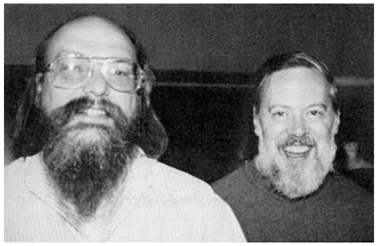
What is UNIX?



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

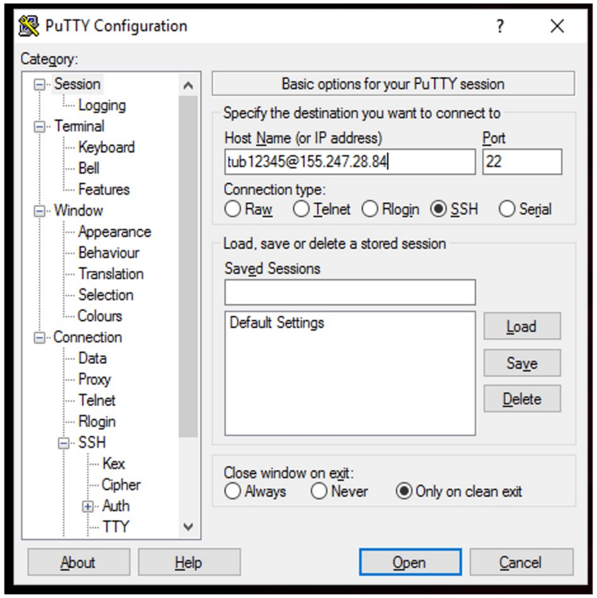
Log onto server

Windows

- Open putty
- Configure your ssh session

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

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



PuTTY Configuration

Host Name (or IP address): tub12345@155.247.28.84

Port: 22

Connection type: ○ Raw ○ Telnet ○ Rlogin ● SSH ○ Serial

Saved Sessions: Default Settings

Close window on exit: ○ Always ○ Never ● Only on clean exit

Mac

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

Log onto server

usernames:

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

Log onto server

- You 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.

- To access the HPC you 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: **pcom-jmadzo@wistar.org**

Get VPN from here:

https://myapps.microsoft.com

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

vpn.apps.wistar.org

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

1. Open a terminal emulator such as:
    1. Built-in Terminal or iTerm2 for MacOS
    2. Windows terminal (cmd) or PuTTy for Windows

2. Use the SSH protocol to connect to the server
    1. ***`ssh <username>@wi-hpc-dev`***
    2. Where <username> is the “Wistar account”
    3. example: ***`ssh pcom-jmadzo@wi-hpc-dev`***

3. You will then be logged into the “Head Node” or sometimes called a “Login Node”.
    1. **This is NOT meant for computational-intensive work**
    2. 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/

Log onto server

Log on server:

```
ssh username@wi-hpc-dev
```

Run bash on server (if you run stuff localy you do not need it):

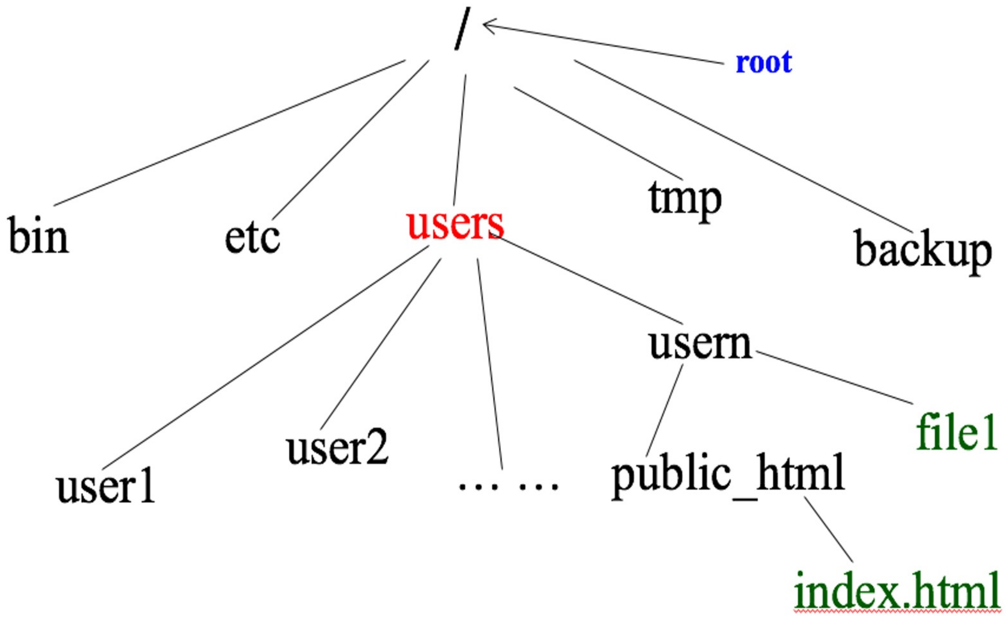
```
srun --cpus-per-task=2 --mem=10G --account=pcom --partition=pcom bash
```

your folder location:

```
/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

UNIX/Linux - basic commands

Look around

