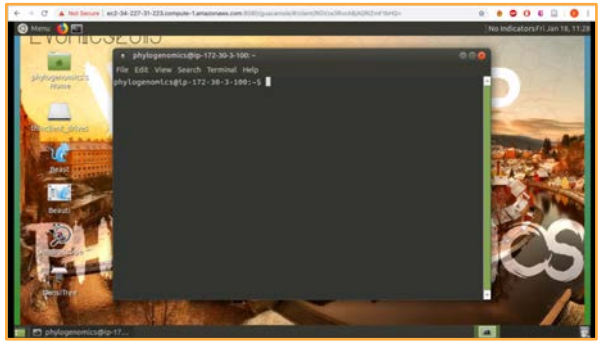
How it Works

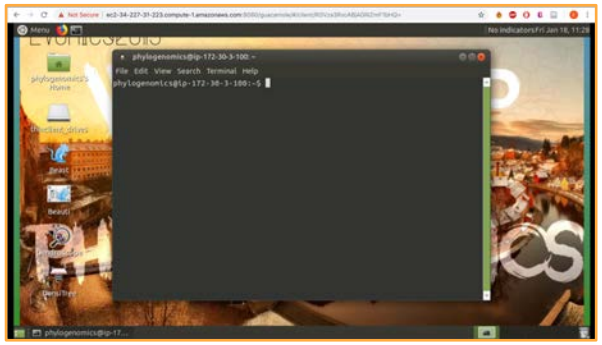
AMI (“Amazon Machine Image”)
Base computer with all data and software



How it Works







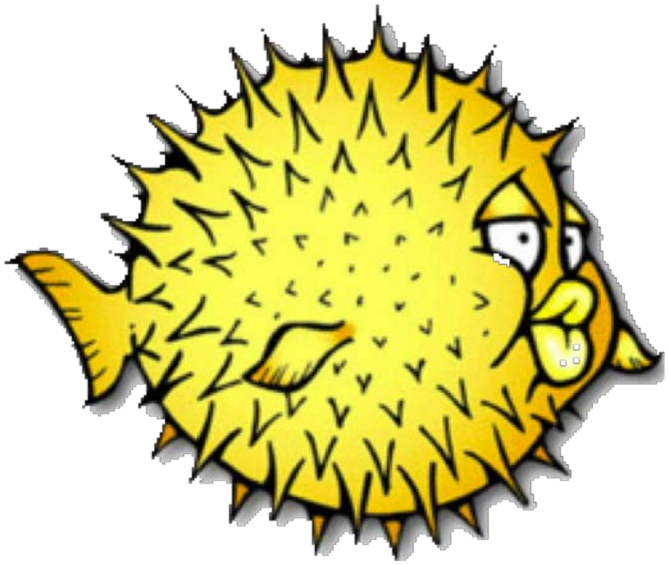
Own copy of the AMI = Instance
(Virtual Machine or VM)

Terminology

- Creating an instance – *buying a brand new computer with software already installed.*
- Starting an instance – *turning that computer on.*
- Stopping an instance – *turning that computer off.*
- Terminating an instance – *setting that computer on fire and throwing it out of the window.*

Connecting to Your Instance

Remote Desktop Software
e.g. Guacamole or X2Go



Secure Shell – "SSH"
e.g. SSH or PuTTY

http://evomics.org/workshops/2019-workshop-on-phylogenomics-cesky-krumlov/

Anna Karnkowska, University of Warsaw

Antonis Rokas, Vanderbilt University

Miscellaneous

- Instance Addresses – Check Daily
- Faculty Lunches – Sign Up!
- T-shirt Competition

SCHEDULE

Week 1: 20-26 January 2019

Workshop on Phylogenomics 2019 Instance List

File Edit View Insert Format Data Tools Add-ons Help

100% $ % .0 .00 123 Arial

fx

	A	B	C	D	E
1	**Name**	**Public Domain**			
2	Eric	ec2-34-227-31-223.compute-1.amazonaws.com			
3	Marina	ec2-3-82-175-48.compute-1.amazonaws.com			
4	Jacob	ec2-3-83-102-107.compute-1.amazonaws.com			
5	Ania	ec2-52-91-1-245.compute-1.amazonaws.com			

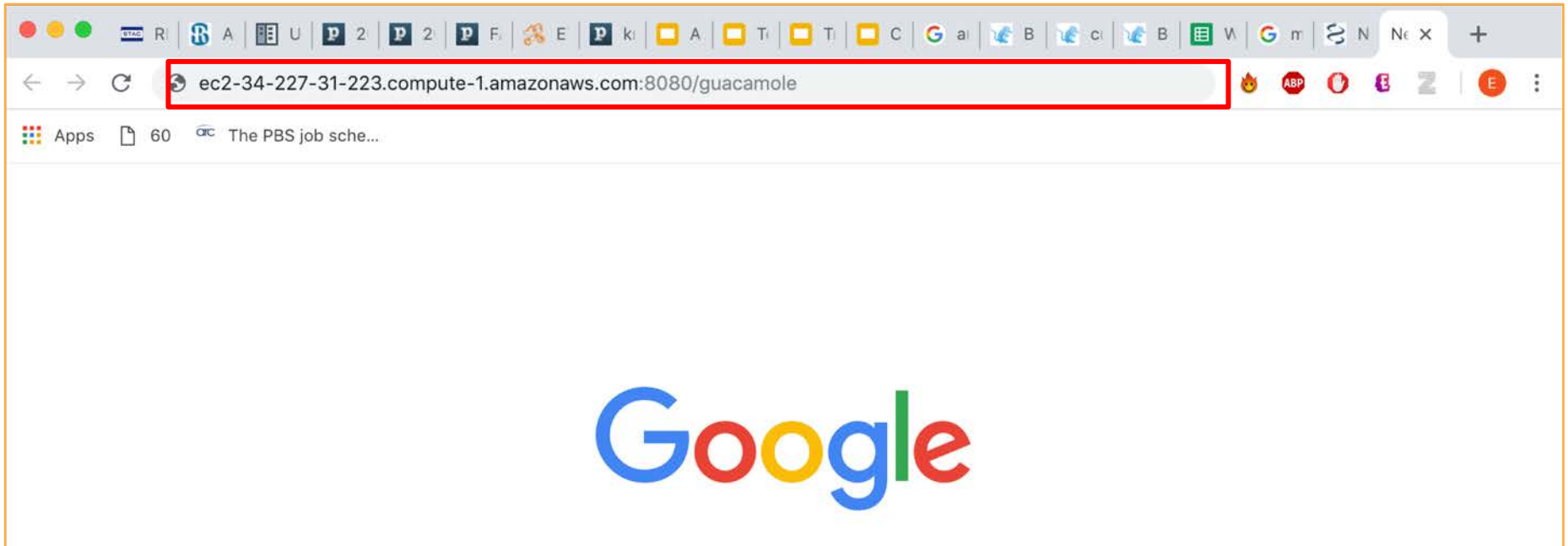
Find your name and copy your public domain

Open your internet browser (e.g. Google Chrome)

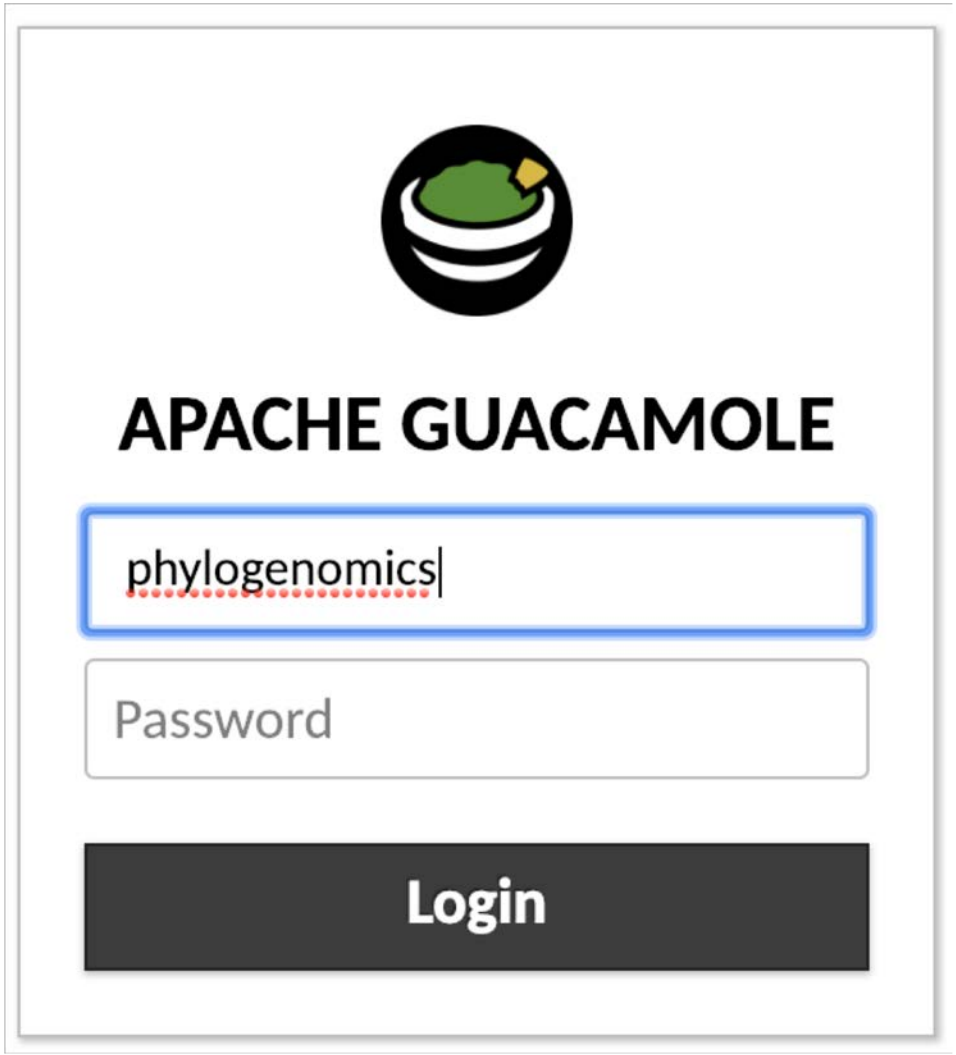
Paste the public domain followed by :8080/guacamole

Example:

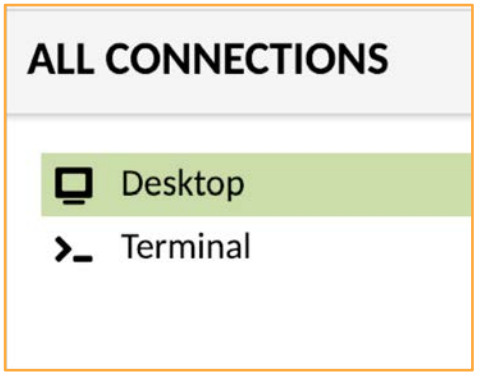
ec2-34-227-31-223.compute-1.amazonaws.com:8080/guacamole



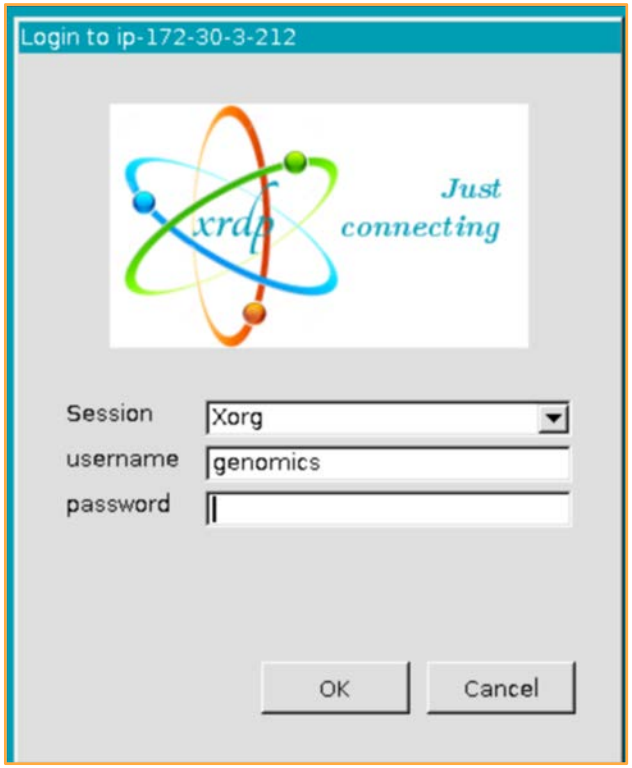
Enter the username “phylogenomics” and password



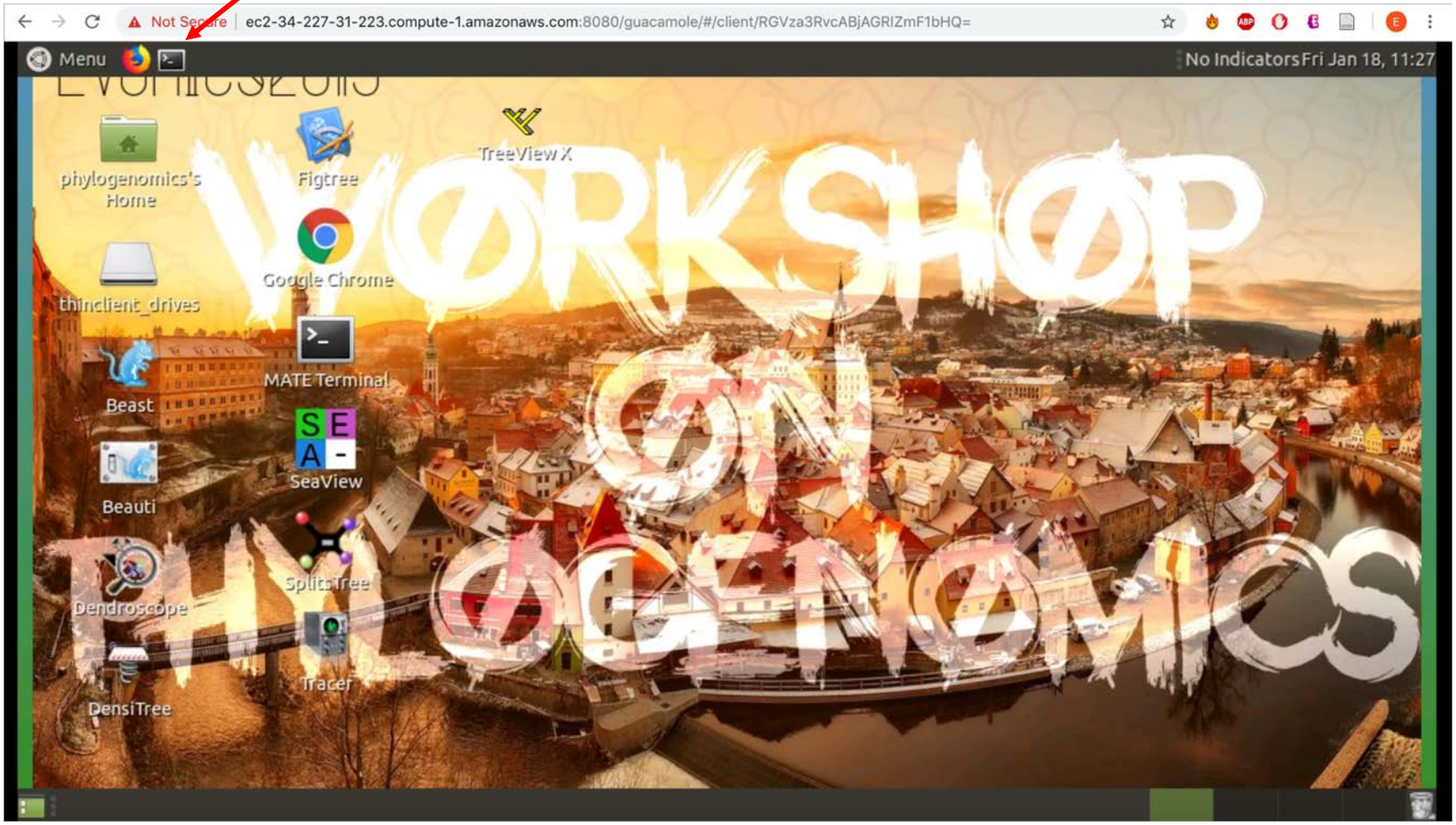
Select Desktop

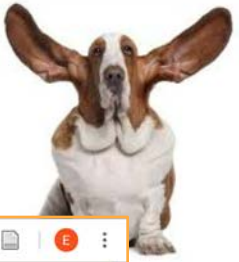


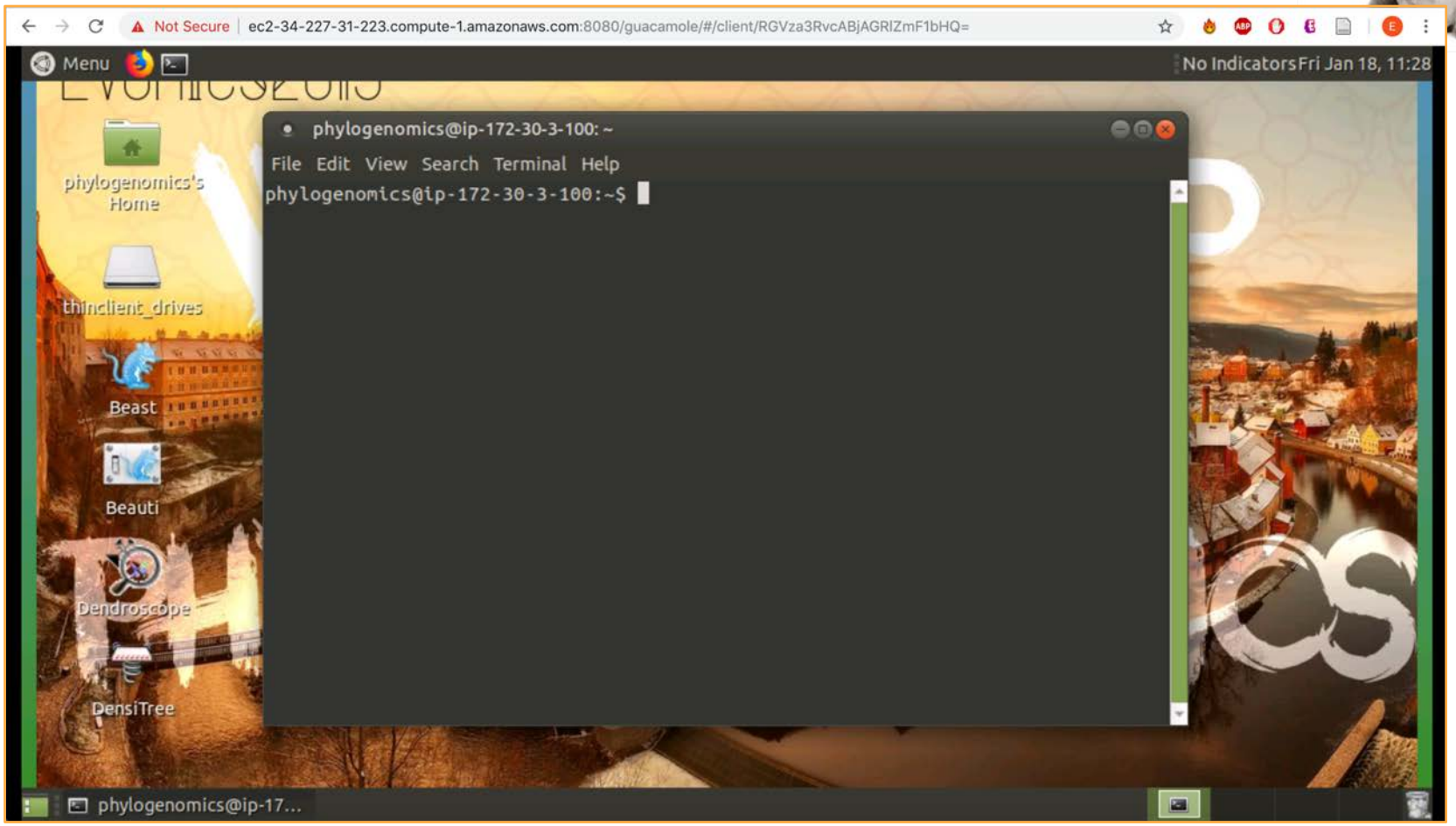
Enter the username “phylogenomics” and password again



Open a Terminal Window using this icon







You're now connected and you're ready to learn some Unix!

But First…
The domain address will change every day after we stop and re-start the instances.
Each morning, you will need to return to the “Instance List” webpage, retrieve your new address and log in again

Workshop on Phylogenomics 2019 Instance List

File Edit View Insert Format Data Tools Add-ons Help

100% $ % .0 .00 123 Arial

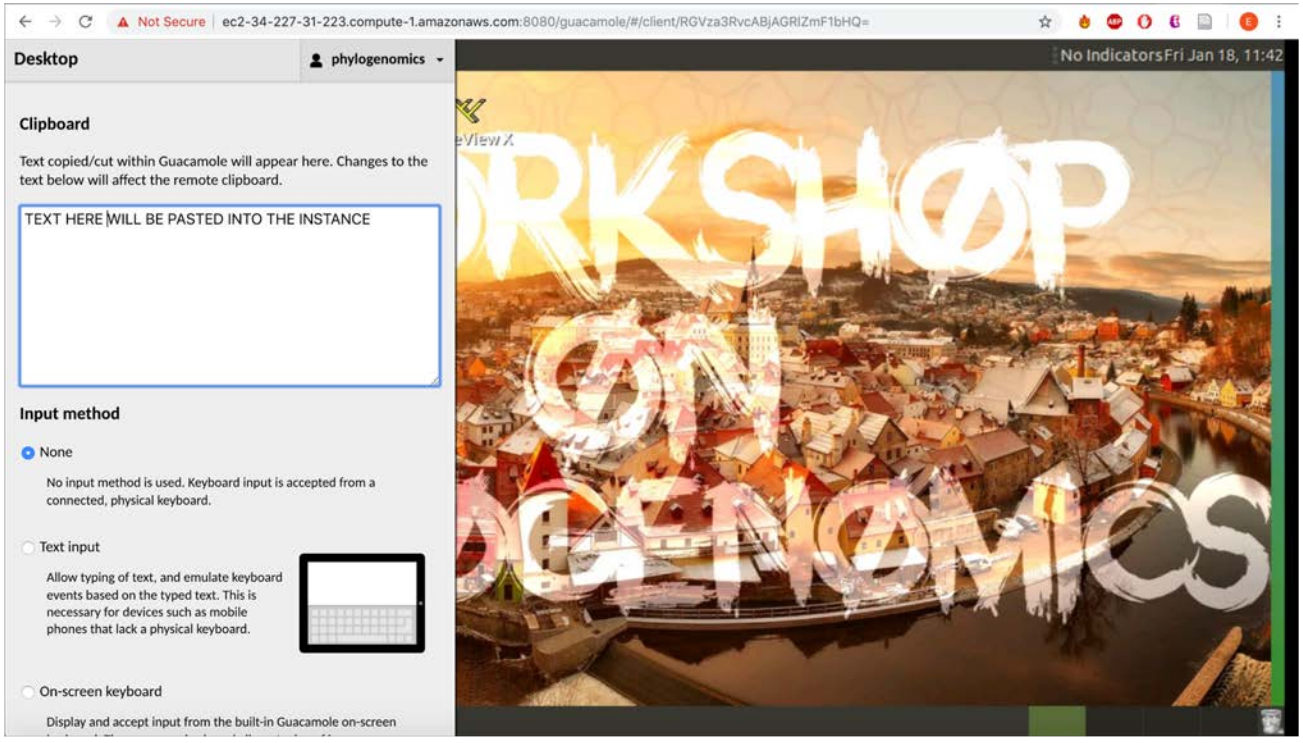
fx

	A	B	C	D	E
1	**Name**	**Public Domain**			
2	Eric	ec2-34-227-31-223.compute-1.amazonaws.com			
3	Marina	ec2-3-82-175-48.compute-1.amazonaws.com			
4	Jacob	ec2-3-83-102-107.compute-1.amazonaws.com			
5	Ania	ec2-52-91-1-245.compute-1.amazonaws.com			

Copying and Pasting

AVOID COPYING AND PASTING WHEREVER POSSIBLE!

