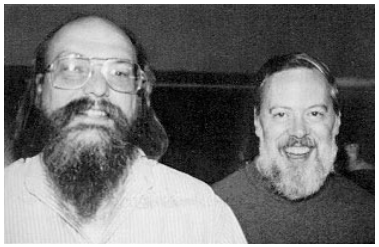
What is UNIX?



Ken Thompson and Dennis Ritchie

- An operating system run on many servers
- Invented by AT&T Bell Labs in 1969
- Linux is a open -source UNIX clone released in 1991
- **Linux** is an operating system kernel
- **Unix/Linux** terms are often used interchangeably

Linus Torvalds

1970's

2020's

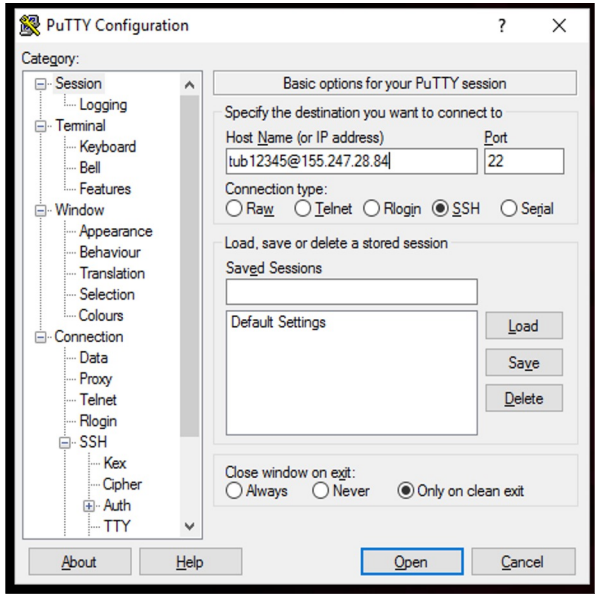
Log onto server

Windows

- Open putty
- Configure your ssh session

  *Host Name or IP =<accessnetid>@**wi-hpc-dev***

  *example: **jmadzo@wi-hpc-dev***
- Click Open
- Enter you temple ID password



Mac

- open terminal
- ***ssh jmadzo@wi-hpc-dev***

abrown
apatel1
asimon
athapar
cnurse
dfarmer
efisher
ekim
gteixeira
hpatel
icross
kcodrington
kjohnson
kpierson
lposadas
mbolis
ndyson
odominguez
sbenkhoukha
smurphy
tdavis
tyang

•You and the students will need to login to our Microsoft My Apps Portal (https://myapps.microsoft.com/) which will require you to reset your password and setup our MFA (Microsoft Authenticator) on your phone. I have included a PDF of the instructions on how to setup the MFA that you can use and share with the class. The default password for everyone for their first time logging in is: **Science7testtube3lab#**

•To access the HPC you will also need to utilize our VPN, Ivanti Secure Access Client, which will be presented to you in the My Apps Portal once you are logged in. The Server URL for the connection is **vpn.apps.wistar.org**

•Your credentials are the following: **jmadzo@wistar.org**

•If you or anyone have an issue with logging in, resetting the password, setting up MFA, setting up the VPN, let us know on this thread.

•If you have any additional questions let us know on this thread.

https://myapps.microsoft.com

https://wistarinstitute.sharepoint.com/IT/SitePages/VPN.aspx

vpn.apps.wistar.org

pw: Science7testtube3lab#

Once you have reset your password and connected to the VPN, you may:

1. Open a terminal emulator such as:
    a. Built-in Terminal or iTerm2 for MacOS
    b. Windows terminal (cmd) or PuTTy for Windows
    c. Do NOT use Visual Studio code to connect to the server

2. Use the SSH protocol to connect to the server
    a. ssh <username>@wi-hpc-dev
    b. Where <username> is the "Wistar account" column below (minus the @wistar.org)
    c. Your login would be: `ssh` ***jmadzo@wi-hpc-dev***

3. You will then be logged into the "Head Node" or sometimes called a "Login Node".
    a. This is NOT meant for computational-intensive work
    b. Rather, please request resources via the Slurm scheduler

HPC Documentation Homepage: https://hpc.apps.wistar.org
FAQ Section: https://hpc.apps.wistar.org/faq/
Quick Start: https://hpc.apps.wistar.org/quick-start/
User Guide: https://hpc.apps.wistar.org/access/
Best Practices: https://hpc.apps.wistar.org/bestpractices/