```
ls
```

Move around

```
cd

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

If you get lost

```
pwd
```

UNIX/Linux - basic commands

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

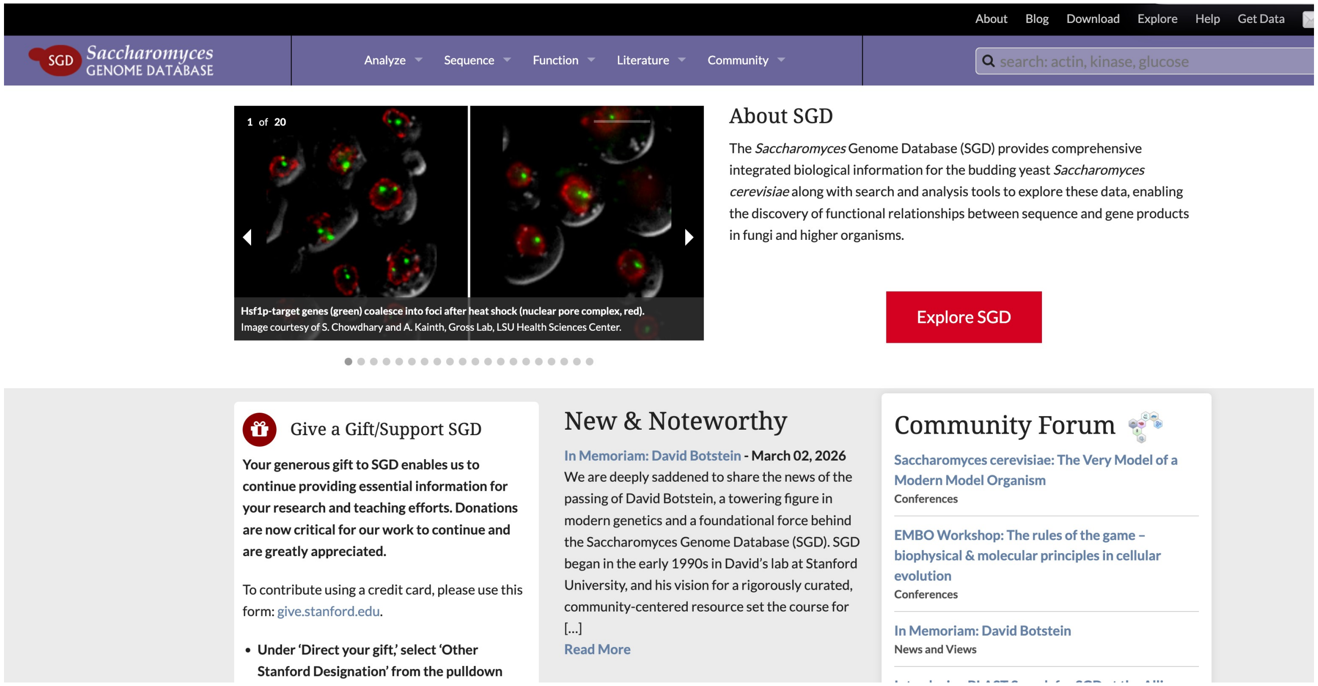
Winscp (between Windows and Linux)

scp (between unix/linux machines)

```
scp file1.txt username@155.247.231.89
```

wget url

```
http://sgd-archive.yeastgenome.org/sequence/S288C_reference/genome_releases/S288C_reference_genome_Current_Release.tgz
```



Hsf1p-target genes (green) coalesce into foci after heat shock (nuclear pore complex, red).
Image courtesy of S. Chowdhary and A. Kainth, Gross Lab, LSU Health Sciences Center.

About SGD

The *Saccharomyces* Genome Database (SGD) provides comprehensive integrated biological information for the budding yeast *Saccharomyces cerevisiae* along with search and analysis tools to explore these data, enabling the discovery of functional relationships between sequence and gene products in fungi and higher organisms.

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Your generous gift to SGD enables us to continue providing essential information for your research and teaching efforts. Donations are now critical for our work to continue and are greatly appreciated.

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- **Under 'Direct your gift,' select 'Other Stanford Designation' from the pulldown**

New & Noteworthy

In Memoriam: David Botstein - **March 02, 2026**

We are deeply saddened to share the news of the passing of David Botstein, a towering figure in modern genetics and a foundational force behind the Saccharomyces Genome Database (SGD). SGD began in the early 1990s in David's lab at Stanford University, and his vision for a rigorously curated, community-centered resource set the course for [...]

Read More

Community Forum

Saccharomyces cerevisiae: The Very Model of a Modern Model Organism
Conferences

EMBO Workshop: The rules of the game – biophysical & molecular principles in cellular evolution
Conferences

In Memoriam: David Botstein
News and Views

https://www.yeastgenome.org/

Download file from web

```
wget http://sgd-archive.yeastgenome.org/curation/chromosomal_feature/saccharomyces_cerevisiae.gff.gz
```

unzip file

```
gunzip saccharomyces_cerevisiae.gff.gz
```

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
```

Some other useful commands

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

```
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
```