But if you do need to…
Press Ctrl+Alt+Shift
Paste the text into the box with right click -> Paste
Press Ctrl+Alt+Shift again
You can now paste into the instance using right click



Your final task before we get started!

Make sure that typing tilde (~), backslash (\), pipe (|), and carat (^) in the terminal works.

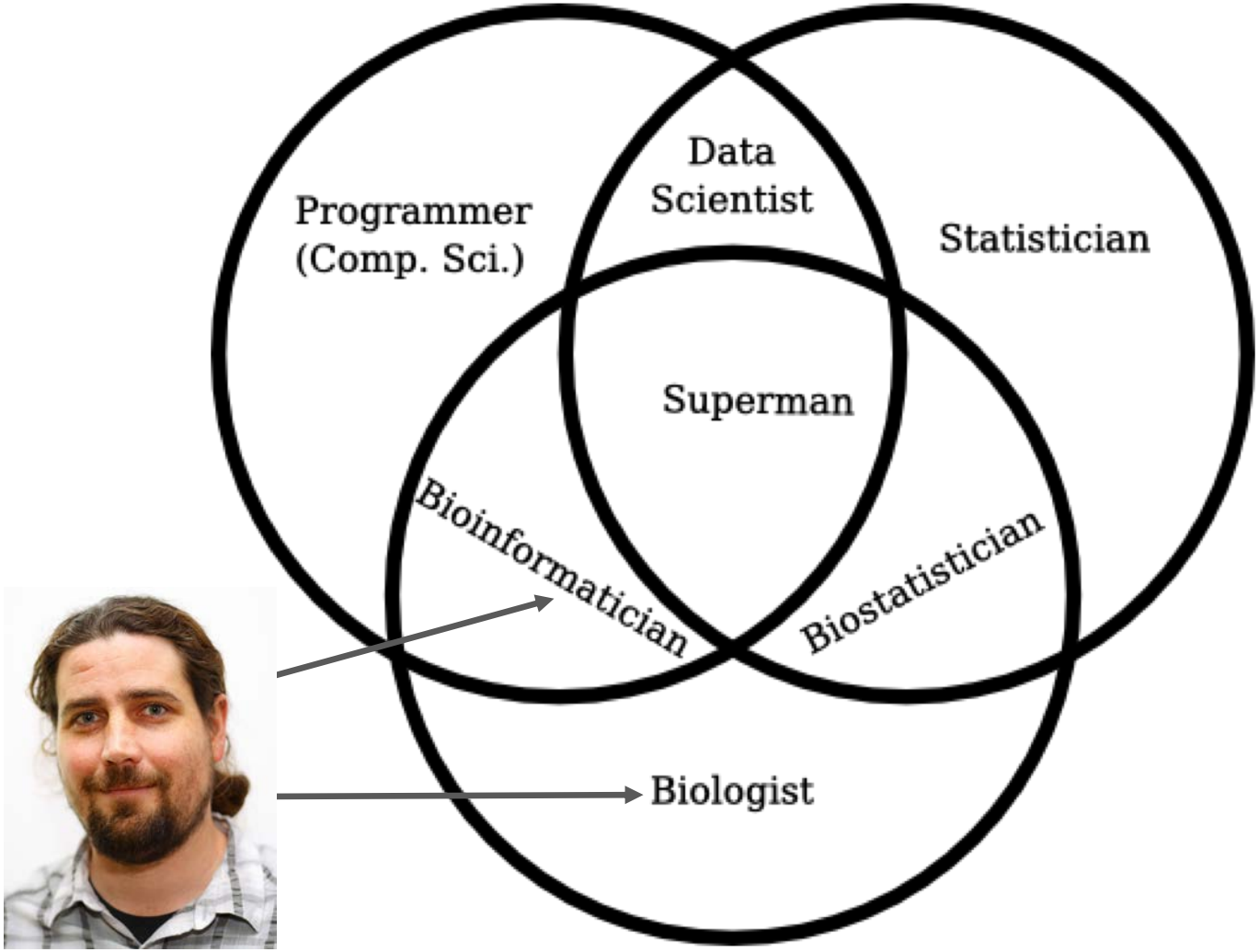
Google search to find these on your computer if you don’t know where they are.


QUESTIONS???

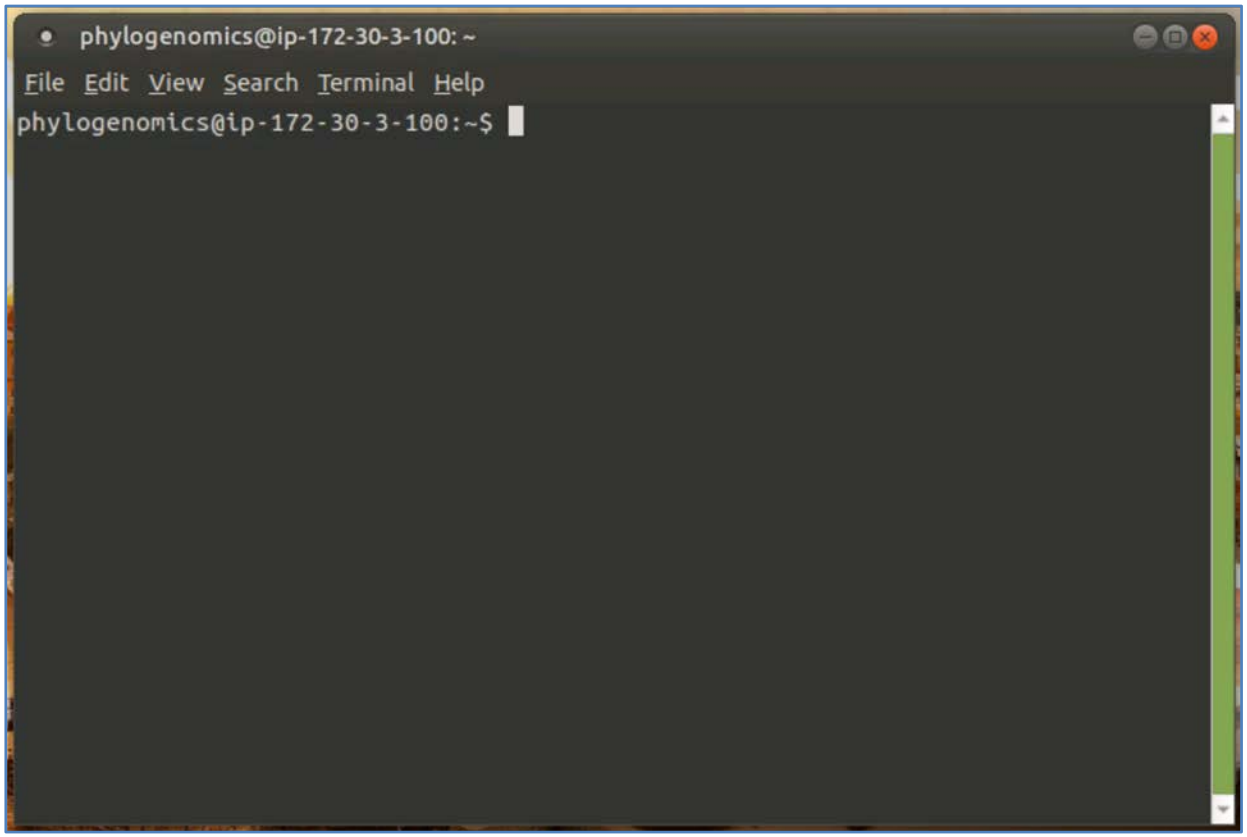
Introduction to Unix

Eric Salomaki

- BA, The Evergreen State College, 2005
- MS, Ohio University, 2012
  - Molecular systematics of freshwater red algae
- PhD, University of Rhode Island, 2017
  - Red algal parasite evolution
- Postdoc, University of Rhode Island, 2017-18
  - Functional ecology of microeukaryotes in the North Atlantic
- Postdoc, Institute of Parasitology, CAS 2018-Present
  - Impact of transitioning to and from parasitism on genome evolution


Programmer
(Comp. Sci.)
Data
Scientist
Statistician
Superman
Bioinformatician
Biostatistician
Biologist

The Terminal



The Command Line, The Shell, The Prompt

Where you see this “$” followed by text, I want you to type the text on your command line

Location is Important

First Task – Where am I?

```
~$ pwd
```

```
phylogenomics@ip-172-30-3-100:~$ pwd
/home/phylogenomics
phylogenomics@ip-172-30-3-100:~$
```

This is your “present working directory”.

/

= ROOT

home

bin

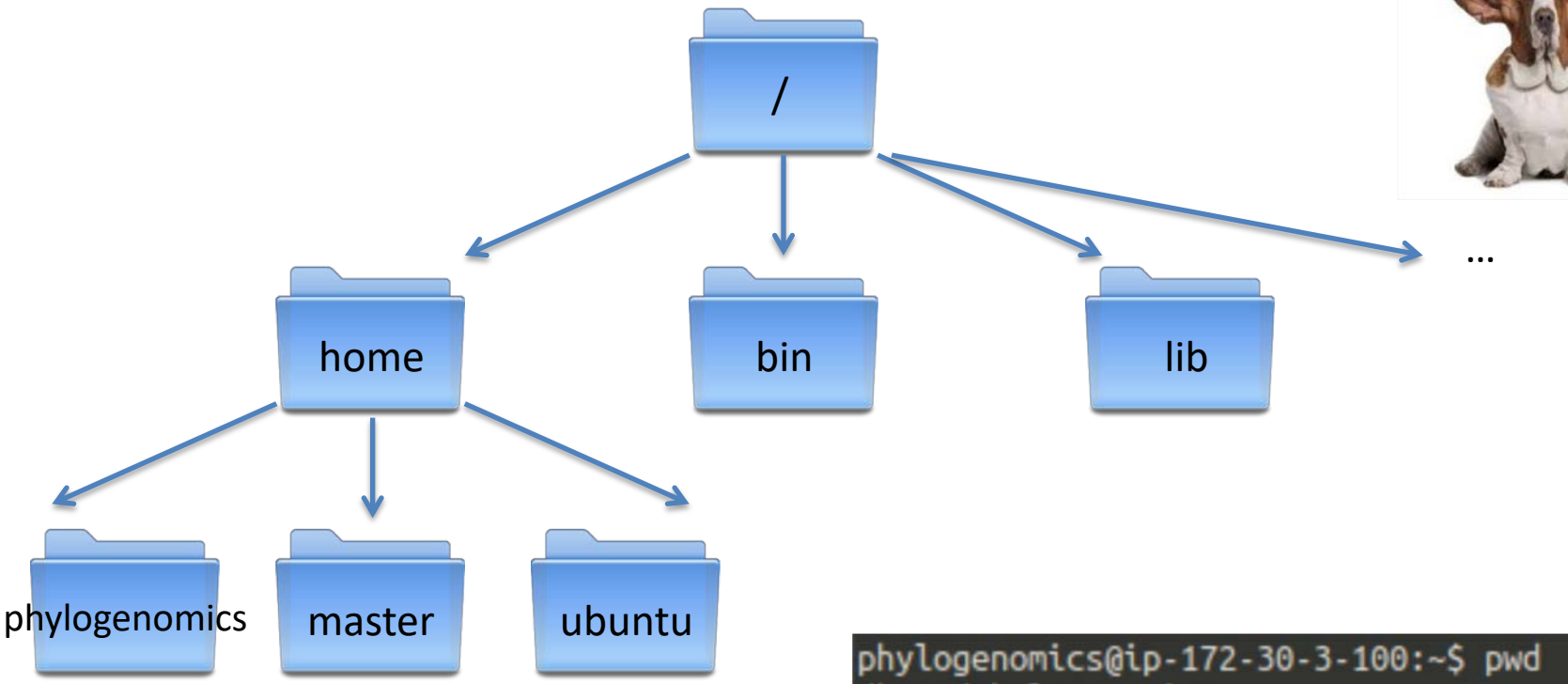
lib

...

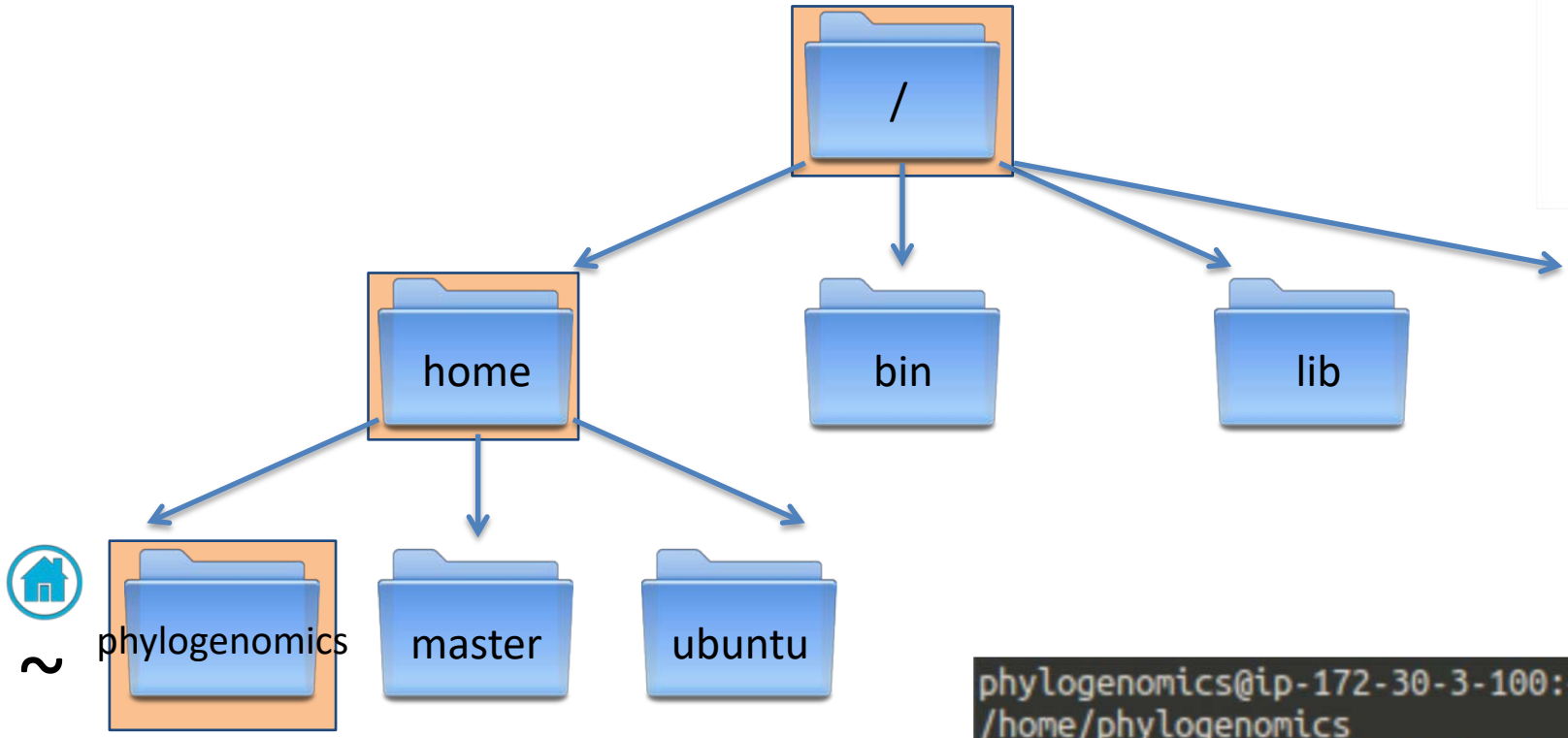
phylogenomics

master

ubuntu




```
phylogenomics@ip-172-30-3-100:~$ pwd
/home/phylogenomics
phylogenomics@ip-172-30-3-100:~$
```




```
phylogenomics@ip-172-30-3-100:~$ pwd
/home/phylogenomics
phylogenomics@ip-172-30-3-100:~$
```

This location is also known as your Home Directory

Tilde is shorthand for Home ~

Now let's create some directories and files

Make a directory

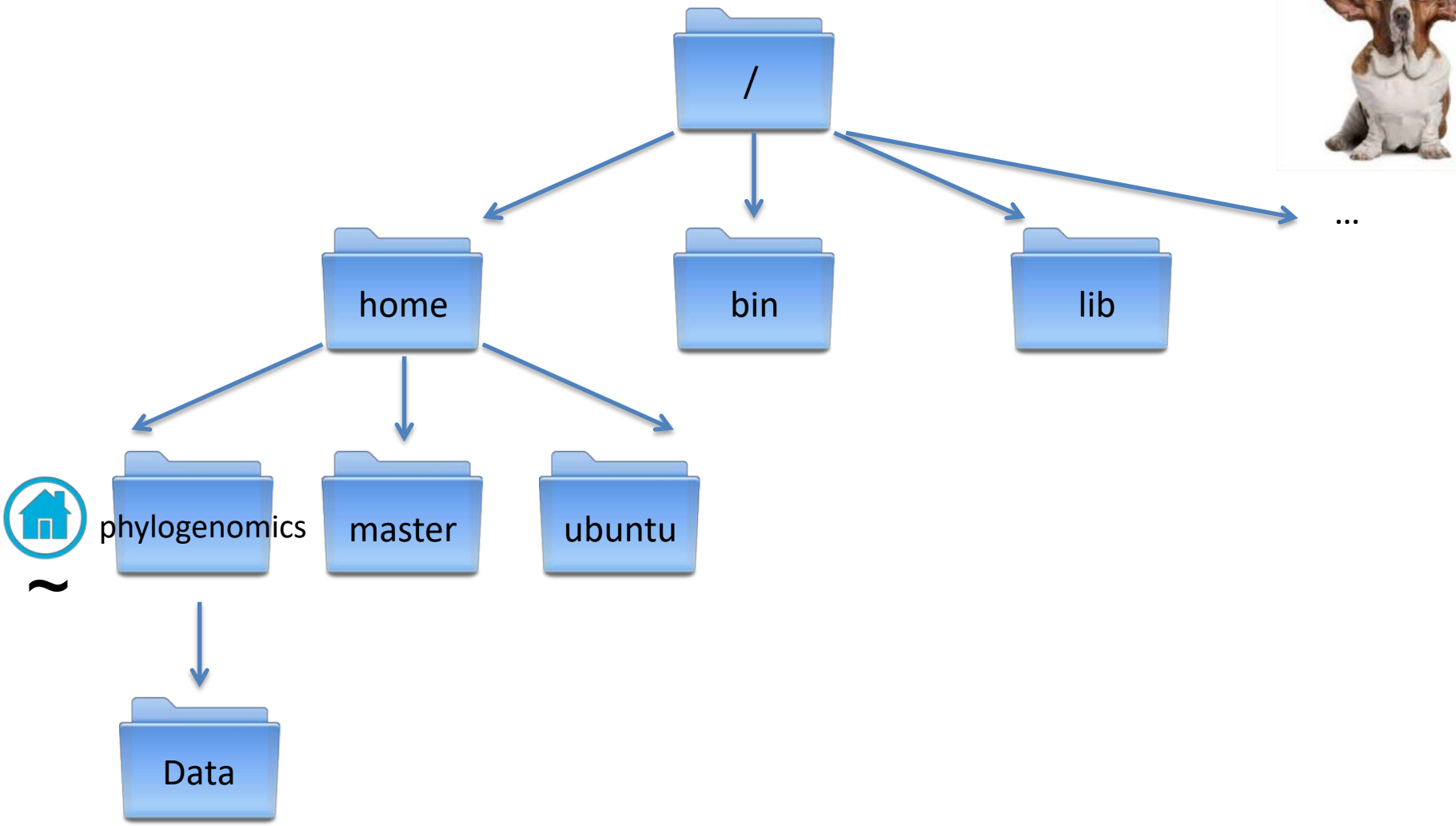
```
~$ mkdir ./Data
```

Change into this directory

```
~$ cd Data
```

Now what is your present working directory?

NOTE! Directory names (and file names for the matter) can not contain spaces. Underscores are often used instead if you want to separate words.


/
home
bin
lib
...
phylogenomics
master
ubuntu
~
Data


```
phylogenomics@ip-172-30-3-100:~$ mkdir ./Data
phylogenomics@ip-172-30-3-100:~$ cd Data
phylogenomics@ip-172-30-3-100:~/Data$ pwd
/home/phylogenomics/Data
phylogenomics@ip-172-30-3-100:~/Data$
```