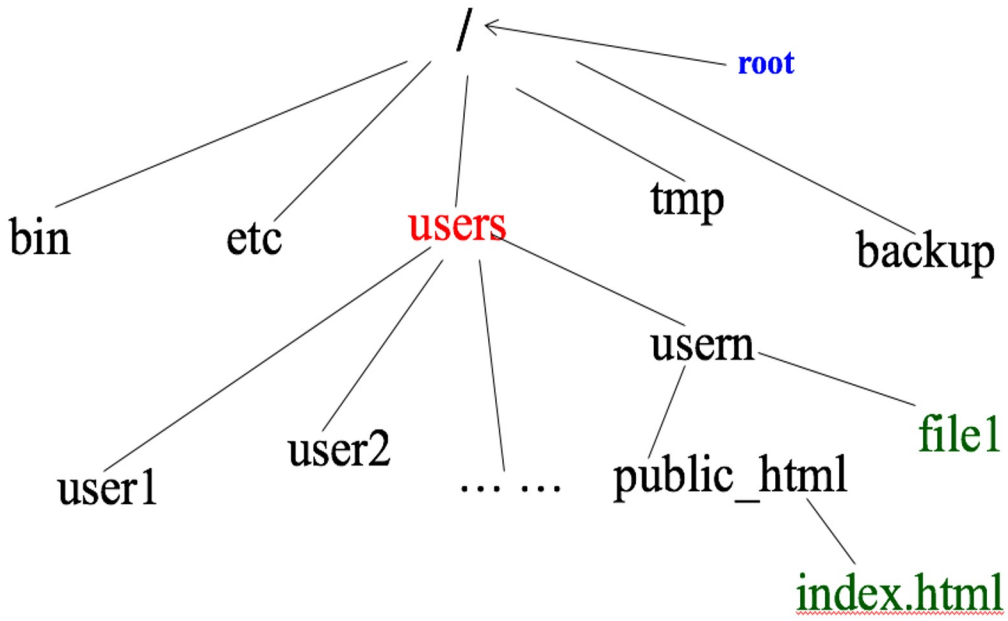
```
ssh username@wi-hpc-dev

srun --cpus-per-task=2 --mem=10G --account=pcom --partition=pcom bash

/wistar/pcom
```

Unix/Linux: What is Directory?

Directories can hold files and other directories



Pathnames

Absolute Pathnames
In the previous tree */users/user1/file1* is an absolute pathname

Relative pathnames
If you are already in the *users* directory, the relative pathname for *file1* is *user1/file1*

UNIX/Linux commands

$ ls -l -r -s tmp

ls (command or utility or program)

-l -r -s (options, or flags –control the flavors of the command)

/tmp (argument – what is been operated on)

UNIX/Linux - basic commands

- ***ls –*** list. Lists folders/files in a directory
- **pwd** - print working directory. Prints the path of the current directory
- **cd** – change directory. "***cd name***" to navigate to directory name
- **mkdir** – make directory create a new directory in the current directory. Can also create multiple directories
- **cp** – copy. "cp file1 file2" to create a new file, file2 which is a copy of file1
- **mv** – move, Same as copy, but deletes the original file

Look around

```
ls
```

Move around

```
cd

./  current position
..  one above current position
../..  two above current position
~   your home
/   root
```

If you get lost

```
pwd
```

Create a new directory

mkdir mydir ### Make a **new** directory

ls

Create a new file in a directory

cd mydir

nano file1.txt #### Use nano to create a **new** file, use Control O to save and Control-X to exit.

ls

Copy a file on your current directory and copy a folder to your home directory.

cp file1.txt file1_copy.txt ### Copy file1.txt to file1_copy.txt

ls

Rename a file or folder

```
mv file1_copy.txt   file12.txt
```

Move file from one folder to another

```
mv folder1/file1.txt folder2
```

File contend

head – first 10 lines of file
tail – last 10 lines of file
more – contend of the file one screen (space next screen)
less – contend of the file one screen (exit with **q**)
cat– contend of one or multiple the file one screen

File manipulation

wc
cut
awk

Compress files

gzip and **gunzip**

I/O redirection and pipe

> file, Output re-direction, overwrite

cat file1.txt > file2.txt

>> file, Output re-direction, append

cat file1.txt >> file2.txt

< file, input re-direction

cat < file1.txt

command A **|** *command B*, pipe output from command A to command B

ls -l | wc -l

Rename a file or folder

```
mv file1_copy.txt   file12.txt
```

Move file from one folder to another

```
mv folder1/file1.txt folder2
```

File contend

mv
less
cat

File manipulation

wc
cut
awk
grep

Compress files

gzip and **gunzip**

UNIX/Linux - more commands

man – manual. Use "***man name***" to bring up a manual
clear – clear. Clears the screen.
cal – calendar

du – disk usage. Shows the disk usage of the current directory

UNIX – remove commands

Be careful with these!

rm – remove. Use “rm file(s)” to delete files

rmdir – remove directory. Use it to delete an empty directory

You can not recover your files after you removed them!

Delete a file or directory

```
rm file1_copy.txt
rm -r temp
```

BE CAREFULL!!!

File transfer between computers

Winscp (between Windows and Linux)

scp (between unix/linux machines)
scp file1.txt username@155.247.231.89

wget url
http://yeastgenome.org/saccharomyces_cerevisiae.gff

Download file from web

wget

```
http://downloads.yeastgenome.org/curation/chromosomal_feature/saccharomyces_cerevisiae.gff
```

Look around file

```
head -10 saccharomyces_cerevisiae.gff
tail -10 saccharomyces_cerevisiae.gff
less saccharomyces_cerevisiae.gff
```

Number of lines

```
wc -l saccharomyces_cerevisiae.gff
```

Look up stuff in file

```
grep CDS saccharomyces_cerevisiae.gff | head
grep CDS saccharomyces_cerevisiae.gff | wc -l

grep chr saccharomyces_cerevisiae.gff | cut -f1 | sort -u

grep chrII saccharomyces_cerevisiae.gff | cut -f 3 | sort | uniq -c | sort -n -r


awk '$3 =="mRNA"' saccharomyces_cerevisiae.gff | head
awk '$3 =="mRNA"' saccharomyces_cerevisiae.gff | wc -l
awk '$3 =="mRNA" {print$1,$4,$5}' saccharomyces_cerevisiae.gff | head
awk -v OFS="\t" '$3 =="mRNA" {print$1,$4,$5}' saccharomyces_cerevisiae.gff >sc.bed
head sc.bed
```

Some other useful commands

```
awk '$1==2 {print$2}' animals.txt
sort
uniq
rev
tr
paste
find ./ name
```