

# Introduction to **Unix command line** & **Shell programming**

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2022 Spring

# Notations of the slides

- Code chunk starts with "➤", e.g.

➤ echo 'Hello world!'

- [Link](#) is underlined

- Practice comes with



# Agenda

- Day 0: Preparation
- Day 1: Introduction to **Unix Command line**
  - Navigating through file system
  - Manipulating files and directories
- Day 2: Advanced **Command line**
  - File processing using **awk**, **grep**, **sed** ...
- Day 3: **Shell scripting** and running jobs on hoffman2

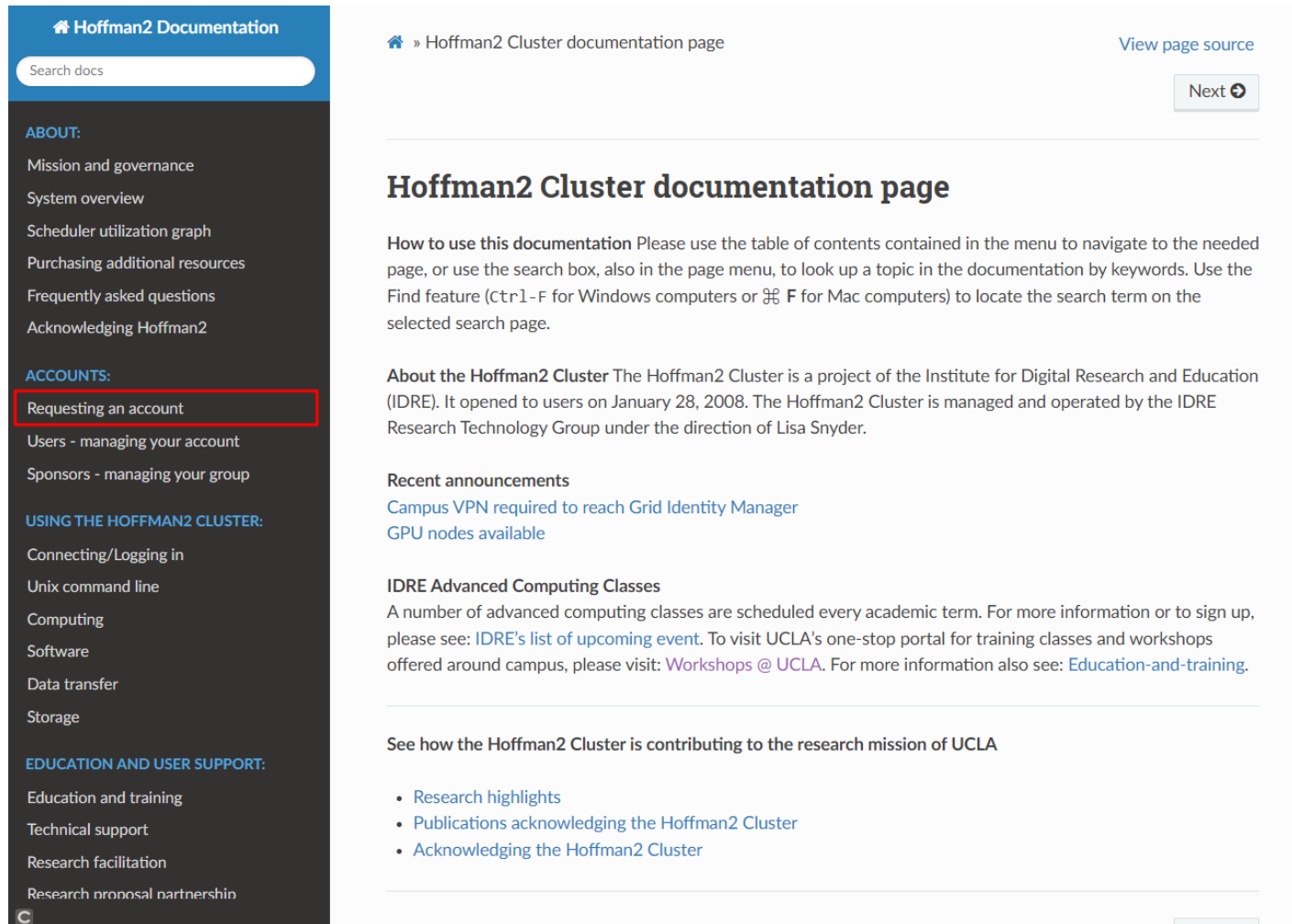


# Day 0: Preparation

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# Step 1: Register a hoffman2 account

- Go to Hoffman2 documentation: <https://www.hoffman2.idre.ucla.edu/>



The screenshot displays the Hoffman2 Documentation website. On the left is a dark sidebar with a search bar and several menu sections. The 'ACCOUNTS:' section is highlighted, and within it, 'Requesting an account' is enclosed in a red rectangular box. The main content area on the right is titled 'Hoffman2 Cluster documentation page' and includes introductory text, a link to 'View page source', a 'Next' button, and sections for 'About the Hoffman2 Cluster', 'Recent announcements', and 'IDRE Advanced Computing Classes'.