Now let's create some directories and files

Make an empty file

```
~/Data$ touch rags
```

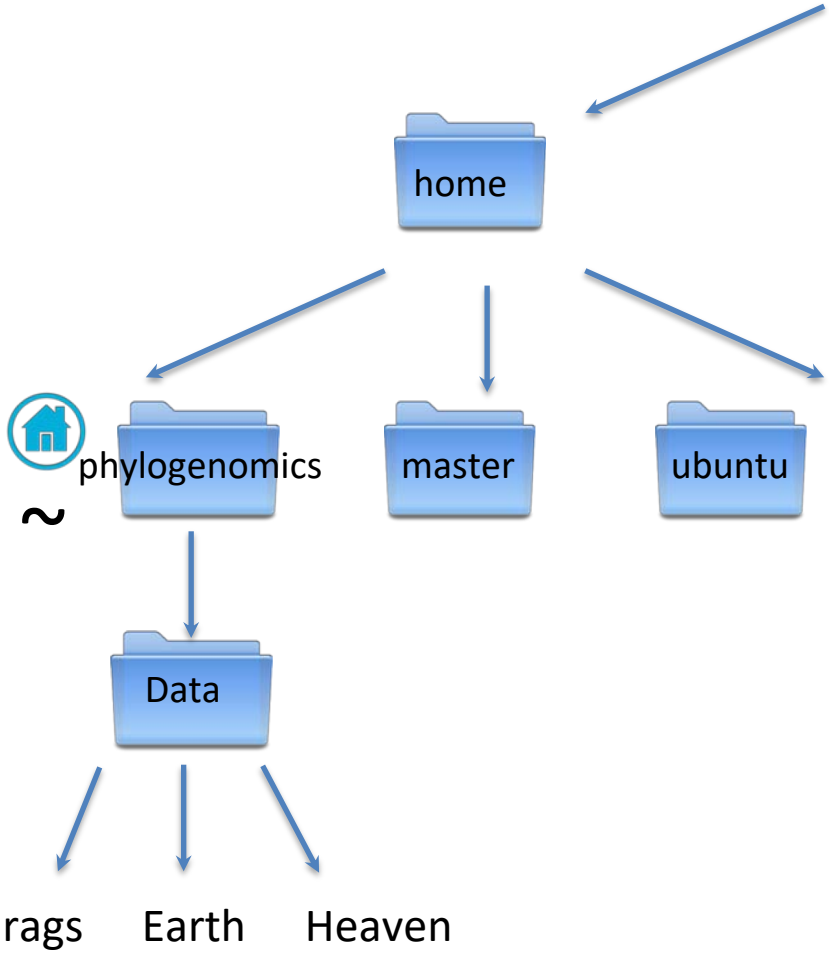
And another two

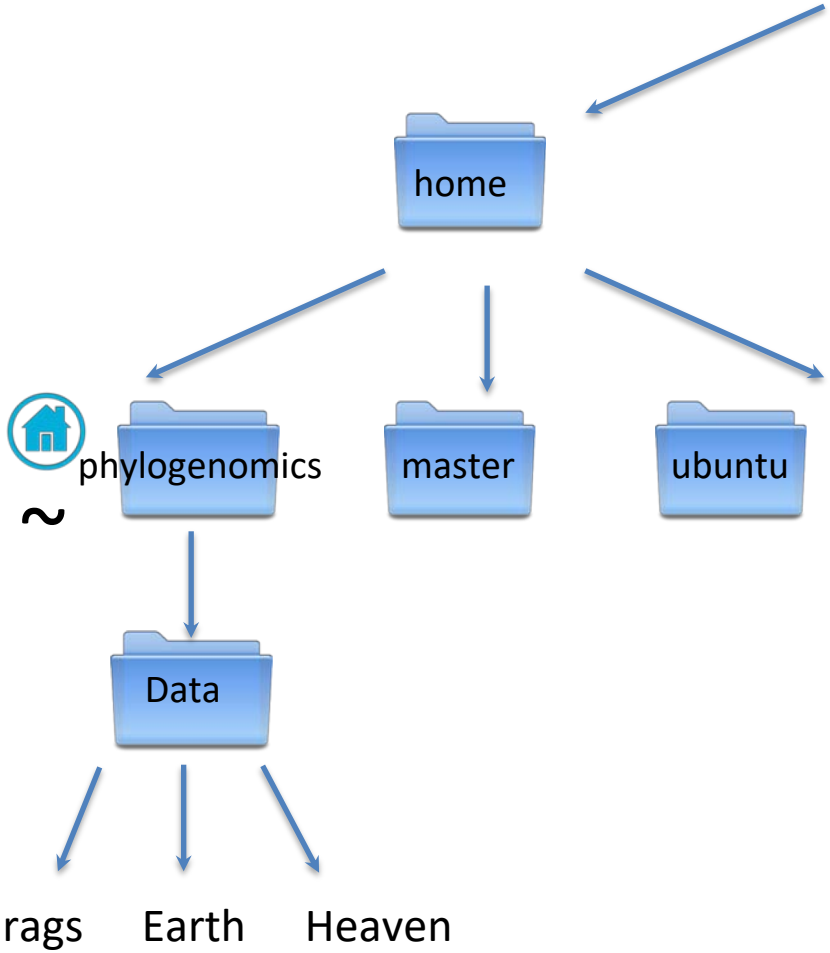
```
~/Data$ touch Heaven Earth
```

Now let's list the contents of the current directory (Data)

```
~/Data$ ls
```

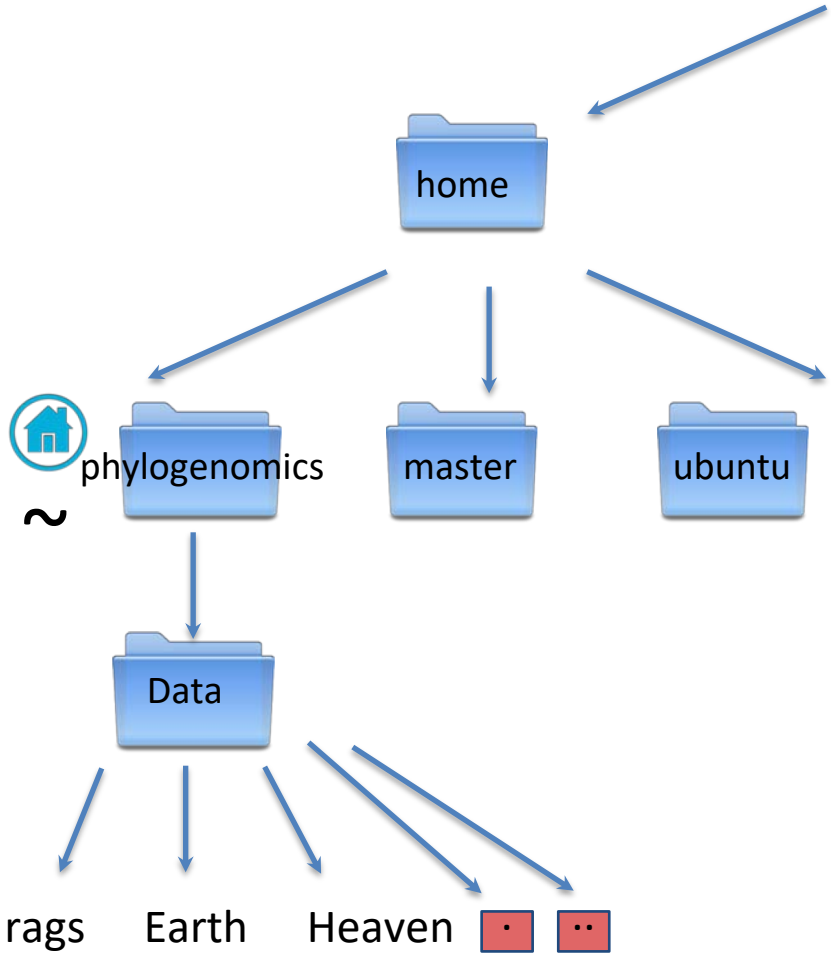
```
phylogenomics@ip-172-30-3-100:~/Data$ touch rags
phylogenomics@ip-172-30-3-100:~/Data$ touch Heaven Earth
phylogenomics@ip-172-30-3-100:~/Data$ ls
Earth  Heaven  rags
```


home
phylogenomics
master
ubuntu
~
Data
rags
Earth
Heaven



Now list ALL of the files

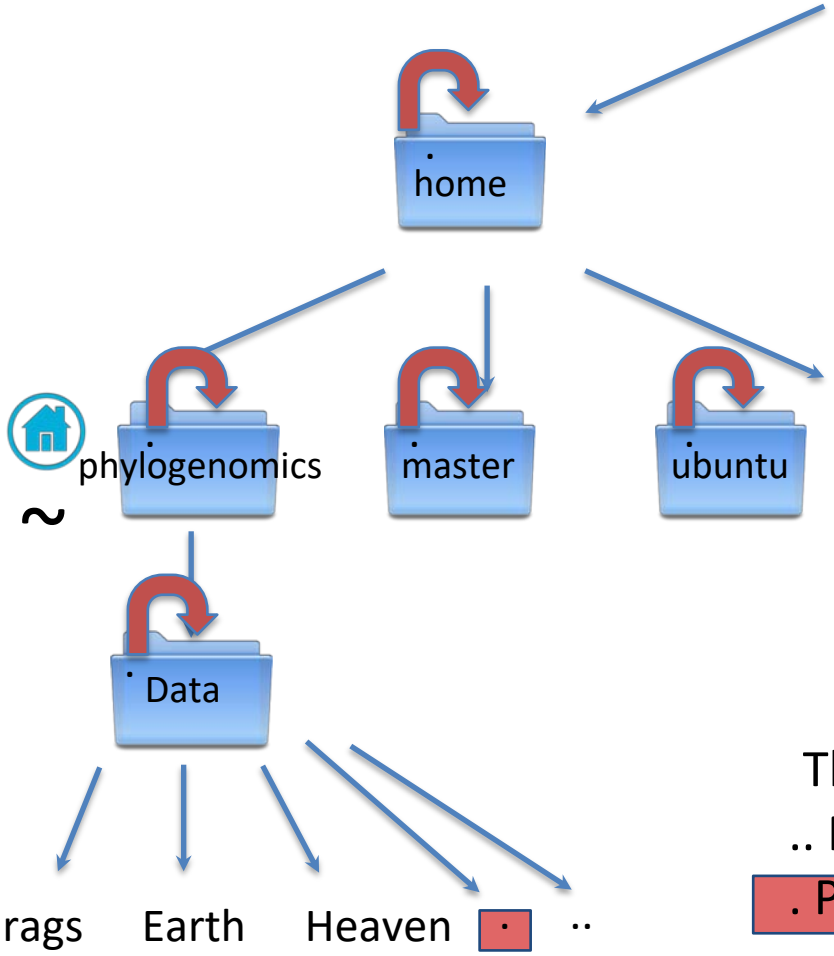
```
~/Data$ ls -a
```



Now list ALL of the files

```
~/Data$ ls -a
```

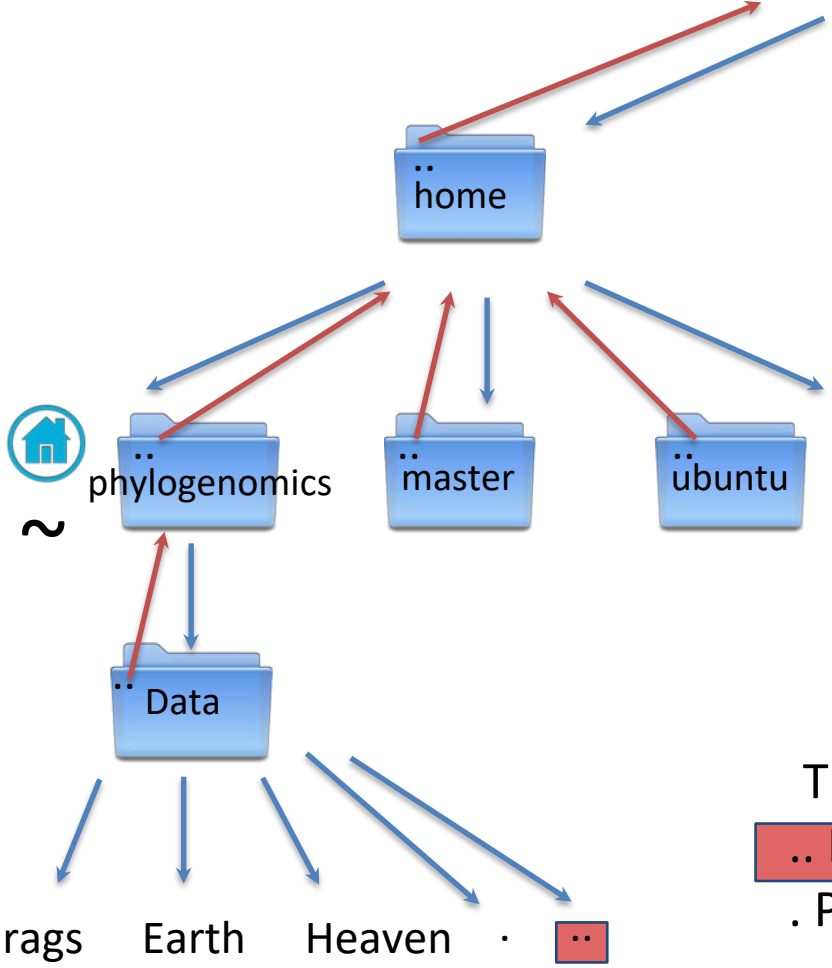
```
phylogenomics@ip-172-30-3-100:~/Data$ ls -a
.  ..  Earth  Heaven  rags
phylogenomics@ip-172-30-3-100:~/Data$
```



These special files are in every directory

.. Points to one directory above

. Points to the current directory



These special files are in every directory

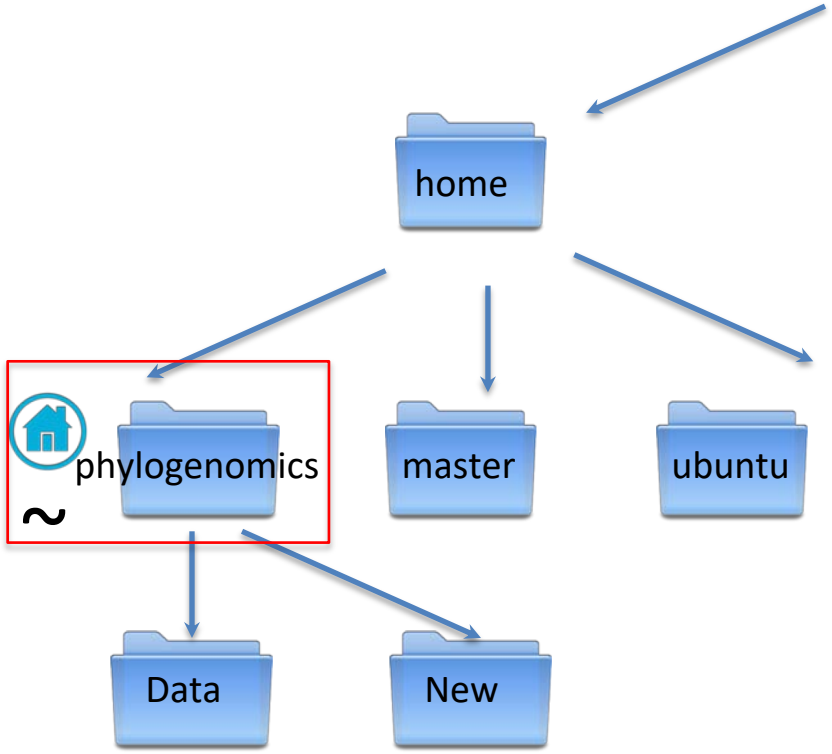
.. Points to one directory above

. Points to the current directory

. and .. are used for specifying location

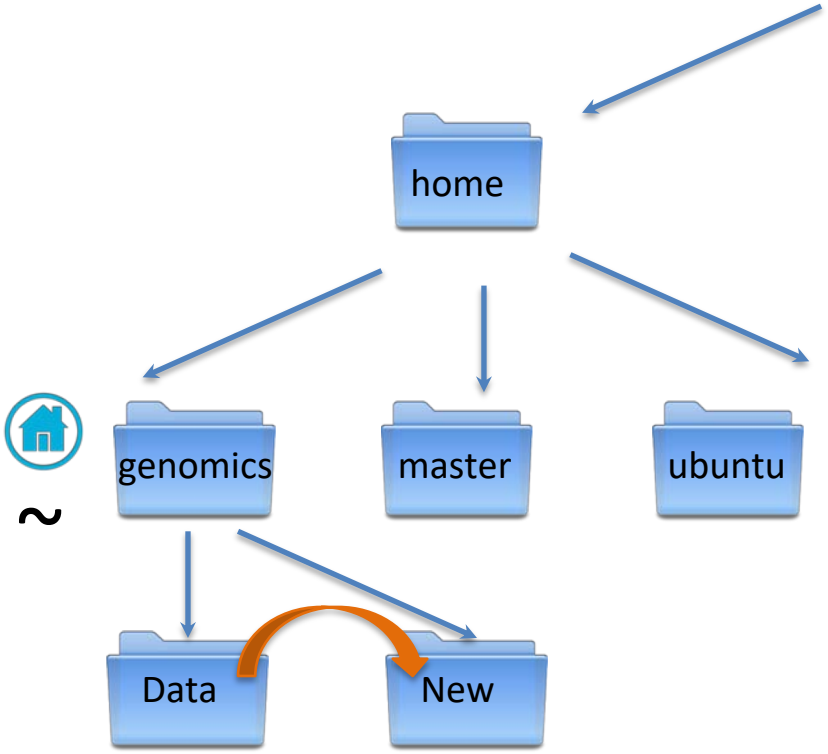
Whenever you do anything on Unix
(move around, move a file, rename a file etc…)
You have to tell the system where that thing is
using a path

. and .. are part of RELATIVE paths



Create a directory called <u>New</u> within the phylogenomics directory using the RELATIVE PATH

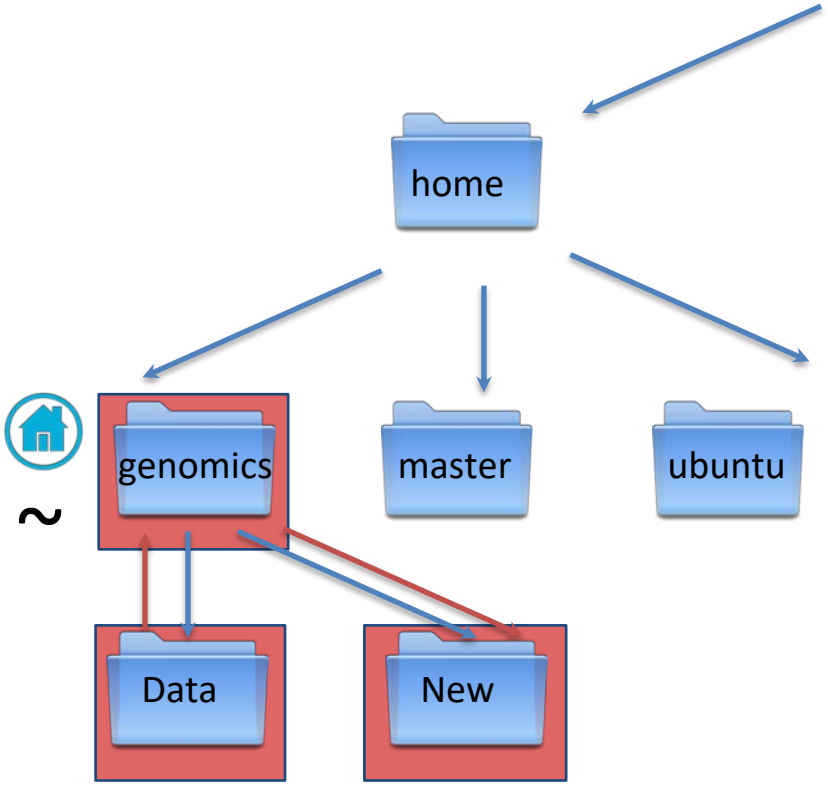
```
~/Data$ mkdir ../New
```



Move from Data to New

RELATIVE PATH

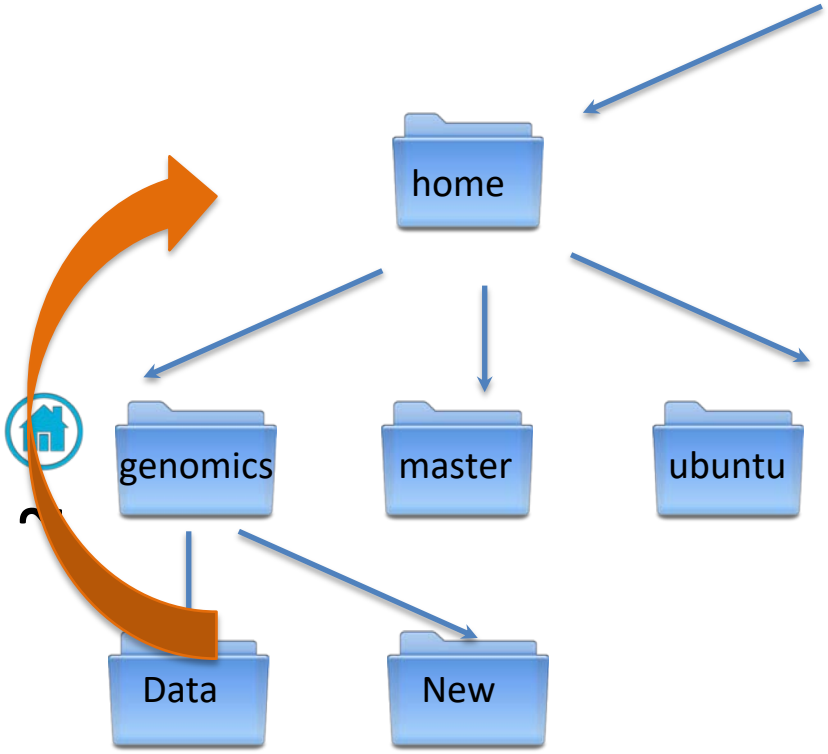
```
~/Data$ cd ../New
```



Moving from Data to New

RELATIVE PATH

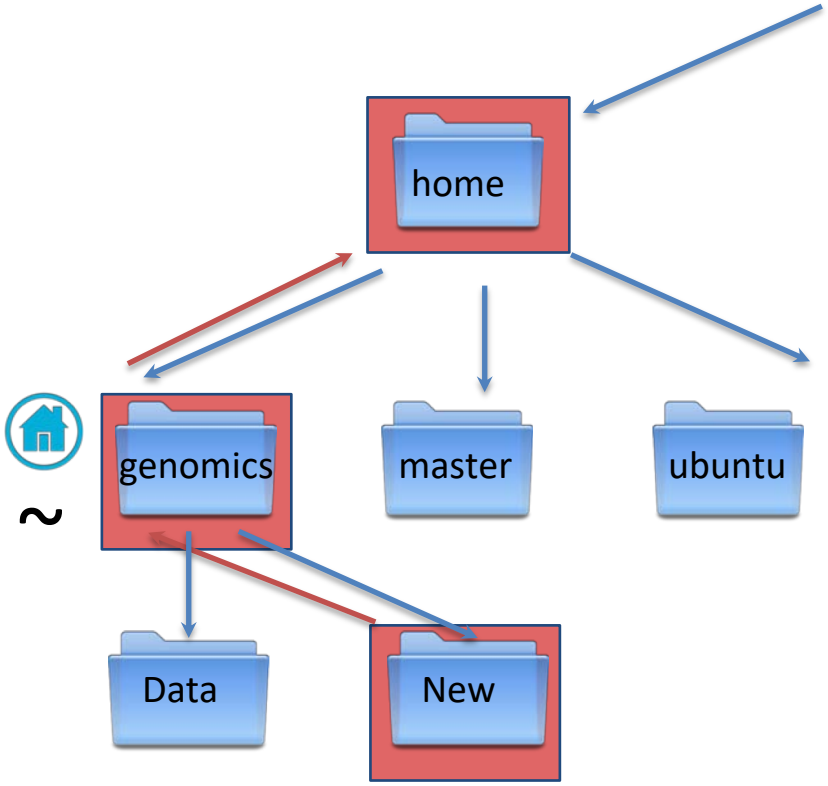
```
phylogenomics@ip-172-30-3-100:~/Data$ cd ../New
phylogenomics@ip-172-30-3-100:~/New$ pwd
/home/phylogenomics/New
```



Moving from New to home

RELATIVE PATH

```
:~/New$ cd ../../
```



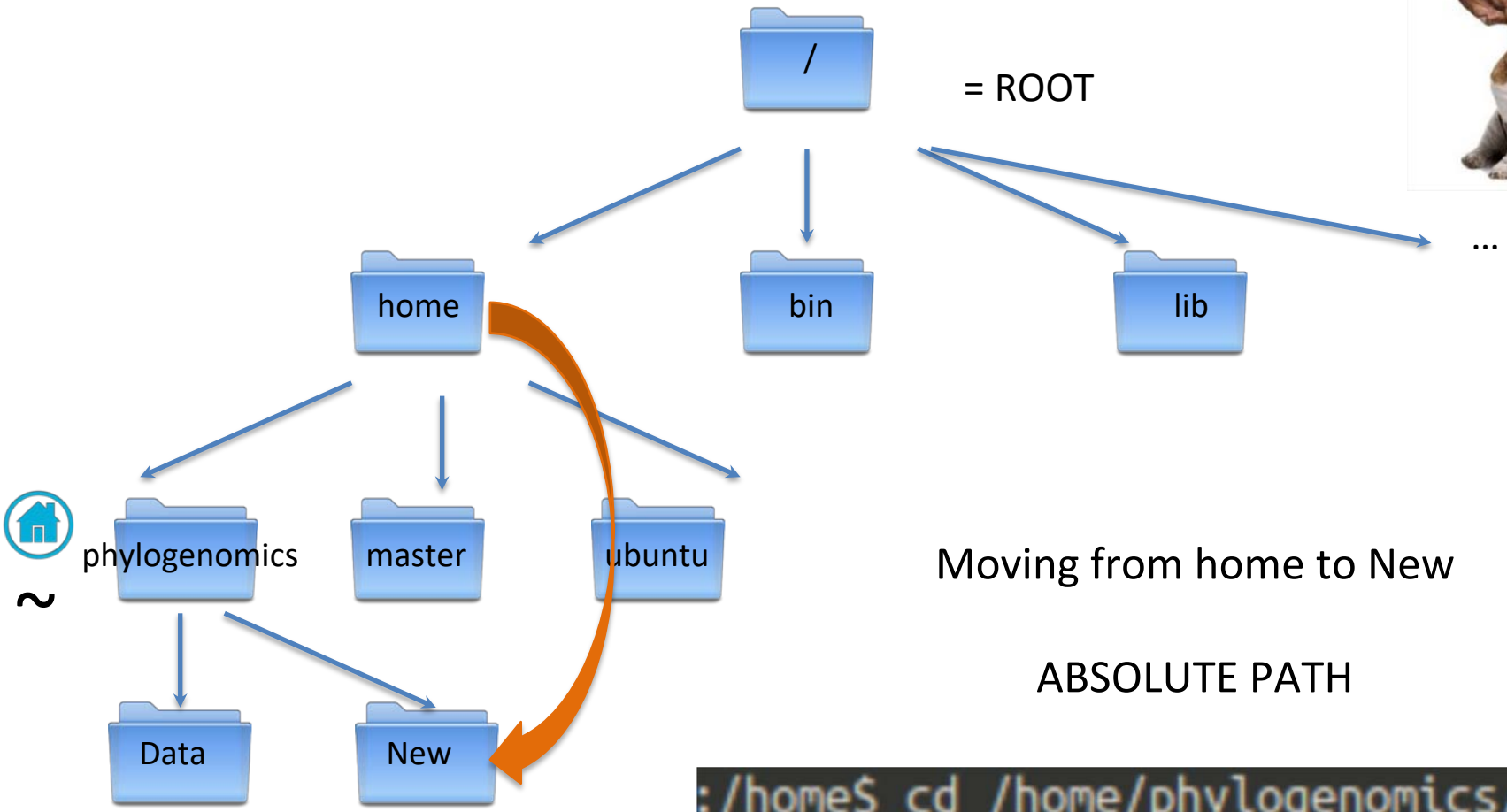
Moving from New to home

RELATIVE PATH

```
:~/New$ cd ../../
:/home$
```

Relative paths will always change depending on your location.

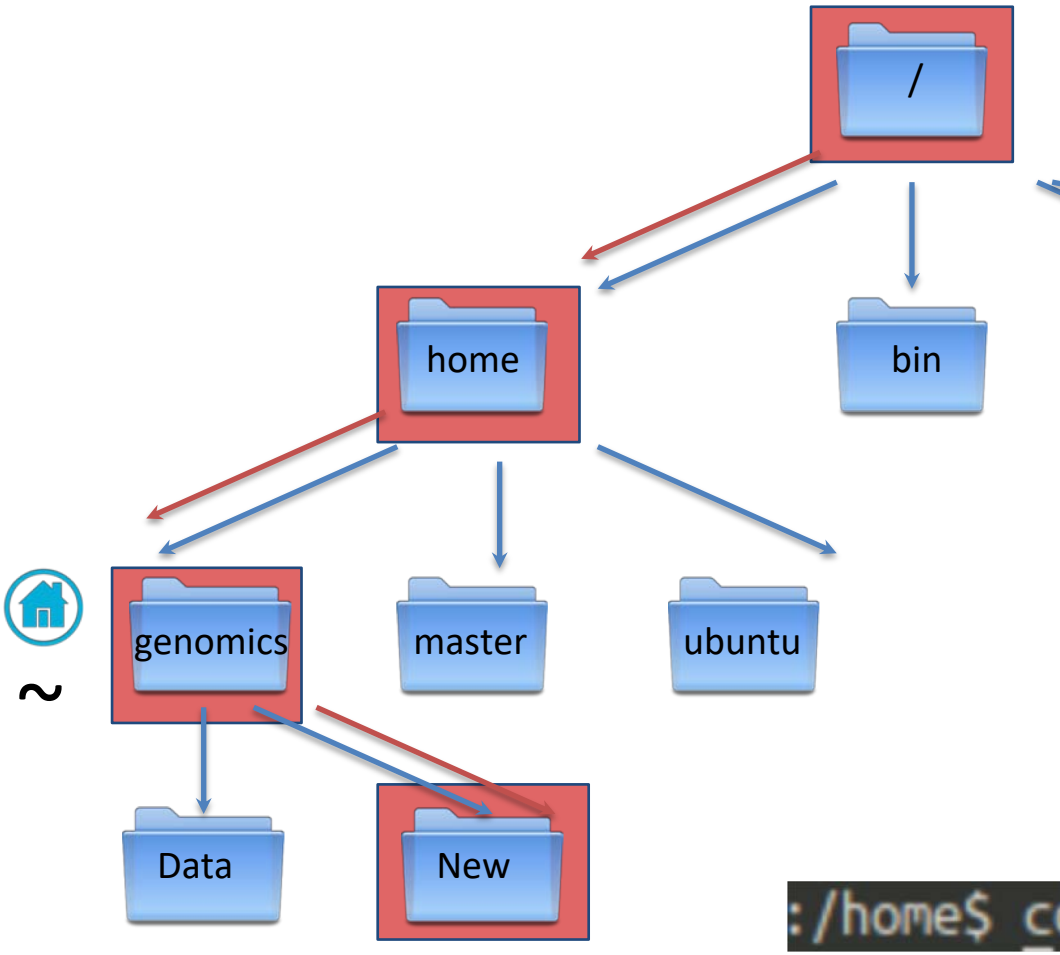
The alternative is ABSOLUTE paths.
These always start from root and will never change.



Moving from home to New

ABSOLUTE PATH

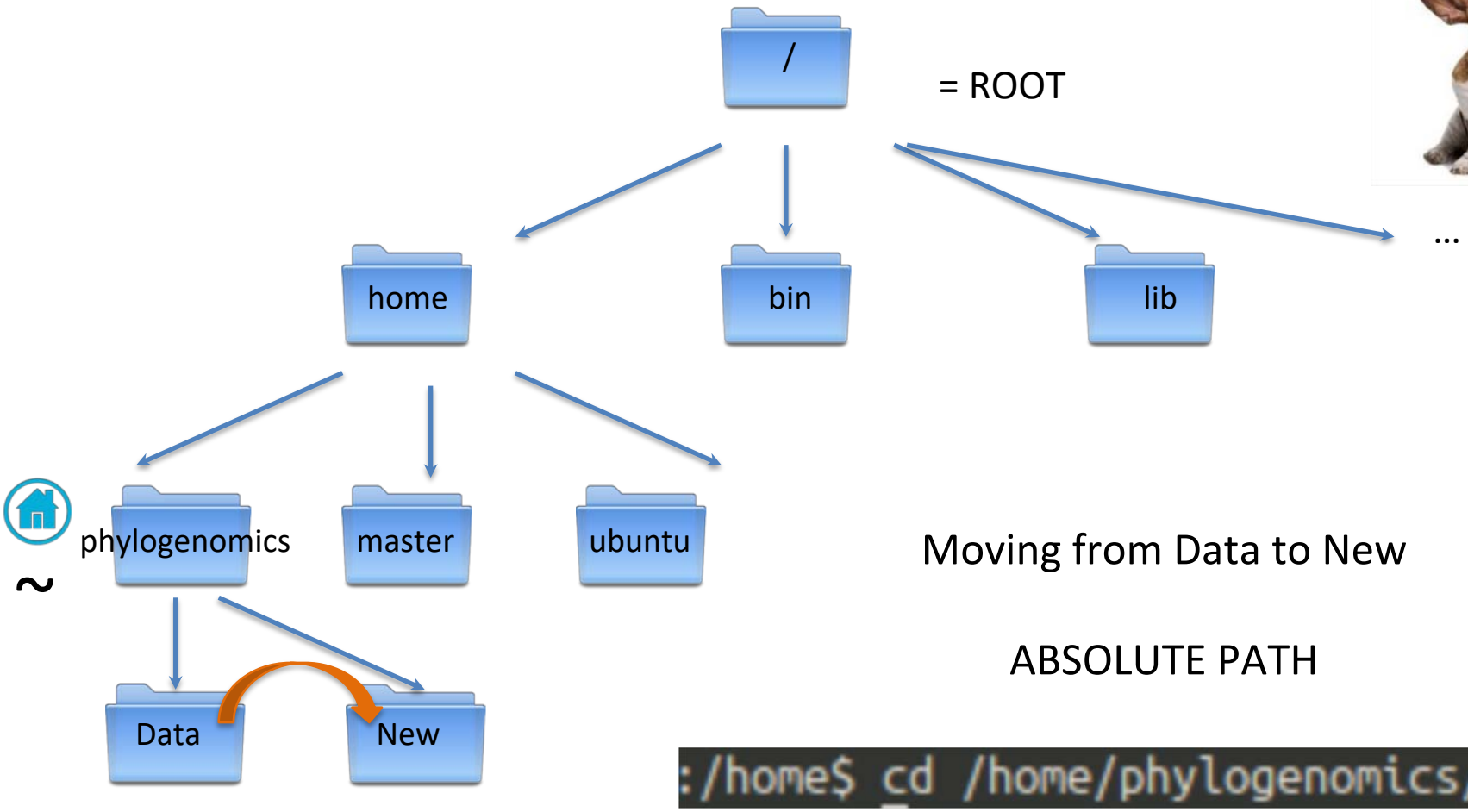
```
:/home$ cd /home/phylogenomics/New/
```



Moving from home to New

ABSOLUTE PATH

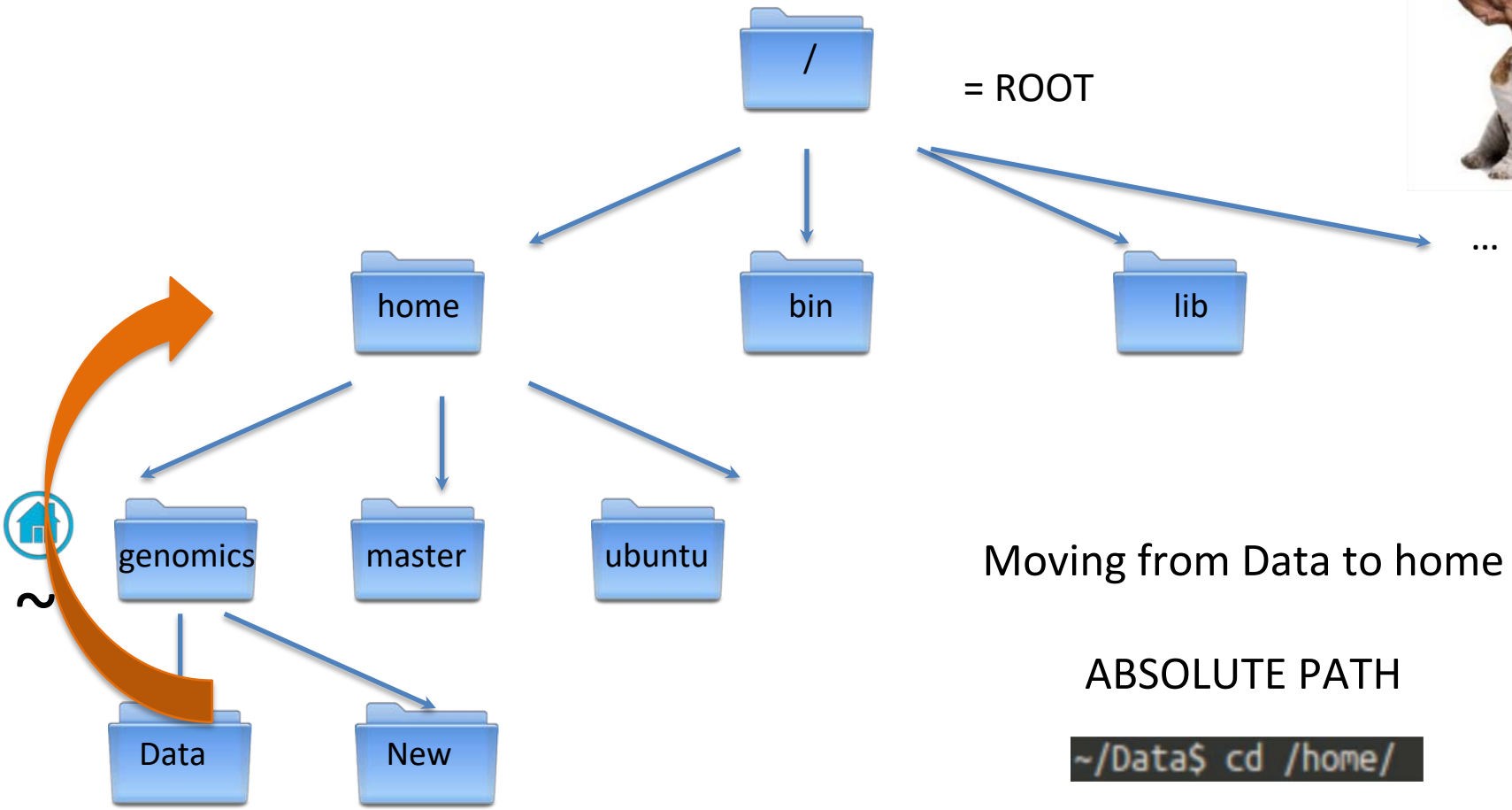
```
:/home$ cd /home/phylogenomics/New/
```



Moving from Data to New

ABSOLUTE PATH

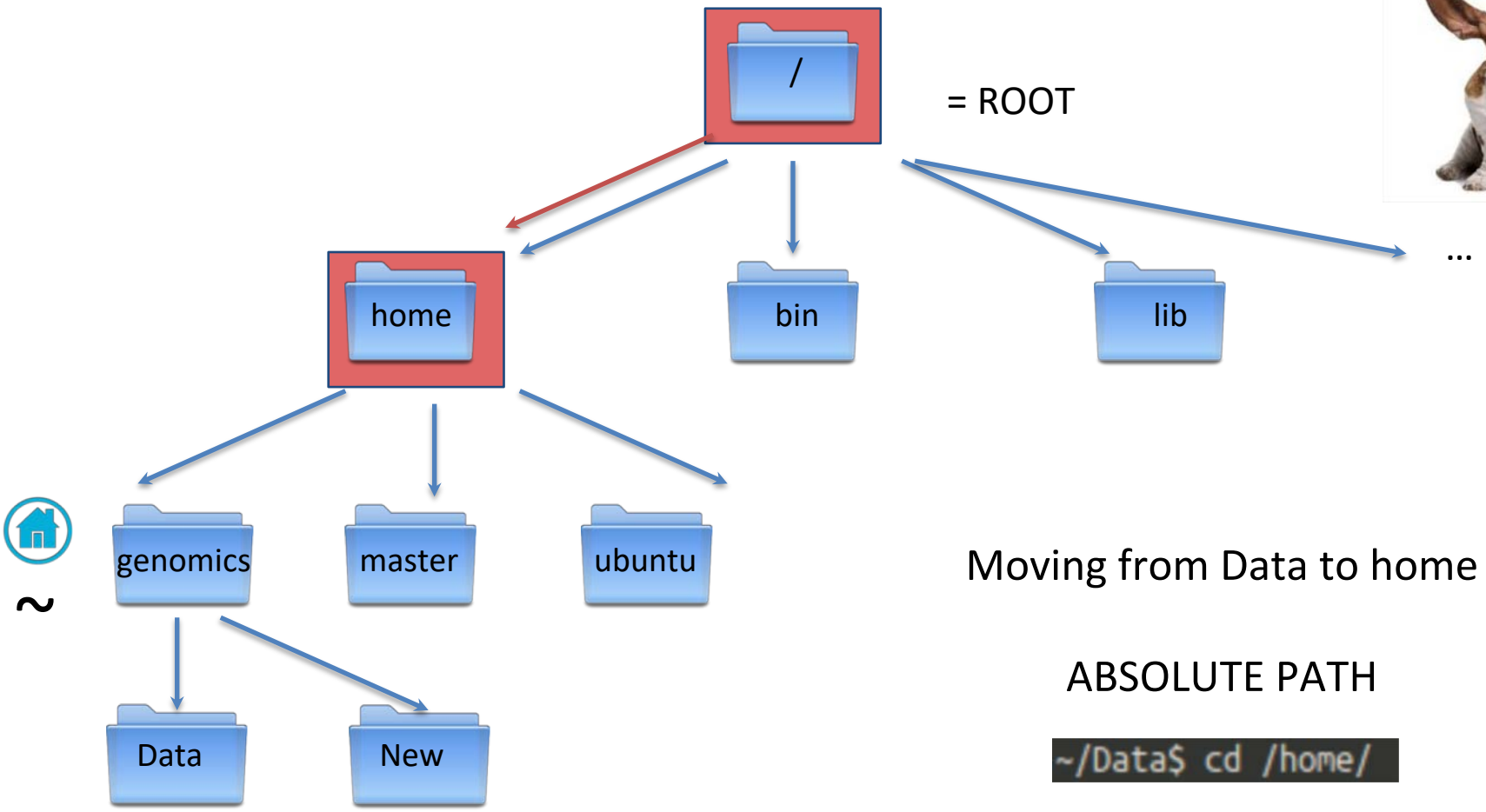
```
:/home$ cd /home/phylogenomics/New/
```



Moving from Data to home

ABSOLUTE PATH

```
~/Data$ cd /home/
```



Moving from Data to home

ABSOLUTE PATH

```
~/Data$ cd /home/
```

A Note About Dot!

. means “In your pwd …”
This command means “List everything that’s in the pwd”

```
$ ls ./
```

This command means “List everything that’s in the pwd within a sub-directory called Data”

```
$ ls ./Data/
```

In most cases, people don’t use ./ at the beginning of a path. As long as the file/directory is within your pwd, the command will work.

```
$ ls ./Data/
```

=

```
$ ls Data
```

Let's put this to practice

Where am I right now? (Should be the Data directory)

```
$ pwd
```

Change to the directory above

```
$ cd ../
```

Let's list the contents of the Data directory

```
$ ls ./Data/
```

CHALLENGE 1!

1. Move into the Data directory and list the contents of your home directory
2. In Data, make a new directory and move into this location
3. From this new directory, move into your home directory IN ONE COMMAND and check your location

Work smarter, not harder!

Tab complete is a nice trick to save you typing paths

For this example we are going to list everything in the directory /home/phylogenomics/workshop_materials/

Start by typing:

```
~$ ls /
```

Followed by tab twice quickly

```
phylogenomics@ip-172-30-3-100:~$ ls /
bin   home            lib64       opt   sbin  tmp       vmlinuz.old
boot  initrd.img      lost+found  proc  snap  usr
dev   initrd.img.old  media       root  srv   var
etc   lib             mnt         run   sys   vmlinuz
phylogenomics@ip-172-30-3-100:~$
```

This shows the contents of the root directory

Work smarter, not harder!

Now type:

```
$ ls /h
```

Followed by tab once. The path to the /home/ directory has filled in.

```
$ ls /home/
```

Now type:

```
$ ls /home/p
```

Followed by tab once. The path to the /home/phylogenomics/ directory has filled in.

```
$ ls /home/phylogenomics
```

Finally type:

```
$ ls /home/phylogenomics/w
```

Followed by tab once to finish the path, and then enter.
You've now listed that directory contents.

Tab complete will fill in paths, save you time in typing and prevent typos!

Work smarter, not harder!

Two more tricks for less typing!

* Represents any character
For example:

```
$ ls /home/phylogenomics/*.txt
```

Will list everything in my home directory ending .txt

The up arrow can be used to re-run commands

Press your up arrow and see

If you want all of these commands listed, simply type

```
$ history
```

Any Questions???

Binary programs

These are all programs installed on the Unix machine.

They can be found in /bin

```
$ ls /bin
```

```
phylogenomics@ip-172-30-3-100:~/Data$ ls /bin
bash                bzmore          fgconsole       lesspipe        netcat          ping                stty                    uncompress
btrfs               cat             fgrep           ln              netstat         ping4               su                      unicode_start
btrfs-debug-tree    chacl           findmnt         loadkeys        networkctl      ping6               sync                    vdir
btrfs-find-root     chgrp           fsck.btrfs      login           nisdomainname   plymouth            systemctl               wdctl
btrfs-image         chmod           fuser           loginctl        ntfs-3g         ps                  systemd                 which
btrfs-map-logical   chown           fusermount      lowntfs-3g      ntfs-3g.probe   pwd                 systemd-ask-password    whiptail
btrfs-select-super  chvt            getfacl         ls              ntfscat         rbash               systemd-escape          ypdomainname
btrfs-zero-log      cp              grep            lsblk           ntfscluster     readlink            systemd-hwdb            zcat
btrfsck             cpio            gunzip          lsmod           ntfscmp         red                 systemd-inhibit         zcmp
btrfstune           dash            gzexe           mkdir           ntfsfallocate   rm                  systemd-machine-id-setup zdiff
bunzip2             date            gzip            mkfs.btrfs      ntfsfix         rmdir               systemd-notify          zegrep
busybox             dd              hciconfig       mknod           ntfsinfo        rnano               systemd-sysusers        zfgrep
bzcat               df              hostname        mktemp          ntfsls          run-parts           systemd-tmpfiles        zforce
bzcmp               dir             ip              more            ntfsmove        sed                 systemd-tty-ask-password-agent zgrep
bzdiff              dmesg           journalctl      mount           ntfsrecover     setfacl             tar                     zless
bzegrep             dnsdomainname   kbd_mode        mountpoint      ntfssecaudit    setfont             tempfile                zmore
bzexe               domainname      kill            mt              ntfstruncate    setupcon            touch                   znew
bzfgrep             dumpkeys        kmod            mt-gnu          ntfsusermap     sh                  true
bzgrep              echo            less            mv              ntfswipe        sh.distrib          udevadm
bzip2               ed              lessecho        nano            open            sleep               ulockmgr_server
bzip2recover        egrep           lessfile        nc              openvt          ss                  umount
bzless              false           lesskey         nc.openbsd      pidof           static-sh           uname
```

These include pwd, mkdir, ls …

Every binary program has a manual

To view the manual page, type man followed by the name of the program

```
$ man <PROGRAM>
```

Open the manual page for ls

```
$ man ls
```

Scroll through (enter) and find the options for:
long listing format (-l), human-readable sizes (-h) and sort by modification time (-t)

Exit the manual page (type q) and give these ls options a go in your Data directory

```
$ ls -l ./Data
```
OR
```
$ ls -t ./Data
```

```
$ ls -l -h ./Data
```
OR
```
$ ls -lh ./Data
```

```
$ ls -l -h -t./Data
```
OR
```
$ ls -lht ./Data
```

```
$ ls -l -h -t -a ./Data
```
OR
```
$ ls -lhta ./Data
```

PATH

The computer needs to know where a program is so that it will run

The PATH environment variable is a list of
locations your computer looks for programs

You can either provide the path to the program you want to run

```
$ /usr/bin/mkdir
```

PATH

The computer needs to know where a program is so that it will run

The PATH environment variable is a list of
locations your computer looks for programs

You can either provide the path to the program you want to run

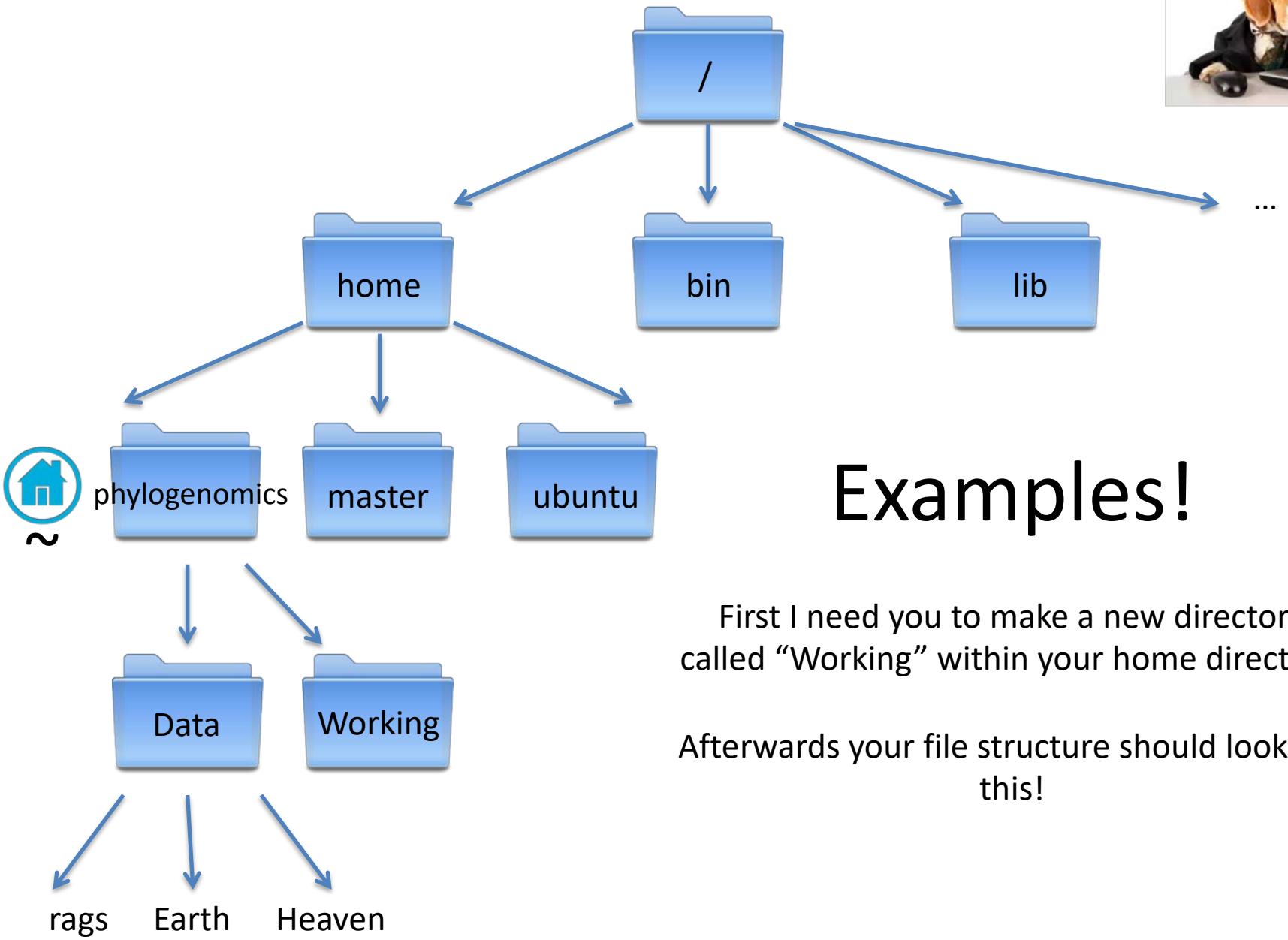
```
$ /usr/bin/mkdir
```

Or make sure the program is in your PATH environment variable

To view locations in your PATH environment variable:

```
$ echo $PATH
```

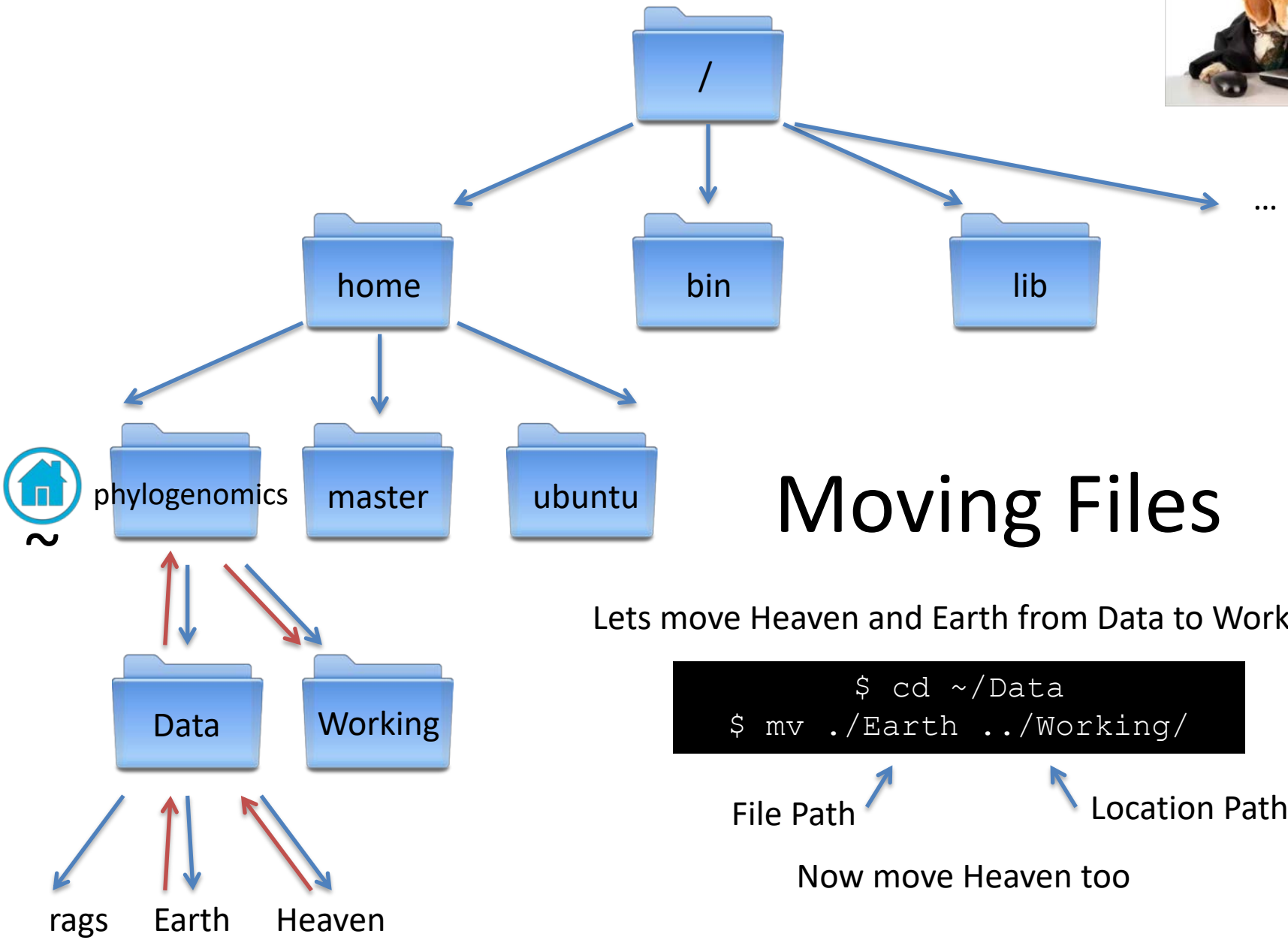
There are ways to add new locations to your PATH, but that is for another time



Examples!

First I need you to make a new directory called “Working” within your home directory.

Afterwards your file structure should look like this!



Moving Files

Lets move Heaven and Earth from Data to Working

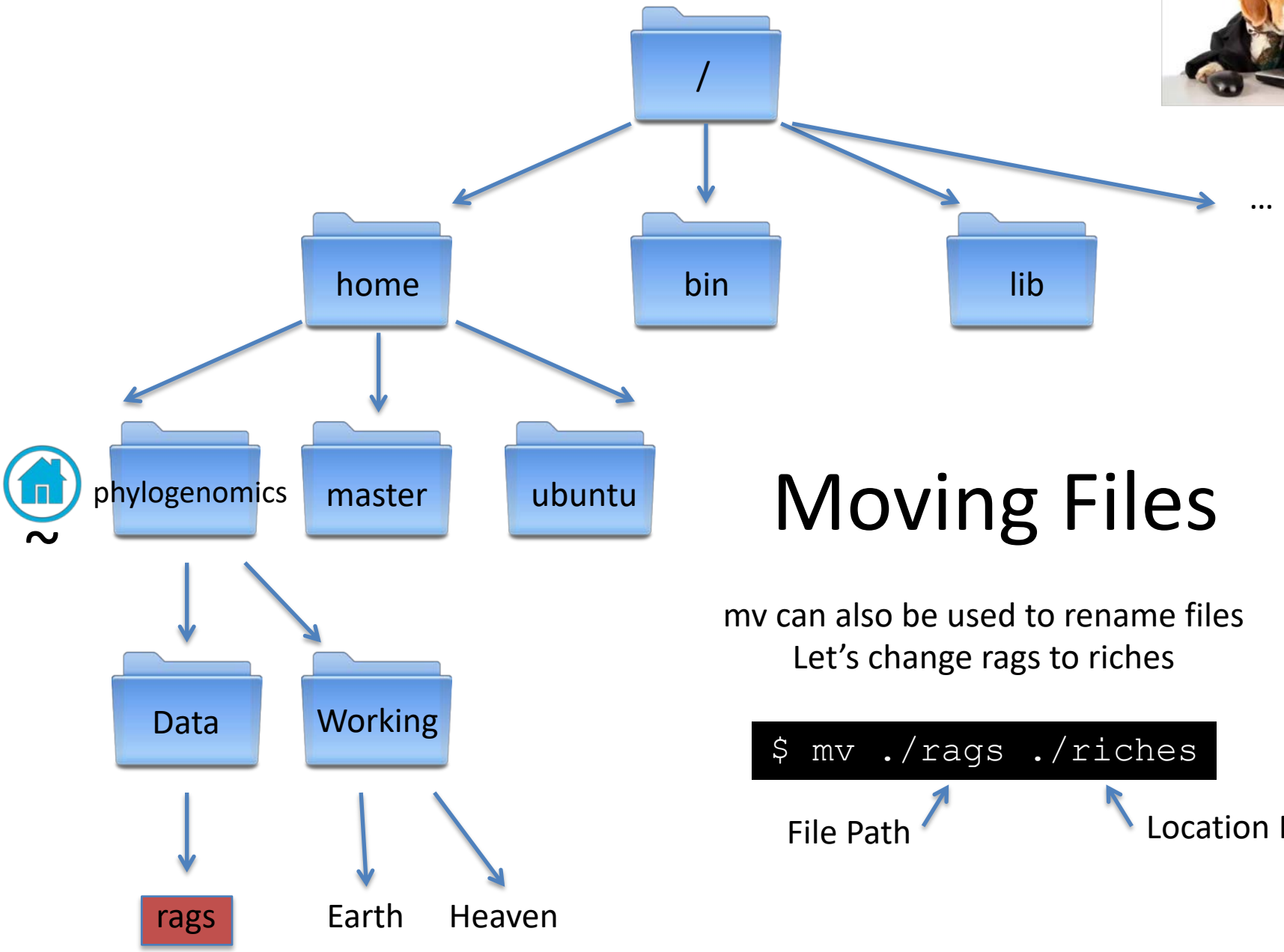
```
$ cd ~/Data
$ mv ./Earth ../Working/
```

File Path

Location Path

Now move Heaven too

REMEMBER TAB COMPLETE!



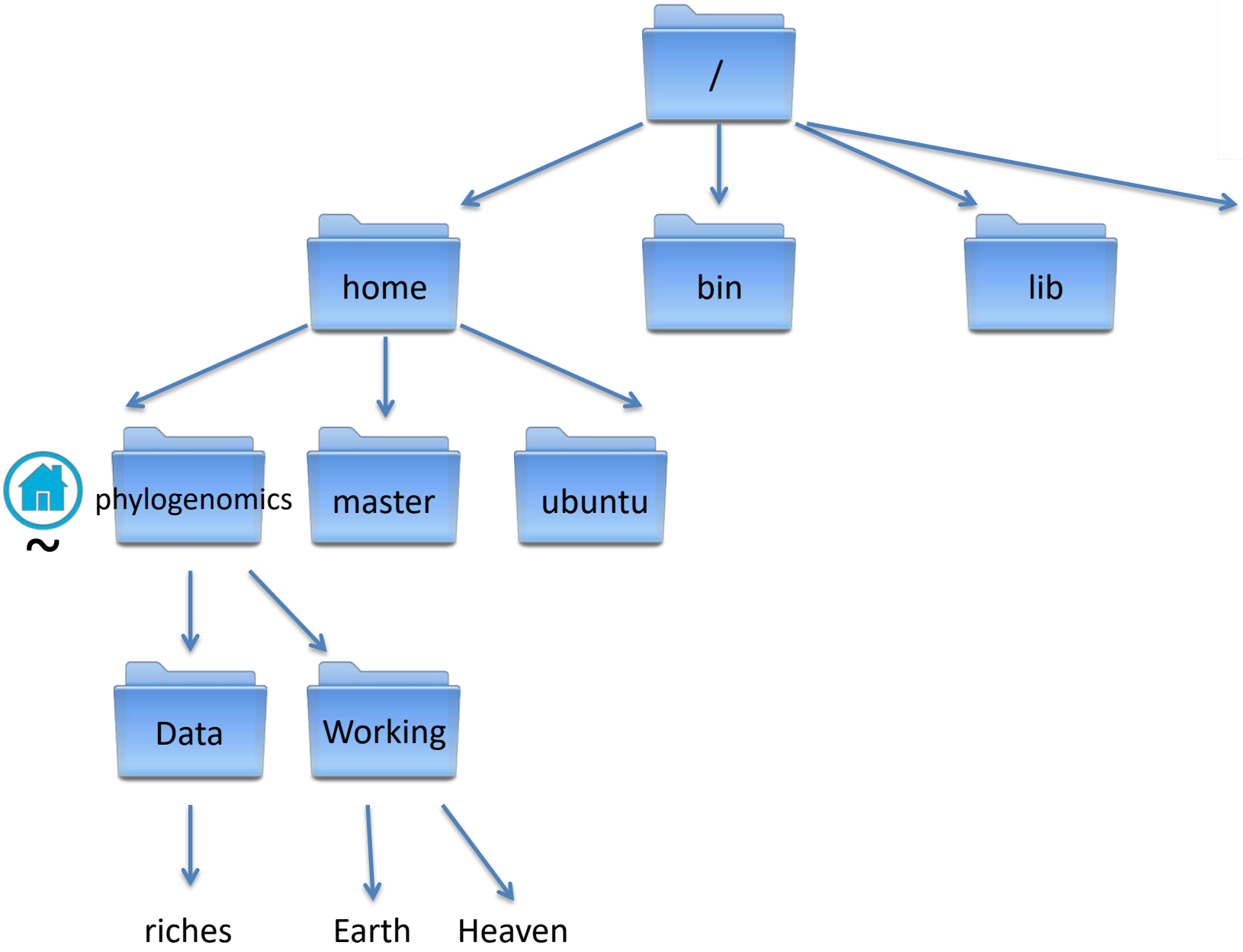
Moving Files

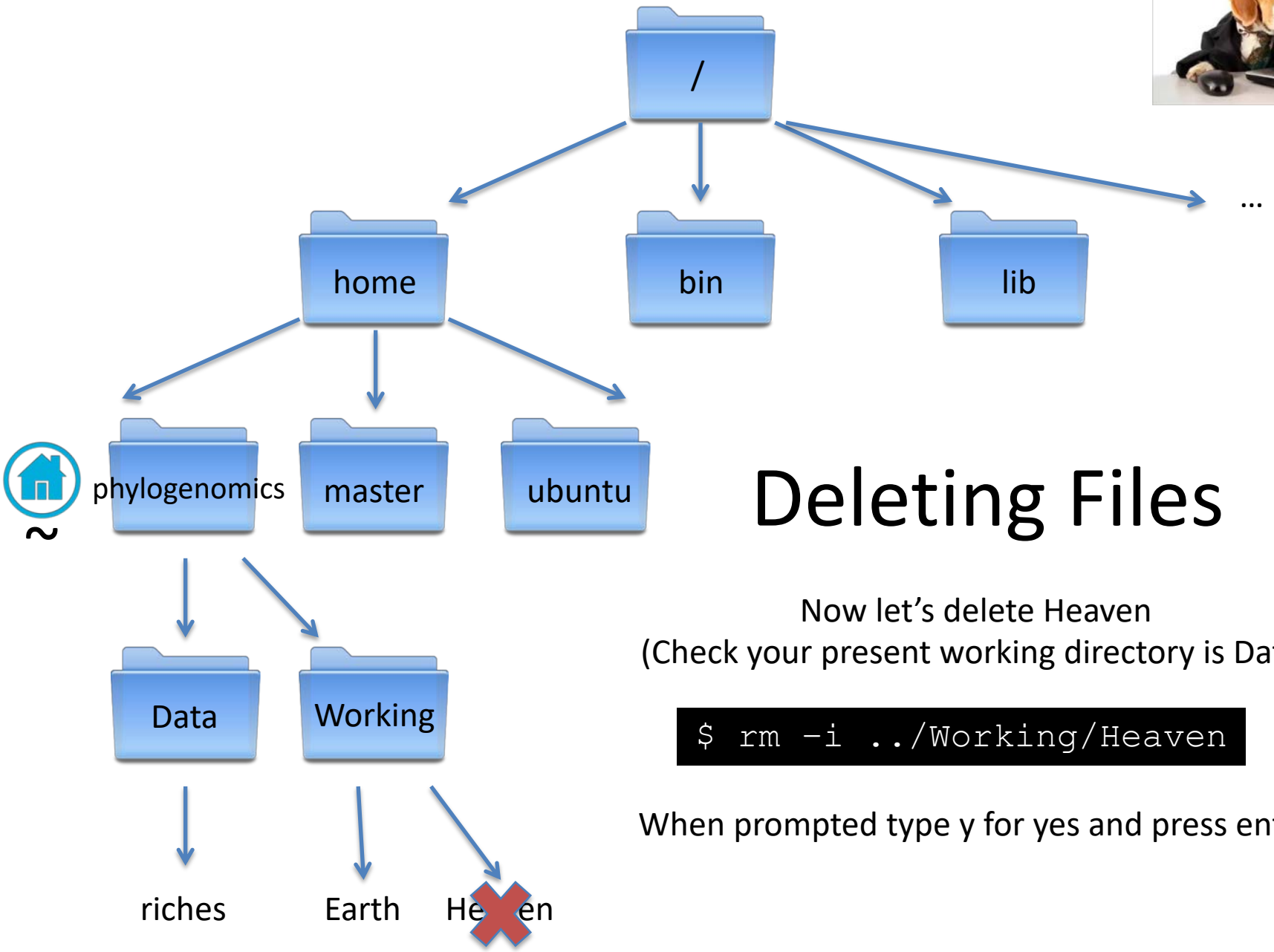
mv can also be used to rename files
Let's change rags to riches

```
$ mv ./rags ./riches
```

File Path

Location Path


/
home
bin
lib
...
phylogenomics
master
ubuntu
~
Data
Working
riches
Earth
Heaven

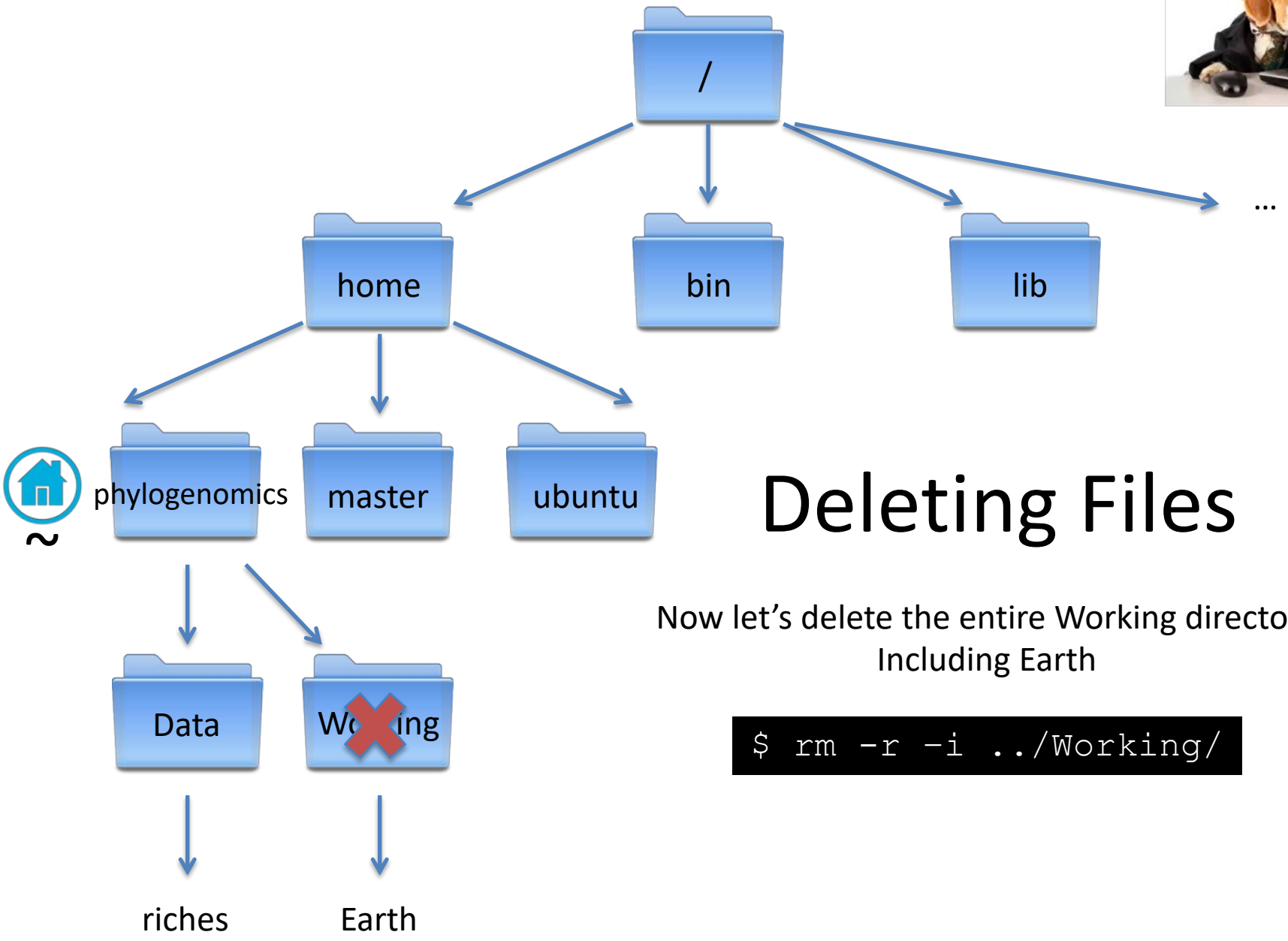


Deleting Files

Now let's delete Heaven
(Check your present working directory is Data)

```
$ rm -i ../Working/Heaven
```

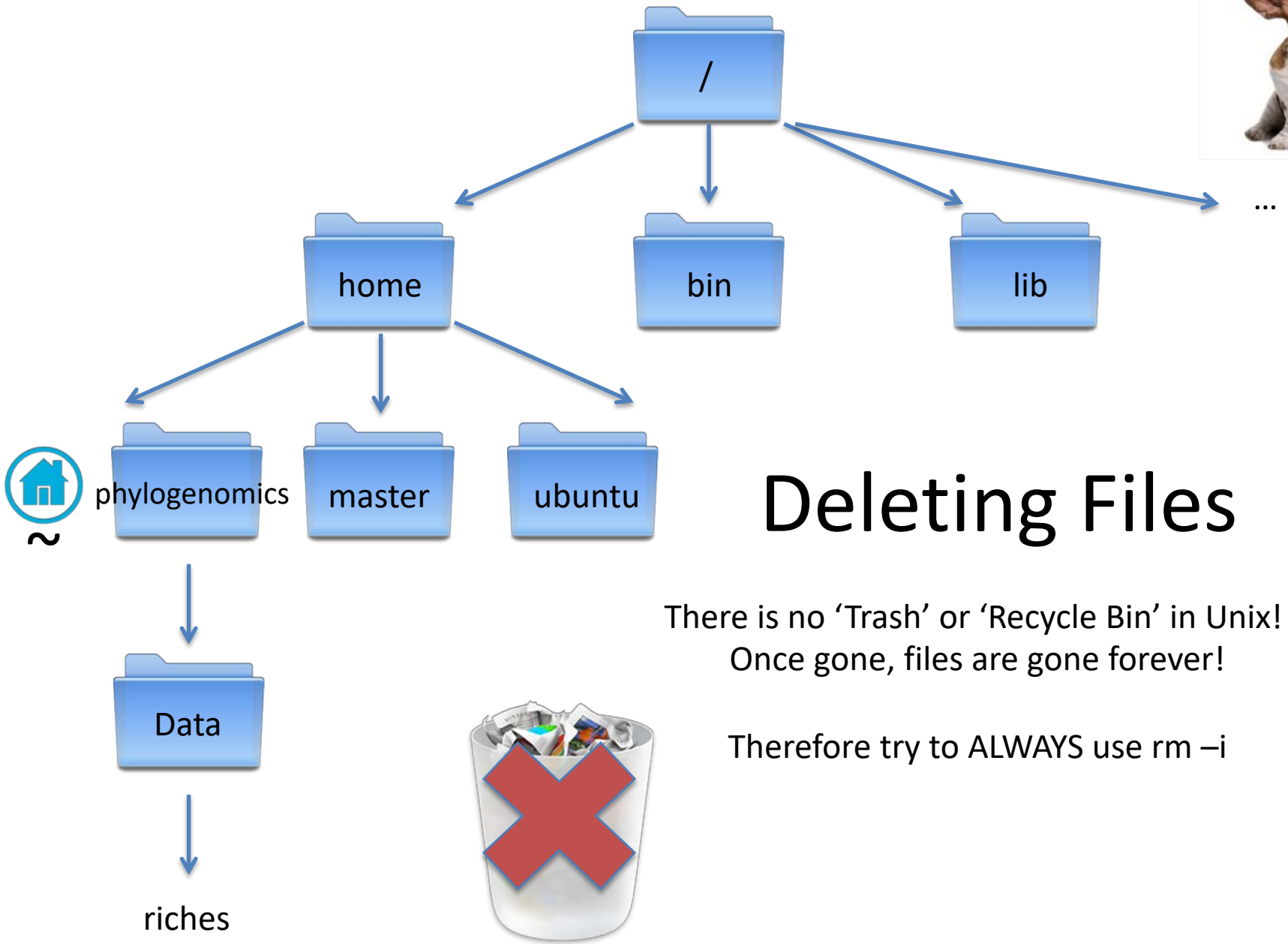
When prompted type y for yes and press enter



Deleting Files

Now let's delete the entire Working directory
Including Earth

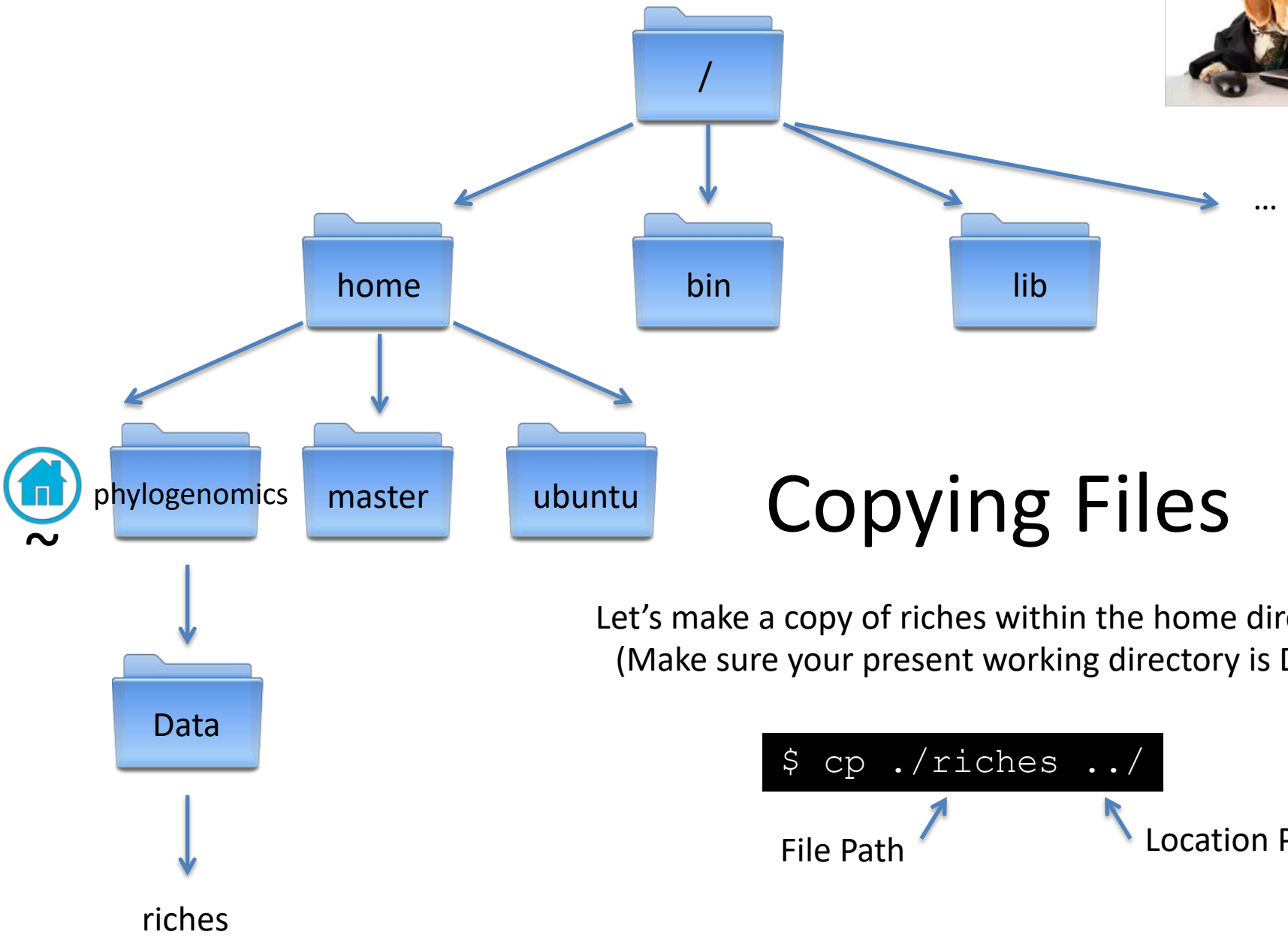
```
$ rm -r -i ../Working/
```



Deleting Files

There is no 'Trash' or 'Recycle Bin' in Unix!
Once gone, files are gone forever!

Therefore try to ALWAYS use rm –i



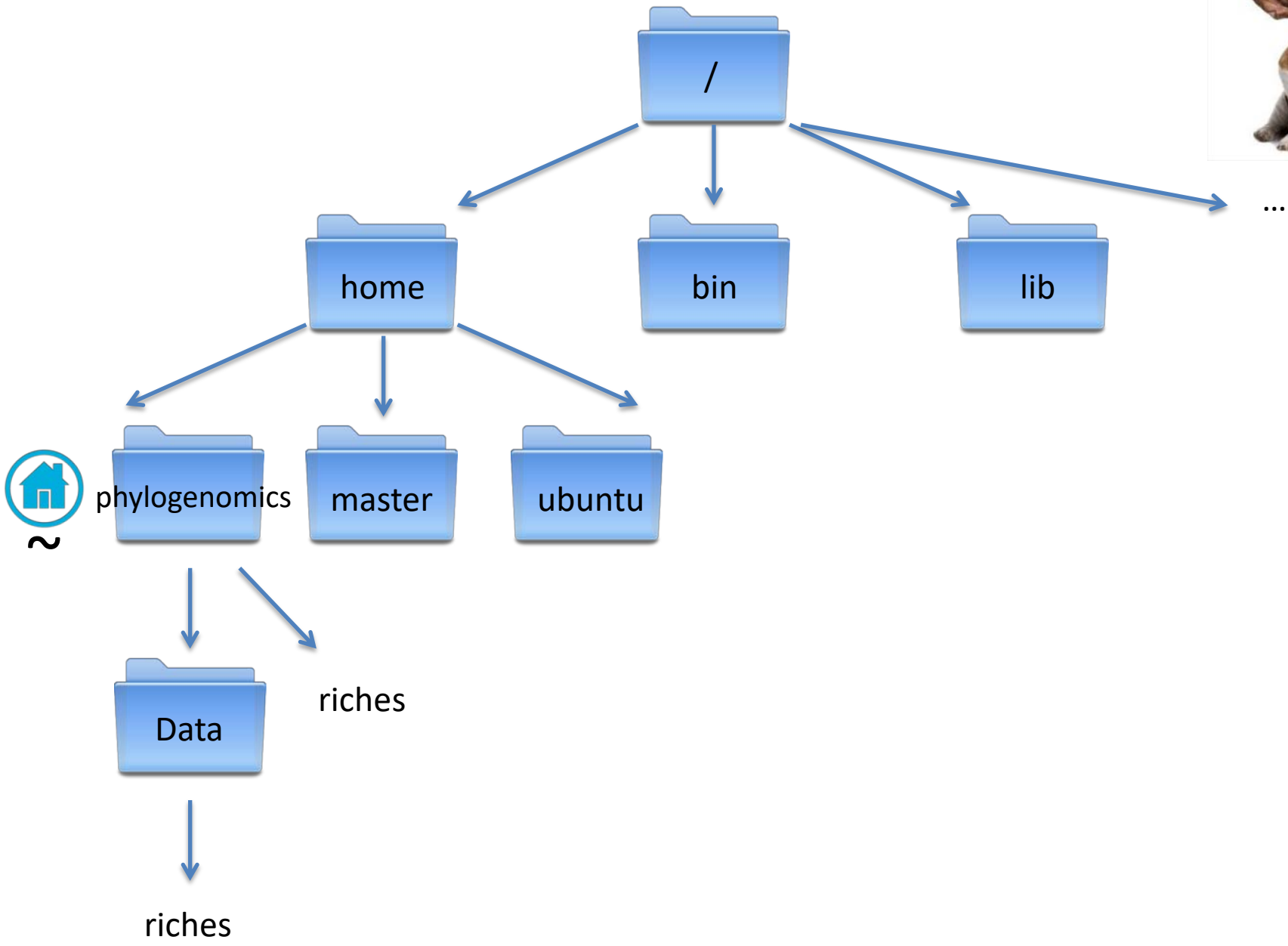
Copying Files

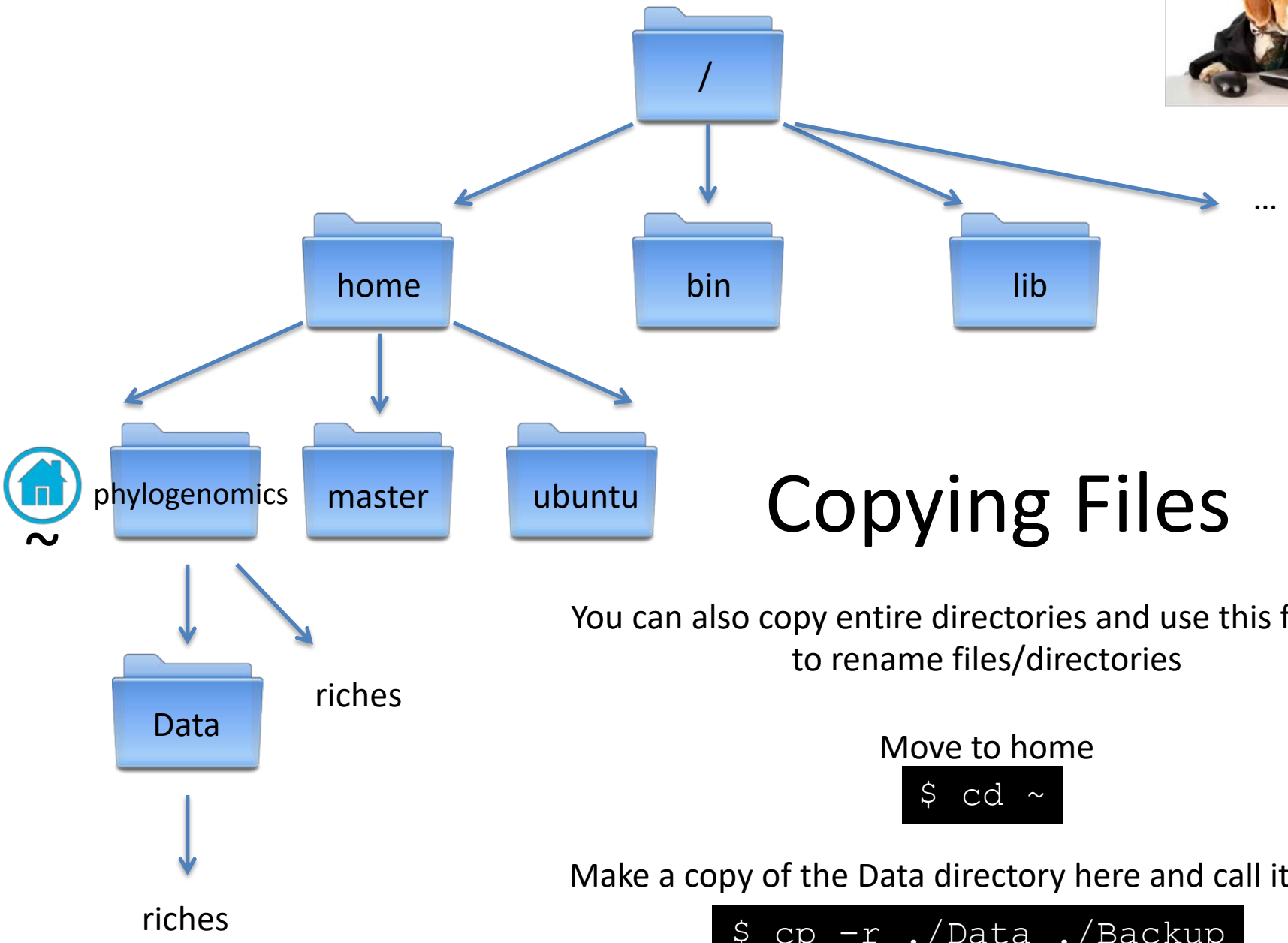
Let's make a copy of riches within the home directory
(Make sure your present working directory is Data)

```
$ cp ./riches ../
```

File Path

Location Path


/
home
bin
lib
...
phylogenomics
master
ubuntu
~
Data
riches
riches



Copying Files

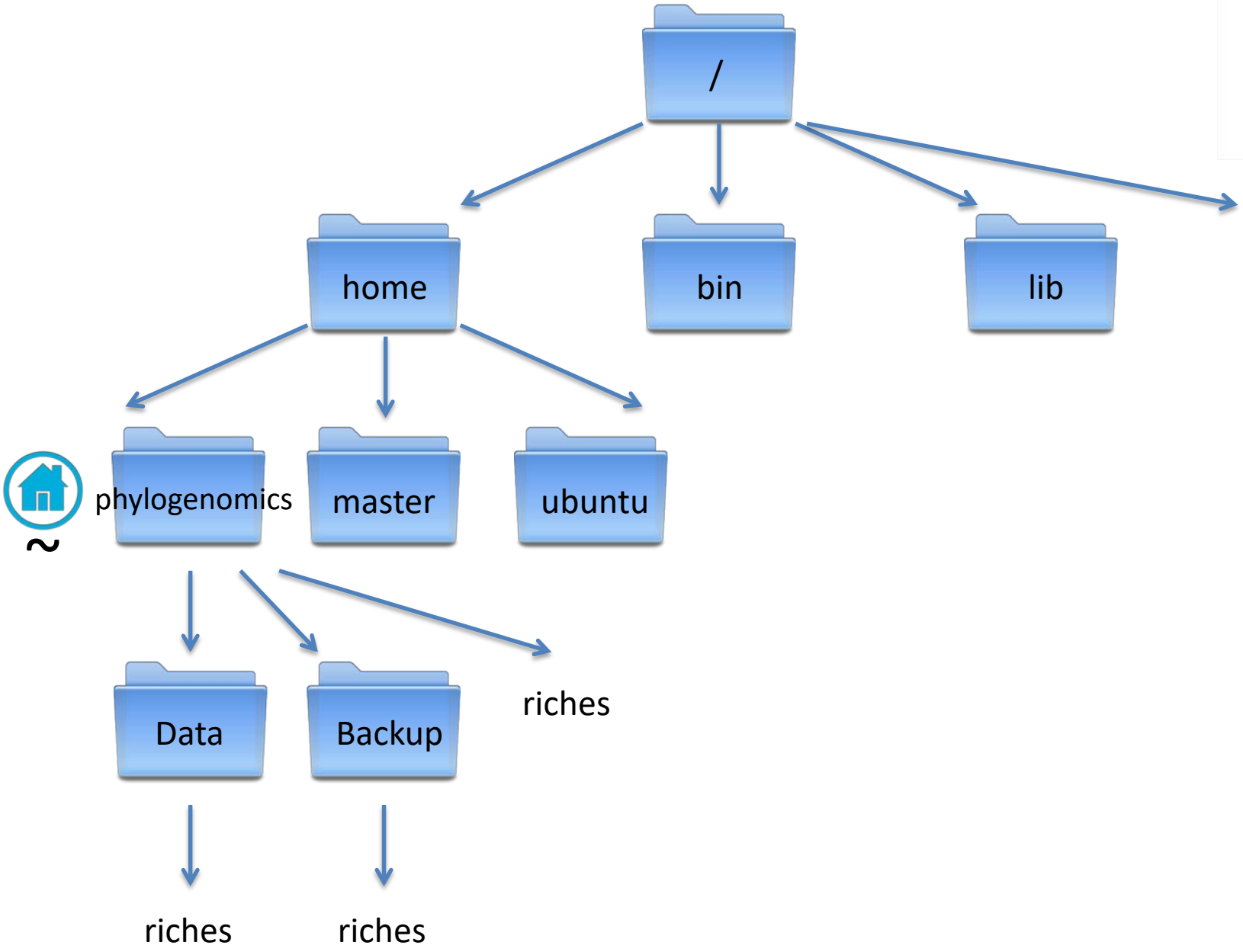
You can also copy entire directories and use this function to rename files/directories

Move to home

```
$ cd ~
```

Make a copy of the Data directory here and call it Backup

```
$ cp -r ./Data ./Backup
```


/
home
bin
lib
...
phylogenomics
master
ubuntu
~
Data
Backup
riches
riches
riches

Typical File Sizes

On the Illumina NextSeq
3,000,000 reads = 1 Gb

But typically your experimental design/sequencing strategies will result in much more than 3,000,000 reads.
You may have different patients, different locations, replicates etc…

The size of the sequencing data file can easily become 100s of Gb

(or even bigger depending on the sequencer used)

Archived/Compressed Files

Commonly, people will archive directories and compress large files so that they are easier to store or share. Here's an example:

sequences.tar.gz

.tar – means that it is a tape archived directory
.gz – means that it is gzipped file

These can be used alone or in combination

To uncompress
A Tar Archive

```
$ tar -xvf <filename>
```

(x = extract, v = verbose, f = all files)

A Gzipped file

```
$ gunzip <filename>
```

A Gzipped Tar archive

```
$ tar -xzvf <filename>
```

Challenge 2!

1. Change to the workshop_materials directory at the following path:

```
~/workshop_materials/unix
```

You should find a compressed directory:

```
Sequences.tar.gz
```

2. Make a copy of this file in the Backup directory you created earlier

3. Un archive the original directory

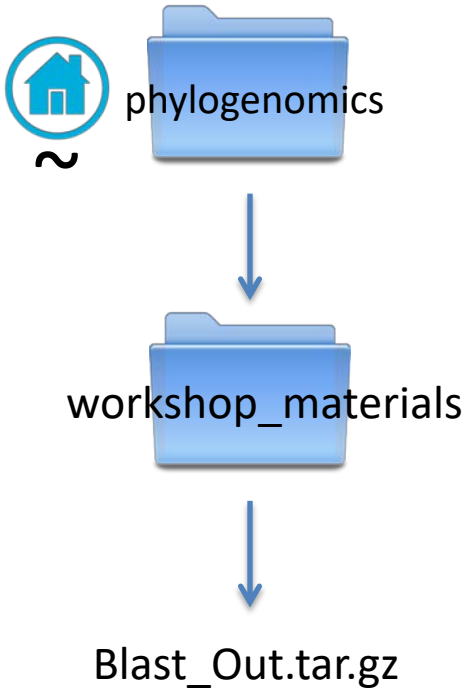
4. Unzip the read files

5. Rename the unarchived files – sequence_1.fq and sequence_2.fq

6. Delete the original .tar file

tar	gunzip
cp	mv
rm –i	mkdir
cd	


YEP. IT'S QUESTION TIME
AGAIN
memegenerator.net



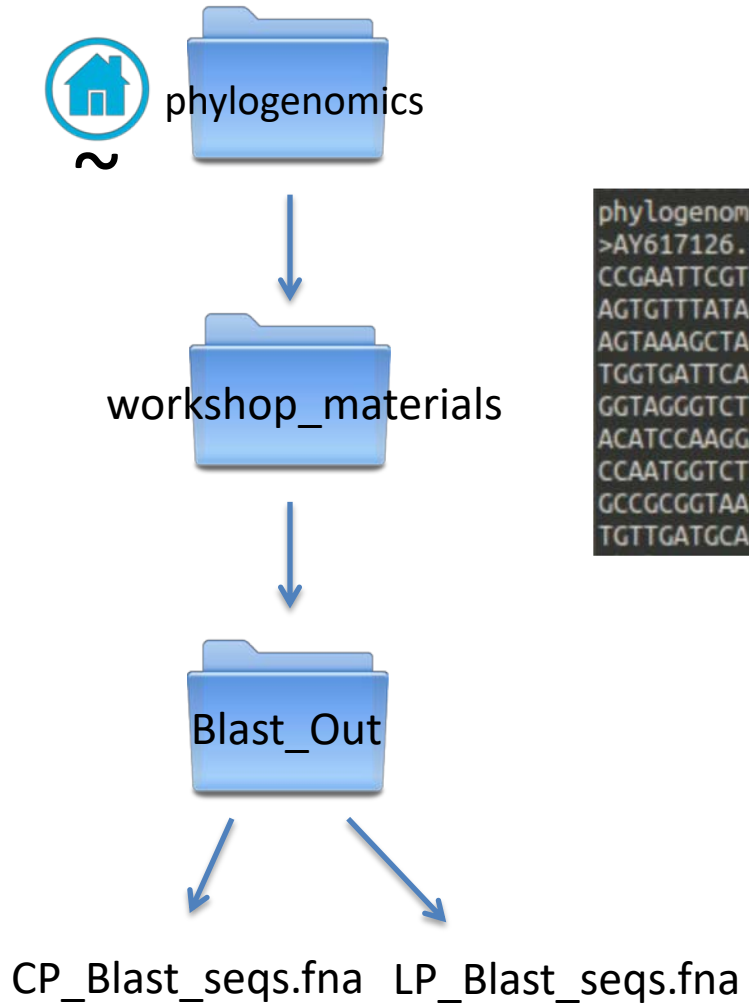
Navigate to the workshop_materials directory

```
$ cd ~/workshop_materials
```

Unarchive the Blast_Out.tar.gz

```
$ tar -xzvf Blast_Out.tar.gz
```

```
phylogenomics@ip-172-30-3-100:~/workshop_materials$ tar -xzvf Blast_Out.tar.gz
Blast_Out/
Blast_Out/LP_blast_seqs.fna
Blast_Out/CP_blast_seqs.fna
phylogenomics@ip-172-30-3-100:~/workshop_materials$
```



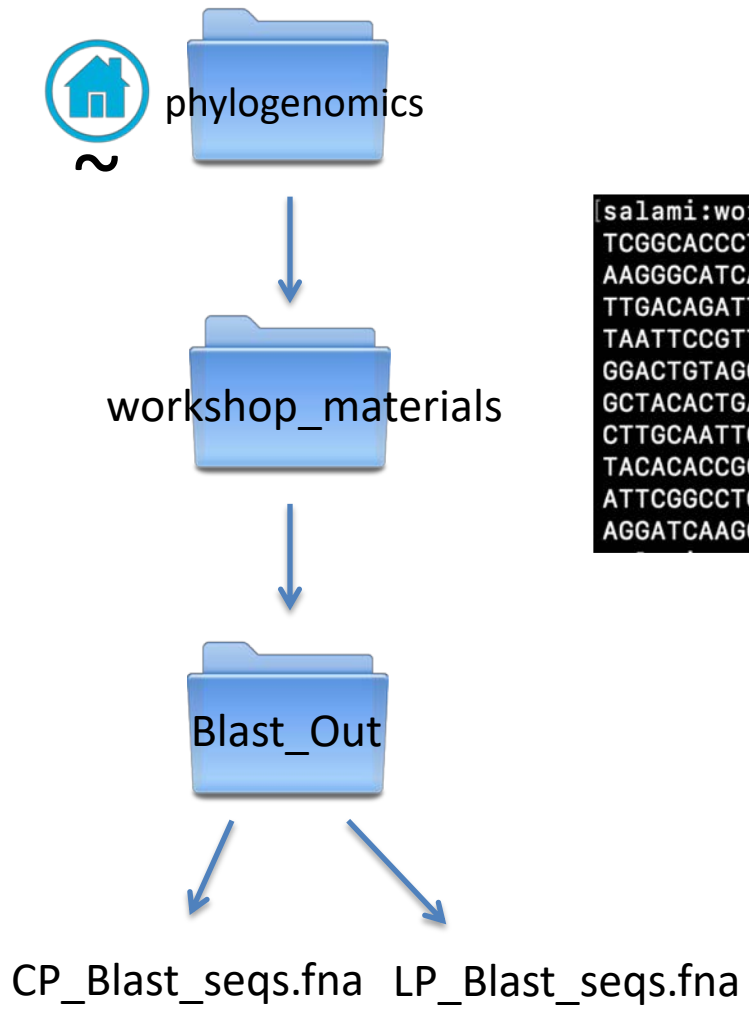
View the first 10 lines of a file

```
$ head CP_blast_seqs.fna
```

```
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ head CP_blast_seqs.fna
>AY617126.1 Choreocolax polysiphoniae 18S ribosomal RNA gene, partial sequence
CCGAATTCGTCGACAACCTGGTTGATCCTGCCACTGGTATATGCTTGTCTCAAAGACTAAGCCATGCAAGTGCCTGTATG
AGTGTTTATACAACGAAACTGCGAATGGCTCGGTAAAACAGCAATAATTTATTCGGGGGTAATACTACTCGGATAACCGT
AGTAAAGCTAGAGCTAATACGTGCAGCGAAGGCGAGAAACGTCTCGTGGTACTAAGTATTAGGTACAAACCAAATATTTT
TGGTGATTCATACTTATCTTCTGATCGCAGGAAACTGCGACGCCCCGAATAAATTTCTGACCTATCAACTATGATGGTAA
GGTAGGGTCTTACCATGGTTGTGACGGGTAACGGACCGTGGGTGCGGGATTCCGGAGAGGGAGCCTGAGAAACGGCTACC
ACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCAATCCGAACTTCGGGAGGTAGTGACAATACATATCAATAGGGGGA
CCAATGGTCTTTCTAATTGGAATGAATACAATGTAAACACATTAATGAGGAACCAGCAGAGGGCAAGTCTGGTGCCAGCA
GCCGCGGTAATTCCAGCTCTGTAAGCGTATACCAAAGTTGTTGCAGTTAAAACGCTCGTAGTCGGATTTTGGCGTGTTTC
TGTTGATGCAGCATTTTGCAGTTGACGCAGGAGCGCCTTTGTGGAAGGGGGTGTGGTGGTACTTTATTGTATTGCTGCAT
```

To view the first 30 lines of the file

```
$ head – 30 CP_blast_seqs.fna
```



View the last 10 lines of a file

```
$ tail CP_blast_seqs.fna
```

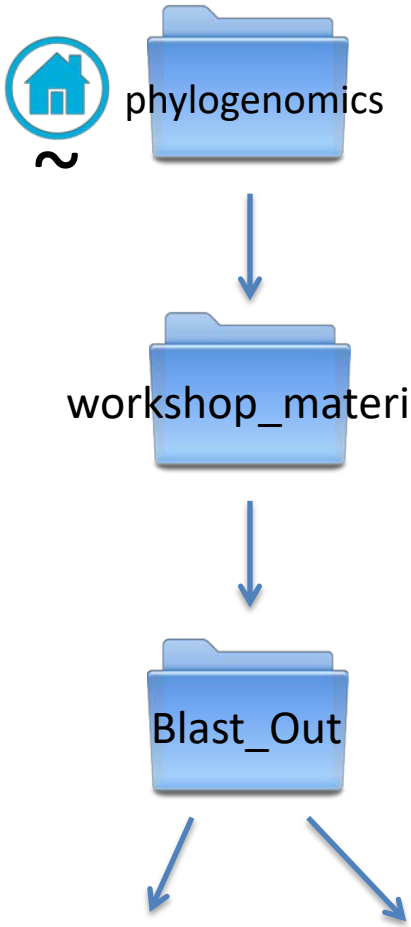
```
salami:workshop_files ericsalomaki$ tail CP_blast_seqs.fna
TCGGCACCCTCCGGGAAACCAAAGTGTTTGCTTTCTGGGGGGAGTATGGTCGCAAGTCTGAAACTTAAAGGAATTGACGG
AAGGGCATCACCGGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTTACCAGGTCCAGACATAATAAGGA
TTGACAGATTGAGAGCTCTTTCTTGATTCTATGGTTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATCTGTCTGGT
TAATTCCGTTAACGAGCGAGACCTGGGCGTGCTAAATAGGGTATGTTATTCTTGTAATAGCAGTTTTGCCCTTCTTAGAC
GGACTGTAGGCTTTTAGTCTATGGAAGCTCCAGGCAATAACAGGTCTGAGATGCCCTTAGATGTTCTGGGCCGCACGCGT
GCTACACTGAACGGTTCAATGGGTGAGGTAGTGCGAAAGCATGACCCAATCTCTAAATCCGTTCGTGCTGGGGATAGAAG
CTTGCAATTCTCCTTCTTGAACGAGGAATACCTTGTAAGCGCGAGTCATCATCTCGCGCTGAATACGTCCCTGCCCTTTG
TACACACCGCCCGTCGCTCCTACCGATTGAGTGGTCCGGTGAGGCTTTGGGAGGGCTGGATGGATTGTGCTTCACAAACT
ATTCGGCCTGAACTTAGTCAAACCTTACTACTTAGAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA
AGGATCAAGCTAA
```

Now view the last 30 lines of the file

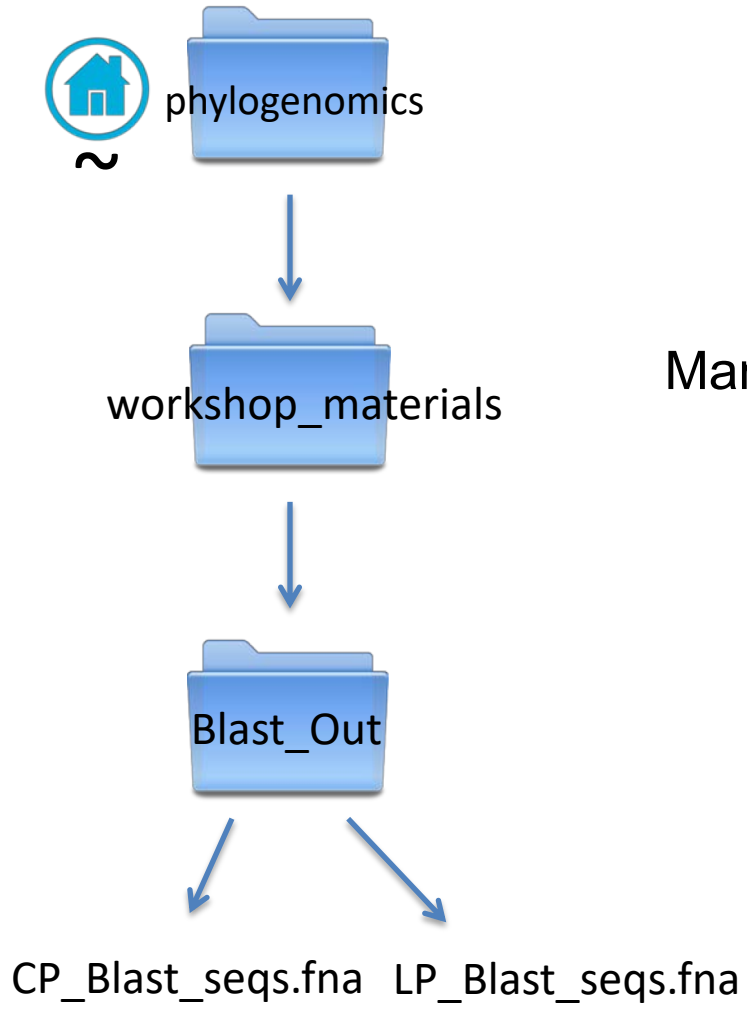
```
$ tail -30 CP_blast_seqs.fna
```

Print the entire file

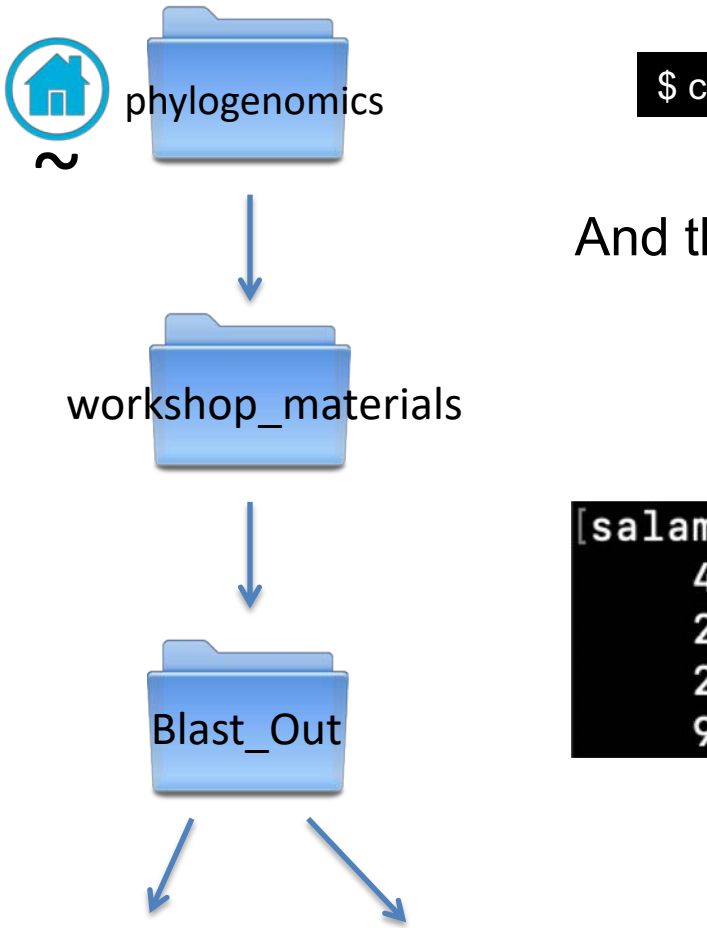
```
$ cat CP_blast_seqs.fna
```




```
GGTGAAATTCTTAGATCCTTGGAAGACAAACAGCTGCGAAAGCGTCTGCCAAGGACGTTTTCATTGATCAAGAACGAAAG
TAAGGGGATCGAAGACGATCAGATACCGTCGTAGTCTTTACTATAAACTATGTGATCTGGGGATTAGCCGAGGCCAATTT
GGTTCGGTTAGCACCCTCCGGGAAACCAAAGATTTTGCATTCTGGGGGGAGTATGGTCGCAAGTCTGAAACTTAAAGGAA
TTGACGGAAGGGCATCACCGGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTTACCAGGTCCAGACATA
ATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTCTATGGTTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATCT
GTCTGGTTAATTCCGTTAACGAGCGAGACCTGGGCGTGCTAAATAGGGTTCATTATTCTTGTAATAGTGGTTCAACTCTT
CTTAGACGGACTGTAGGCTTTTAGTCTATGGAAGCTCCAGGCAATAACAGGTCTGAGATGCCCTTAGATGTTCTGGGCCG
CACGCGTGCTACACTGAACGGTTCAATGGGTGAGGTAGTGCGAAAGCATGACCTAATCTCGAAATCCGTTCGTGCTGGGG
ATAGAAGCTTGCAATTATCCTTCTTGAACGAGGAATACCTTGTAGGCGTGAGTCATCATCTCACGCCGAATACGTCCCTG
CCCTTTGTACACACCGCCCGTCGCTCCTACCGATTGAGTGTTCCGGTGAGGCTTTGGGAGAACTGGGTGGATTGTGTTCC
ACAAACTGCTCGGTTTGAACTTAGTCAAACCTTATCACTTAGAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAAC
CTGCAGAAGGATCAAGCT
>AY237287.1 Osmundaria spiralis 18S ribosomal RNA gene, partial sequence
CCCCCACCTGGTTGATCCTGCCAGTGGTATATGCTTGTCTCAAAGACTAAGCCATGCAAGTGCCTGTATGAGTGTTTATA
CAACGAAACTGCGAATGGCTCGGTAAAACAGCAATAATTTCTTCGGGGGTAATACTACTCGGATAACCGTAGTAAAGCTA
GAGCTAATACGTGCTACAAAGGCGAGATCGCTCTCGTGGTACTAAGTATTAGGTACAAGCCAGTTTTTCTGGTGATTCAT
ACTTATCTTCTGATCGCACTCTGTGCGACGCCCCGATCAAATTTCTGACCTATCAACTATGATGGTAAGGTAGTGTCTTA
CCATGGTTGTGACGGGTAACGGACCGTGGGTGCGGGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCANNNNNNNNNN
NNNNNNNNNNNNNNNNNNNACCCAATCCGAACTTCGGGAGGTAGTGACAAAAAATATCAATAGGGGGACCGATGGTCTTC
CTAATTGGAATGAAAACAATGTAAACACCTTATTGAGGAACCAGCAGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATT
CCAGCTCTGTAAGCGTATACCAAAGTTGTTGCAGTTAAAACGCTCGTAGTCGGATTTTGGCGTGTGCTGCAGAAACTCCG
TAAGGAGGTTGATGTAGCTCCGCCTTTGTGGAGGGGGGTGTGGTGGTACTTTATTGTATTGCTGCATTTCCACCACTGTT
TACTGTGAAAAAATTAGAGTGTTCAAAGCGAGCGATTGCCATGAATACATTAGCATGGAATAATAGAATAGGACCTGGTC
CTGTTTTATTGGTTTGTCGGTATCAGGTAATGATTAAGAGGGACGGTCGGGGGCATTTGTATTCCAGCGCTAGAGGTGAA
ATTCTTGGATTGCTGGAAGACAAACAGCTGCGAAAGCGTCTGCCAAGGACGTTTTCATTGATCAAGAACGAAAGTAAGGG
GATCGAAGACGATCAGATACCGTCGTAGTCTTTACTATAAACGATGAGGACTGGGGATCGGATGTATGCTTATGGTACTT
TCGGCACCCTCCGGGAAACCAAAGTGTTTGCTTTCTGGGGGGAGTATGGTCGCAAGTCTGAAACTTAAAGGAATTGACGG
AAGGGCATCACCGGGTGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGAAAACTTACCAGGTCCAGACATAATAAGGA
TTGACAGATTGAGAGCTCTTTCTTGATTCTATGGTTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATCTGTCTGGT
TAATTCCGTTAACGAGCGAGACCTGGGCGTGCTAAATAGGGTATGTTATTCTTGTAATAGCAGTTTTGCCCTTCTTAGAC
GGACTGTAGGCTTTTAGTCTATGGAAGCTCCAGGCAATAACAGGTCTGAGATGCCCTTAGATGTTCTGGGCCGCACGCGT
GCTACACTGAACGGTTCAATGGGTGAGGTAGTGCGAAAGCATGACCCAATCTCTAAATCCGTTCGTGCTGGGGATAGAAG
CTTGCAATTCTCCTTCTTGAACGAGGAATACCTTGTAAGCGCGAGTCATCATCTCGCGCTGAATACGTCCCTGCCCTTTG
TACACACCGCCCGTCGCTCCTACCGATTGAGTGGTCCGGTGAGGCTTTGGGAGGGCTGGATGGATTGTGCTTCACAAACT
ATTCGGCCTGAACTTAGTCAAACCTTACTACTTAGAGGAAGGAGAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCAGA
AGGATCAAGCTAA
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$
```



Many files are too long to meaningfully view in terminal or to edit in a unix text editor



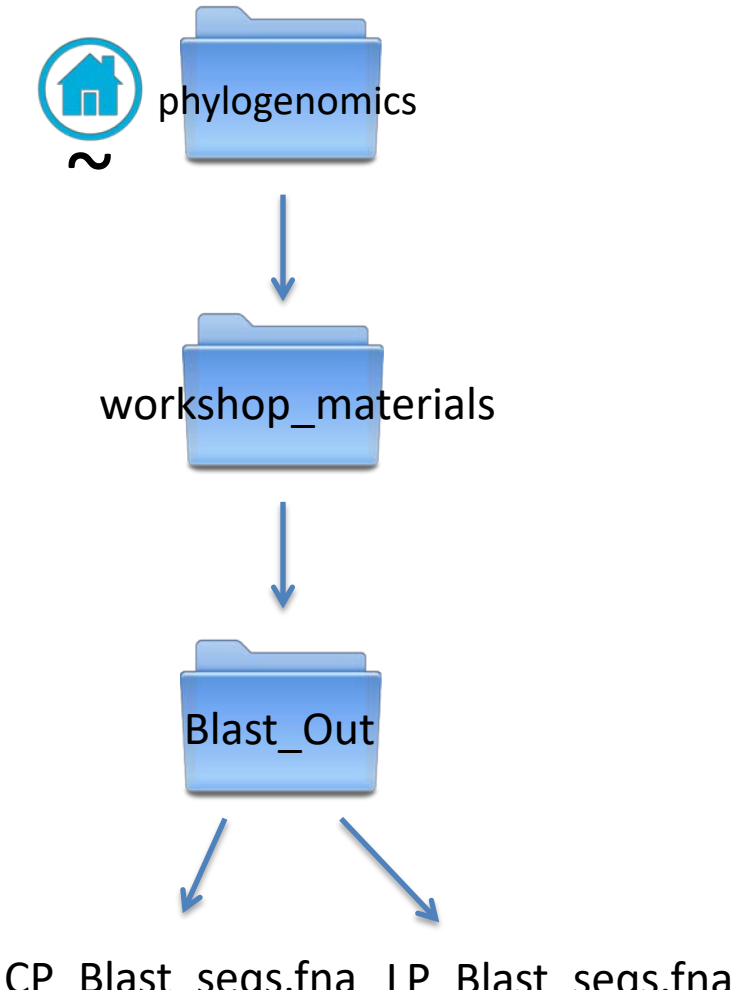
‘cat’ can also combine multiple files

```
$ cat CP_blast_seqs.fna LP_blast_seqs.fna > All_blast_seqs.fna
```

And then count the number of lines in each fasta file to confirm they have been combined

```
$ wc –l *.fna
```

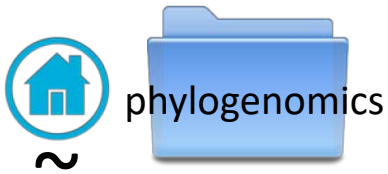
```
salami:workshop_files ericsalomaki$ wc -l *.fna
    4703 All_blast_seqs.fna
    2369 CP_blast_seqs.fna
    2334 LP_blast_seqs.fna
    9406 total
```



Use ‘grep’ to print occurrences of a pattern

```
$ grep “>” CP_blast_seqs.fna
```

```
>MG272245.1 Neochondria nidifica voucher UC2026095 18S ribosomal RNA gene, partial sequence
>AF427537.1 Womersleyella setacea small subunit ribosomal RNA gene, complete sequence
>MF093929.1 Gredgaria maugeana isolate PD1230 18S ribosomal RNA gene, partial sequence
>HM560626.1 Digenea simplex voucher Dig sim 18S ribosomal RNA gene, partial sequence
>MG272238.1 Chondria crassicaulis voucher SAP115362 18S ribosomal RNA gene, partial sequence
>AF339897.1 Lenormandia sp. MELU_000065 18S ribosomal RNA gene, complete sequence
>MF093941.1 Periphykon beckeri isolate JH1427 18S ribosomal RNA gene, partial sequence
>MF093947.1 Polysiphonia scopulorum isolate PD0899 18S ribosomal RNA gene, partial sequence
>JX828186.1 Pterosiphonia pennata voucher CH816 small subunit ribosomal RNA gene, partial sequence
>AF427526.1 Boergeseniella fruticulosa small subunit ribosomal RNA gene, complete sequence
>MF093935.1 Lophocladia kuetzingii isolate PD1509 18S ribosomal RNA gene, partial sequence
>JX828165.1 Boergeseniella thuyoides voucher CH824 small subunit ribosomal RNA gene, partial sequence
>HM582914.1 Osmundaria obtusiloba voucher 03151 small subunit ribosomal RNA gene, partial sequence
>AF427527.1 Enelittosiphonia stimpsonii small subunit ribosomal RNA gene, complete sequence
>JX828192.1 Polysiphonia brodiei voucher CH410 small subunit ribosomal RNA gene, partial sequence
>AF203890.1 Heterocladia australis small subunit ribosomal RNA gene, complete sequence
>KX499570.1 Brongniartella australis isolate PD931 small subunit ribosomal RNA gene, partial sequence
>FJ153773.2 Uncultured eukaryote clone 53 18S ribosomal RNA gene, partial sequence
>AB219915.1 Polysiphonia sp. SNI07 gene for 18S rRNA, complete sequence
>MF093961.1 Vertebrata thuyoides isolate PD0546 18S ribosomal RNA gene, partial sequence
>JX828170.1 Leptosiphonia schousboei voucher CH826 small subunit ribosomal RNA gene, partial sequence
>JX828189.1 Symphyocladia linearis voucher CH419 small subunit ribosomal RNA gene, partial sequence
>JX828171.1 Neosiphonia elongella voucher CH415 small subunit ribosomal RNA gene, partial sequence
>AF427530.1 Polysiphonia fucoides small subunit ribosomal RNA gene, complete sequence
>AF203892.1 Heterocladia umbellata small subunit ribosomal RNA gene, complete sequence
>AB219910.1 Polysiphonia sp. BRI50 gene for 18S rRNA, complete sequence
>AF203885.1 Neosiphonia savatieri small subunit ribosomal RNA gene, complete sequence
>JX828179.1 Polysiphonia atlantica voucher CH1268 small subunit ribosomal RNA gene, partial sequence
>JX828175.1 Neosiphonia yendoi voucher CH420 small subunit ribosomal RNA gene, partial sequence
>JX828181.1 Polysiphonia elongata voucher CH1416 small subunit ribosomal RNA gene, partial sequence
>MF093943.1 Polysiphonia brodiei isolate PD0516 18S ribosomal RNA gene, partial sequence
>AF427534.1 Polysiphonia nigra small subunit ribosomal RNA gene, complete sequence
>JX828168.1 Ceramiales sp. HGC-2012 voucher CH1414 small subunit ribosomal RNA gene, partial sequence
>MF093937.1 Melanothamnus harveyi isolate PD0890 18S ribosomal RNA gene, partial sequence
>AF427529.1 Polysiphonia elongata small subunit ribosomal RNA gene, complete sequence
>AY237287.1 Osmundaria spiralis 18S ribosomal RNA gene, partial sequence
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$
```



CP_blast_seqs.fna

LP_blast_seqs.fna

CP_blast_headers.txt

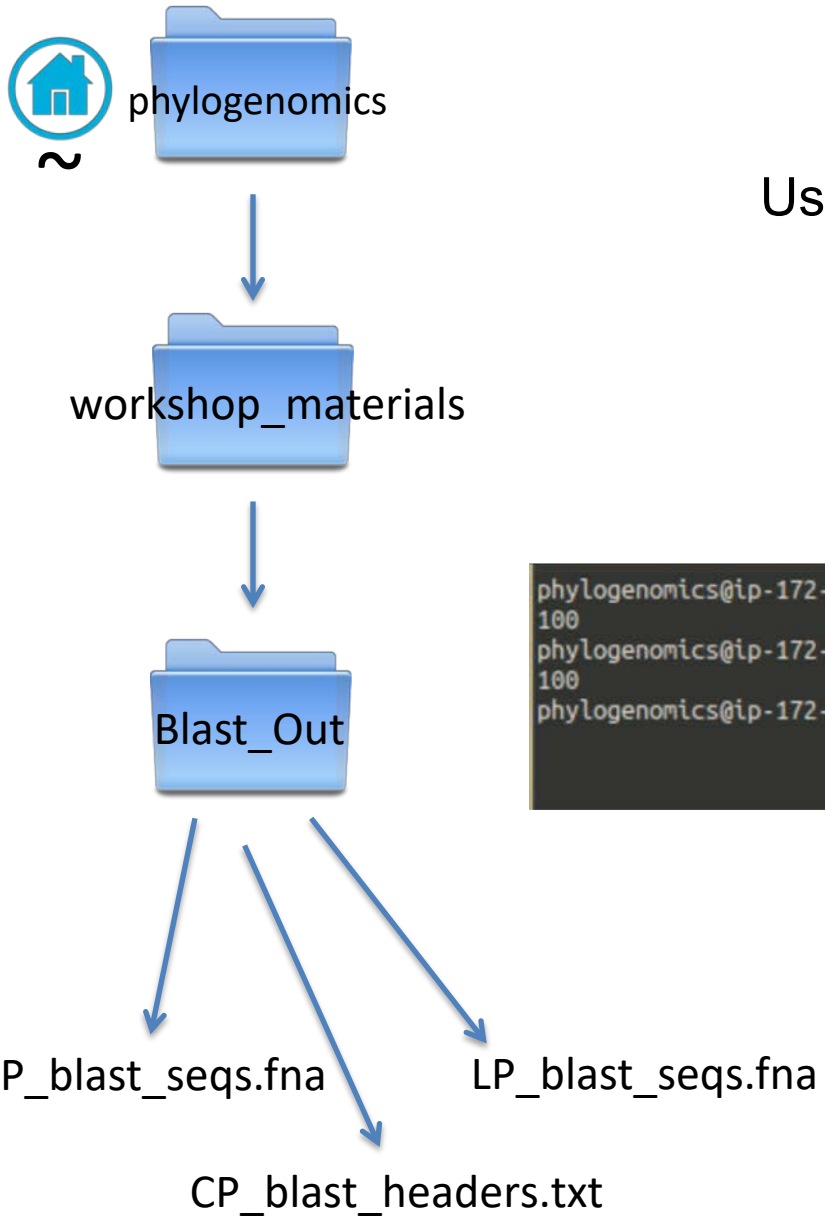
Use ‘grep’ to print occurrences of a pattern

```
$ grep “>” CP_blast_seqs.fna
```

Create a new file of the fasta headers

```
$ grep “>” CP_blast_seqs.fna > CP_blast_headers.txt
```

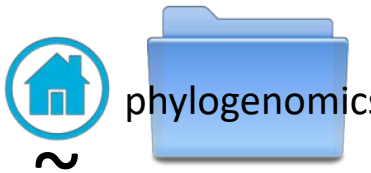
```
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ grep "^>" CP_blast_seqs.fna > CP_blast_headers.txt
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ head CP_blast_headers.txt
>AY617126.1 Choreocolax polysiphoniae 18S ribosomal RNA gene, partial sequence
>AY617142.1 Odonthalia washintoniensis 18S ribosomal RNA gene, partial sequence
>AY617140.1 Neorhodomela larix 18S ribosomal RNA gene, partial sequence
>AY617141.1 Odonthalia floccosa 18S ribosomal RNA gene, partial sequence
>MF093958.1 Thaumatella adunca isolate PD1388 18S ribosomal RNA gene, partial sequence
>MF093926.1 Digenea simplex isolate PD1820 18S ribosomal RNA gene, partial sequence
>JX828176.1 Odonthalia corymbifera voucher OK230 small subunit ribosomal RNA gene, partial sequence
>AY617145.1 Rhodomela confervoides 18S ribosomal RNA gene, partial sequence
>MF093954.1 Rhodomela confervoides isolate PD508 18S ribosomal RNA gene, partial sequence
>L26203.1 Rhodomela confervoides DNA fragment
```

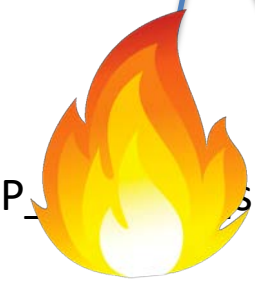


Use ‘grep’ for to count the number of times a pattern occurs

```
$ grep –c “>” CP_Blast_seqs.fna
```

```
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ grep -c "^>" CP_blast_seqs.fna
100
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ grep -c ">" CP_blast_seqs.fna
100
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$
```





CP_ .fna

LP_blast_seqs.fna

CP_blast_headers.txt

Quotation marks are important

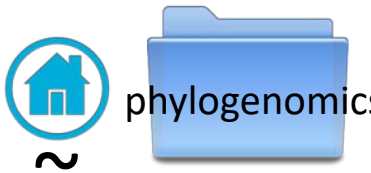
$ grep –c “>” CP_blast_seqs.fna

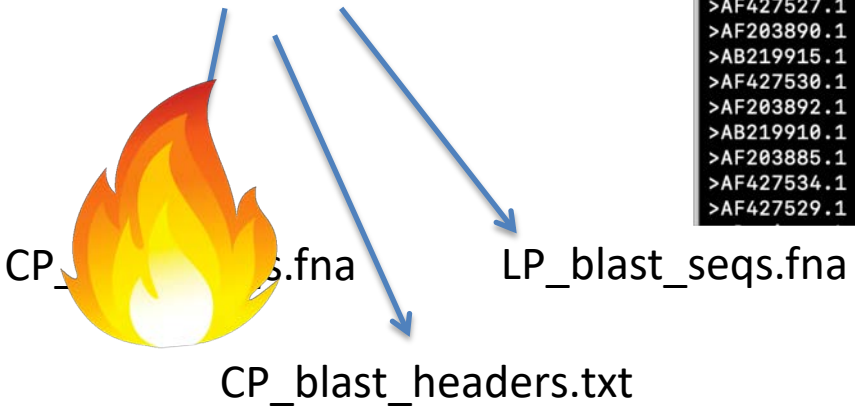
```
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ grep -c "^>" CP_blast_seqs.fna
100
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ grep -c ">" CP_blast_seqs.fna
100
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$
```

$ grep –c > CP_blast_seqs.fna

```
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ grep -c > CP_blast_seqs.fna
Usage: grep [OPTION]... PATTERN [FILE]...
Try 'grep --help' for more information.
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ grep -c ">" CP_blast_seqs.fna
0
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ head CP_blast_seqs.fna
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$
```

CP_Blast_seqs.fna is empty

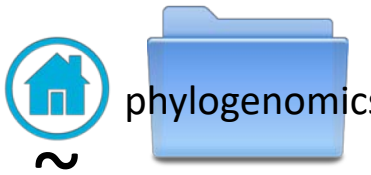




Search for headers that are not partial sequences

```
$ grep –v “partial” CP_blast_headers.txt
```

```
[salami:workshop_files ericsalomaki$ grep -v "partial" CP_blast_headers.txt
>L26203.1 Rhodomela confervoides DNA fragment
>AF339893.1 Lenormandia latifolia 18S ribosomal RNA gene, complete sequence
>AF203897.1 Lenormandia muelleri small subunit ribosomal RNA gene, complete sequence
>AF339899.1 Neurymenia fraxinifolia 18S ribosomal RNA gene, complete sequence
>AF203889.1 Melanamansia mamillaris small subunit ribosomal RNA gene, complete sequence
>AF339896.1 Lenormandia spectabilis 18S ribosomal RNA gene, complete sequence
>AF339901.1 Protokuetzingia australasica 18S ribosomal RNA gene, complete sequence
>AF339895.1 Lenormandia smithiae 18S ribosomal RNA gene, complete sequence
>AF203895.1 Lenormandia prolifera small subunit ribosomal RNA gene, complete sequence
>AF339900.1 Osmundaria prolifera 18S ribosomal RNA gene, complete sequence
>AF203896.1 Micropeuce strobiliferum small subunit ribosomal RNA gene, complete sequence
>AF251513.1 Halopithys incurva 18S ribosomal RNA gene, complete sequence
>AF339892.1 Lenormandia angustifolia 18S ribosomal RNA gene, complete sequence
>AF203894.1 Laurencia filiformis small subunit ribosomal RNA gene, complete sequence
>AF251512.1 Melanamansia glomerata 18S ribosomal RNA gene, complete sequence
>AF203887.1 Murrayella periclados small subunit ribosomal RNA gene, complete sequence
>AF203886.1 Polysiphonia lanosa small subunit ribosomal RNA gene, complete sequence
>AF339898.1 Lenormandia sp. MELU_000064 18S ribosomal RNA gene, complete sequence
>AF427537.1 Womersleyella setacea small subunit ribosomal RNA gene, complete sequence
>AF339897.1 Lenormandia sp. MELU_000065 18S ribosomal RNA gene, complete sequence
>AF427526.1 Boergeseniella fruticulosa small subunit ribosomal RNA gene, complete sequence
>AF427527.1 Enelittosiphonia stimpsonii small subunit ribosomal RNA gene, complete sequence
>AF203890.1 Heterocladia australis small subunit ribosomal RNA gene, complete sequence
>AB219915.1 Polysiphonia sp. SNI07 gene for 18S rRNA, complete sequence
>AF427530.1 Polysiphonia fucoides small subunit ribosomal RNA gene, complete sequence
>AF203892.1 Heterocladia umbellata small subunit ribosomal RNA gene, complete sequence
>AB219910.1 Polysiphonia sp. BRI50 gene for 18S rRNA, complete sequence
>AF203885.1 Neosiphonia savatieri small subunit ribosomal RNA gene, complete sequence
>AF427534.1 Polysiphonia nigra small subunit ribosomal RNA gene, complete sequence
>AF427529.1 Polysiphonia elongata small subunit ribosomal RNA gene, complete sequence
```



Replacing Text in Large files

sed ’s/**FIND**/**REPLACE**/g’ filename > output_file

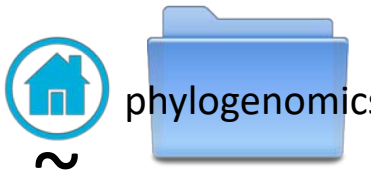
```
$ sed ‘s/ /_/g’ CP_blast_headers.txt
```

```
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ sed 's/ /_/g' CP_blast_headers.txt > CP_blast_headers_clean.txt
phylogenomics@ip-172-30-3-100:~/workshop_materials/Blast_Out$ head CP_blast_headers_clean.txt
>AY617126.1_Choreocolax_polysiphoniae_18S_ribosomal_RNA_gene,_partial_sequence
>AY617142.1_Odonthalia_washintoniensis_18S_ribosomal_RNA_gene,_partial_sequence
>AY617140.1_Neorhodomela_larix_18S_ribosomal_RNA_gene,_partial_sequence
>AY617141.1_Odonthalia_floccosa_18S_ribosomal_RNA_gene,_partial_sequence
>MF093958.1_Thaumatella_adunca_isolate_PD1388_18S_ribosomal_RNA_gene,_partial_sequence
>MF093926.1_Digenea_simplex_isolate_PD1820_18S_ribosomal_RNA_gene,_partial_sequence
>JX828176.1_Odonthalia_corymbifera_voucher_OK230_small_subunit_ribosomal_RNA_gene,_partial_sequence
>AY617145.1_Rhodomela_confervoides_18S_ribosomal_RNA_gene,_partial_sequence
>MF093954.1_Rhodomela_confervoides_isolate_PD508_18S_ribosomal_RNA_gene,_partial_sequence
>L26203.1_Rhodomela_confervoides_DNA_fragment
```

CP_blast_seqs.fna

LP_blast_seqs.fna

CP_blast_headers.txt



Replacing Text in Large files

Use the –i flag to make changes inplace

```
$ sed -i 's/,//g' CP_blast_headers.txt
$ head CP_blast _headers.txt
```

```
>AY617126.1 Choreocolax polysiphoniae 18S ribosomal RNA gene partial sequence
>AY617142.1 Odonthalia washintoniensis 18S ribosomal RNA gene partial sequence
>AY617140.1 Neorhodomela larix 18S ribosomal RNA gene partial sequence
>AY617141.1 Odonthalia floccosa 18S ribosomal RNA gene partial sequence
>MF093958.1 Thaumatella adunca isolate PD1388 18S ribosomal RNA gene partial sequence
>MF093926.1 Digenea simplex isolate PD1820 18S ribosomal RNA gene partial sequence
>JX828176.1 Odonthalia corymbifera voucher OK230 small subunit ribosomal RNA gene partial sequence
>AY617145.1 Rhodomela confervoides 18S ribosomal RNA gene partial sequence
>MF093954.1 Rhodomela confervoides isolate PD508 18S ribosomal RNA gene partial sequence
>L26203.1 Rhodomela confervoides DNA fragment
```

CP_blast_seqs.fna

LP_blast_seqs.fna

CP_blast_headers.txt

Regular Expressions

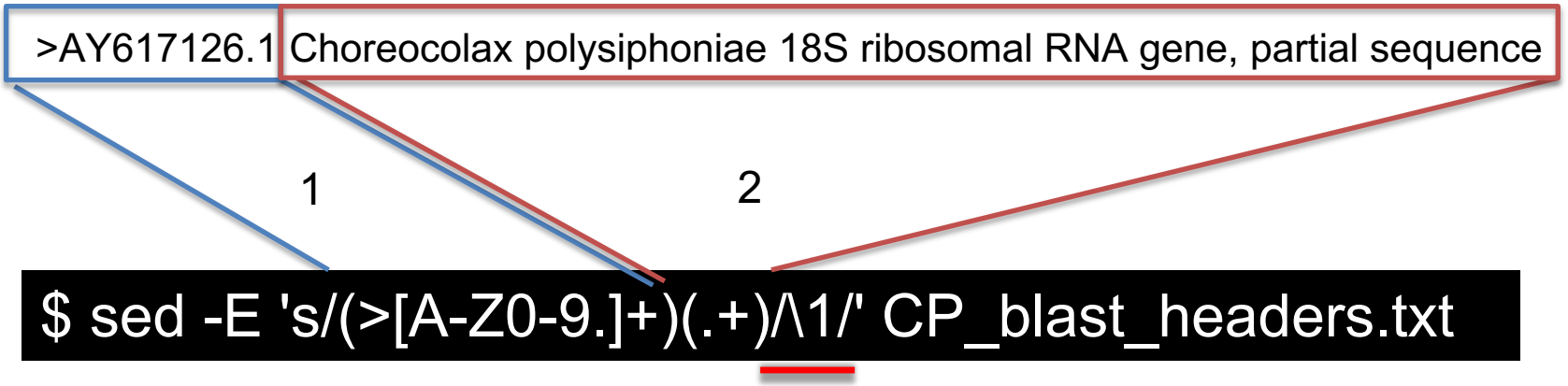
Encoding	Modern Equivalent	Pattern Type
`.`		a single character
`.+`		one or more characters
`.*`		zero or more characters
`.?`		Maybe present
`^`		first on the line
`$`		last on the line
`[0-9]`	`\d`	digits
`[a-zA-Z]`	`\w`	letters
`' '`	`\s \t`	space
`{3}`		must be exactly 3 characters long
`{3,5}`		between 3-5 characters long
`[ACGT]`		a specific set of characters (a class)

Regular Expressions

Use –E with sed and grep to use extended regular expressions

Store pattern in memory using parentheses

Print out only the GenBank accessions



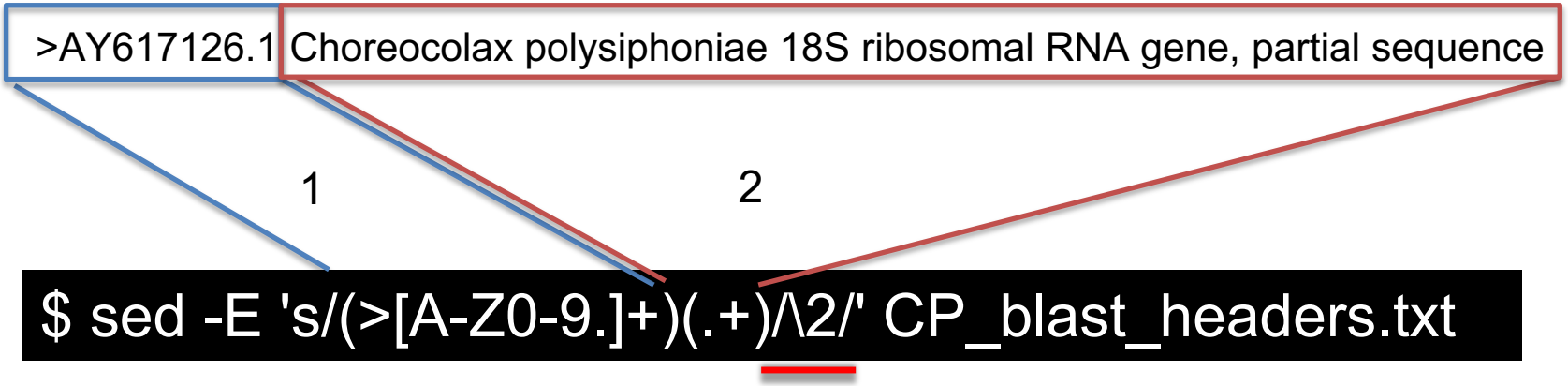

```
salami:workshop_files ericsalomaki$ sed -E 's/(>[A-Z0-9.]+)(.+)/\1/' CP_blast_headers.txt
>AY617126.1
>AY617142.1
>AY617140.1
>AY617141.1
>MF093958.1
```

Regular Expressions

Use –E with sed and grep to use extended regular expressions

Store pattern in memory using parentheses

Print out everything except the GenBank accessions




```
salami:workshop_files ericsalomaki$ sed -E 's/(>[A-Z0-9.]+)(.+)/\2/' CP_blast_headers.txt
 Choreocolax polysiphoniae 18S ribosomal RNA gene, partial sequence
 Odonthalia washintoniensis 18S ribosomal RNA gene, partial sequence
 Neorhodomela larix 18S ribosomal RNA gene, partial sequence
 Odonthalia floccosa 18S ribosomal RNA gene, partial sequence
 Thaumatella adunca isolate PD1388 18S ribosomal RNA gene, partial sequence
 Digenea simplex isolate PD1820 18S ribosomal RNA gene, partial sequence
 Odonthalia corymbifera voucher OK230 small subunit ribosomal RNA gene, partial sequence
 Rhodomela confervoides 18S ribosomal RNA gene, partial sequence
```

Pipes

Use “|” to string multiple commands together

Combine the fasta files from the blast output and identify how many sequences there are

```
cat CP_blast_seqs.fna LP_blast_seqs.fna | grep ">" | wc -l
```

```
salami:workshop_files ericsalomaki$ cat CP_blast_seqs.fna LP_blast_seqs.fna | grep ">" | wc -l
     200
```

Pipes

Use the pipe “|” to string multiple commands together

Combine the fasta files from the blast output and identify how many sequences there are

```
cat CP_blast_seqs.fna LP_blast_seqs.fna | grep ">" | wc -l
```

```
[salami:workshop_files ericsalomaki$ cat CP_blast_seqs.fna LP_blast_seqs.fna | grep ">" | wc -l
     200
```

Other built-in unix binaries that are great to use with pipes

‘sort’ – sort lines of text files
‘uniq’ – report or omit repeated lines (only works on a sorted file)

String together many commands to count the number of unique accessions from these blast results

```
$ cat *.fna |
```
Print out all fasta files

```
$ cat *.fna | grep ">" |
```
Find all the fasta headers

```
$ cat *.fna | grep ">" | sed -E 's/(>[A-Z0-9.]+)(.+)/\1/' |
```
Remove everything except accessions

```
$ cat *.fna | grep ">" | sed -E 's/(>[A-Z0-9.]+)(.+)/\1/' | sort |
```
Sort accessions

```
$ cat *.fna | grep ">" | sed -E 's/(>[A-Z0-9.]+)(.+)/\1/' | sort | uniq |
```
Keep only unique accessions

```
$ cat *.fna | grep ">" | sed -E 's/(>[A-Z0-9.]+)(.+)/\1/' | sort | uniq | wc -l
```
Count unique accessions

```
salami:Blast_Out ericsalomaki$ cat *.fna | grep ">" | sed -E 's/(>[A-Z0-9.]+)(.+)/\1/' | sort | uniq | wc -l
     144
```

Using a Loop

Using for loops allow you to apply a command to multiple files at once

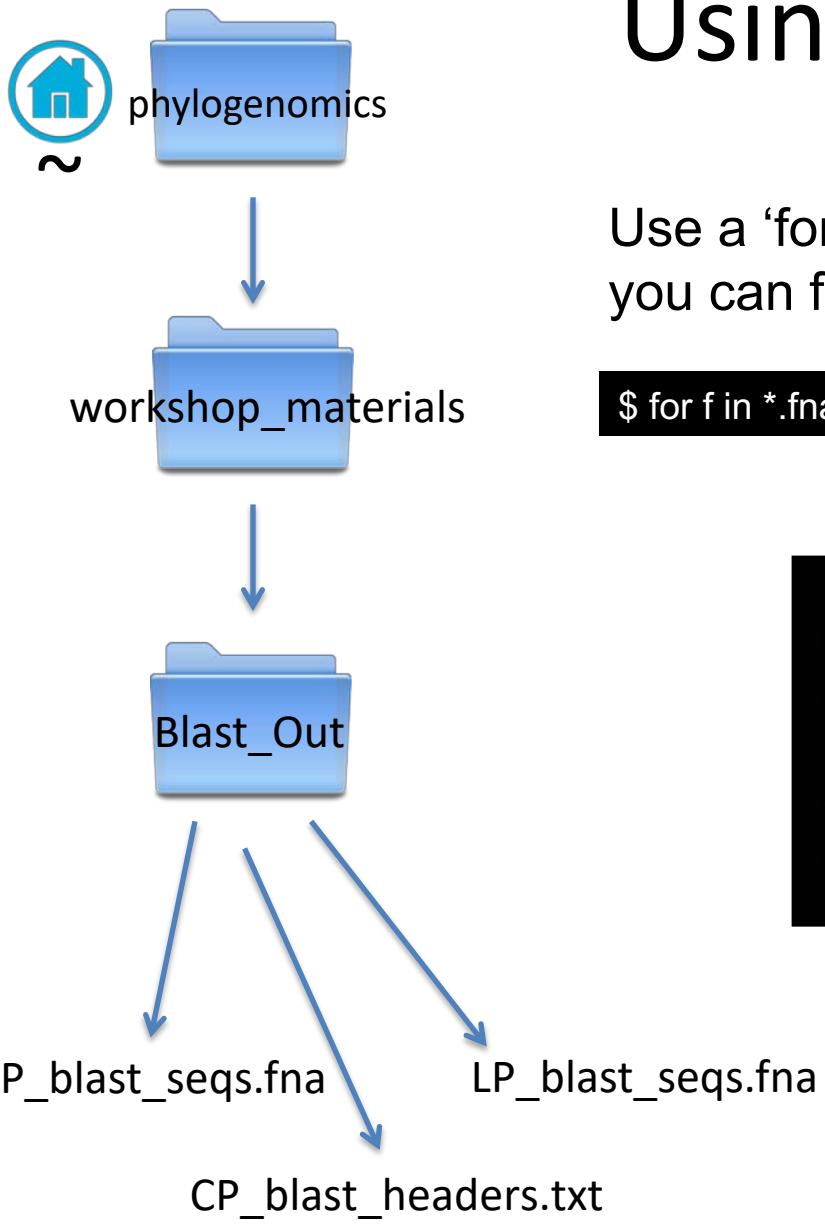
```
$ for f in *.fna; do grep -c "ACT" $f ; done
```

Assign variable “f” to all files that end in .fna
Then carry out command on all values of “f”

```
salami:Blast_Out ericsalomaki$ for f in *.fna; do grep -c "ACT" $f ; done
1354
1291
```

I often use loops to make several single gene trees at once

Using a Loop



Use a ‘for loop’ to find how many times you can find “CAT” in these fasta files

```
$ for f in *.fna; do grep -c ”CAT" $f ; done
```

```
1257
1319
```

Online Downloads

wget will download to your pwd
Use the –P option

```
wget –P /path/to/desired/location/  File_To_Download.txt
```

Online Downloads

Use wget –P to download these slides to a new directory
-P will make a new directory if it does not yet exist

```
wget –P ./wget_dir/  http://evomics.org/wp-content/uploads/2019/01/Introduction_to_Unix_Krumlov2019_Jan21_red.pdf
```

http://evomics.org/wp-content/uploads/2019/01/Introduction_to_Unix_Krumlov2019_Jan21_red.pdf

Then use ls to see the new directory and then again to look inside the directory to ensure the slides have been downloaded

Final Unix Challenge

Download the challenge and view it in terminal

http://evomics.org/wp-content/uploads/2019/01/Final_Unix_Challenge.txt

Save Your Data Everyday

We will launch new instance tonight so everything you have done today will be gone tomorrow

Use scp or rsync to transfer files

scp –r username@IP.address:/Location/On/Instance /Location/On/Your/Computer

```
$ scp  -r phyogenomics@ec2-34-227-31-223.compute-1.amazonaws.com:~/workshop_materials/Unix
~/Location/On/Your/Computer
```

Any questions?