**Hoffman2 Documentation**

Search docs

**ABOUT:**

- Mission and governance
- System overview
- Scheduler utilization graph
- Purchasing additional resources
- Frequently asked questions
- Acknowledging Hoffman2

**ACCOUNTS:**

- Requesting an account**
- Users - managing your account
- Sponsors - managing your group

**USING THE HOFFMAN2 CLUSTER:**

- Connecting/Logging in
- Unix command line
- Computing
- Software
- Data transfer
- Storage

**EDUCATION AND USER SUPPORT:**

- Education and training
- Technical support
- Research facilitation
- Research proposal partnership

» Hoffman2 Cluster documentation page

View page source

Next

## Hoffman2 Cluster documentation page

**How to use this documentation** Please use the table of contents contained in the menu to navigate to the needed page, or use the search box, also in the page menu, to look up a topic in the documentation by keywords. Use the Find feature (Ctrl-F for Windows computers or ⌘ F for Mac computers) to locate the search term on the selected search page.

**About the Hoffman2 Cluster** The Hoffman2 Cluster is a project of the Institute for Digital Research and Education (IDRE). It opened to users on January 28, 2008. The Hoffman2 Cluster is managed and operated by the IDRE Research Technology Group under the direction of Lisa Snyder.

**Recent announcements**

- Campus VPN required to reach Grid Identity Manager
- GPU nodes available

**IDRE Advanced Computing Classes**

A number of advanced computing classes are scheduled every academic term. For more information or to sign up, please see: [IDRE's list of upcoming event](#). To visit UCLA's one-stop portal for training classes and workshops offered around campus, please visit: [Workshops @ UCLA](#). For more information also see: [Education-and-training](#).

See how the Hoffman2 Cluster is contributing to the research mission of UCLA

- Research highlights
- Publications acknowledging the Hoffman2 Cluster
- Acknowledging the Hoffman2 Cluster

# Step 1: Register a hoffman2 account

- Click [Register here!](#)

**ACCOUNTS:**

- Requesting an account
  - Overview
  - Applying for a user account
  - Register as a Sponsor
- Users - managing your account
- Sponsors - managing your group

**USING THE HOFFMAN2 CLUSTER:**

- Connecting/Logging in
- Unix command line
- Computing
- Software
- Data transfer
- Storage

**EDUCATION AND USER SUPPORT:**

- Education and training
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- Research facilitation
- Research proposal partnership

**POLICIES:**

- User account policy
- Backup policy
- Job scheduling policy
- Role of the login nodes
- Role of GPU nodes
- Security
- Software installation

**RESEARCH SHOWCASE:**

Previous Next

## Requesting an account

**Note**

If you are using a computer on Mednet in the David Geffen School of Medicine (DGSOM) you may need to first connect to the [campus VPN](#) in order to reach GIM. If you still have an issue, please submit a ticket to our [helpdesk](#).

### Overview

In order to use the Hoffman2 Cluster, you will need to apply for a user account. All user accounts need to be sponsored by a UCLA faculty or researcher that qualifies under [UCLA Policy 900](#) as a principal investigator.

We use a web-based account management application, **Grid Identity Manager (GIM)** for sponsor registration, user account requests, and to manage your Hoffman2 Cluster account. Please note, the GIM uses the UCLA Federated Authentication Service to authenticate access, therefore you need to have a [UCLA Logon ID](#) in order to access GIM. [UCLA Logon ID](#) is not a service of the IDRE Research Technology Group, if you have difficulty with it consider contacting the [UCLA IT Support Center](#).

### Applying for a user account

After acquiring a [UCLA Logon ID](#) you are ready to register as a user of the Hoffman2 Cluster provided that your academic advisor is already registered as a [Hoffman2 Cluster Sponsor](#). Please note, each person is allowed only one Hoffman2 Cluster user account. If you require access to multiple research groups, please submit a request to add/join a secondary group via our [online helpdesk](#).

**Important**

New users: [Register here!](#)

Should your academic advisor not be listed in the sponsor pull-down menu on the [New User Registration](#) web form, he or she will need to apply following directions given in [Register as a Sponsor](#). If you are a UCLA faculty or researcher that qualifies under [UCLA Policy 900](#) as a principal investigator, please register as a [Hoffman2 Cluster sponsor](#) first, before applying for a user account.

(Campus VPN might be required to access the registration website)

# Step 1: Register a hoffman2 account

- Fill in the information

(Note: if you don't have a **sponsor** or your PI is not in the sponsor faculty list, you can choose **Collaboratory Workshops**)

English

## Grid Identity Manager

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### Grid Identity Manager

#### New User Registration

If you don't have a cluster login id and/or Grid Username, please fill out the following form. An e-mail will be sent to your chosen sponsor for approval. If the sponsor you select is not correct, your application may be denied. You use your Grid Username and Grid Password when you access a cluster via the web, so it is important to remember them.

Select a Resource: Hoffman2 Cluster

Select a Sponsor: Choose a faculty sponsor

Proposed Username:

- Passwords can only contain the characters: a-z A-Z 0-9 @#\_ /
- Passwords must be at least 6 characters long.
- Passwords must contain at least one letter and one non-letter from: 0-9 @#\_ /

New Grid Password:

New Grid Password Confirm:

First Name:

Last Name:

Email Address:

Department, Center or Organization: Choose a department

Preferred Shell: Bash

#### Create the shared secret

- You will need the following shared secret to retrieve your initial cluster login password.
- You will also need it if you forget your password and need to have it reset in future.
- The secret answer can not contain special characters. It must be alpha-numeric.

Secret Challenge Question:

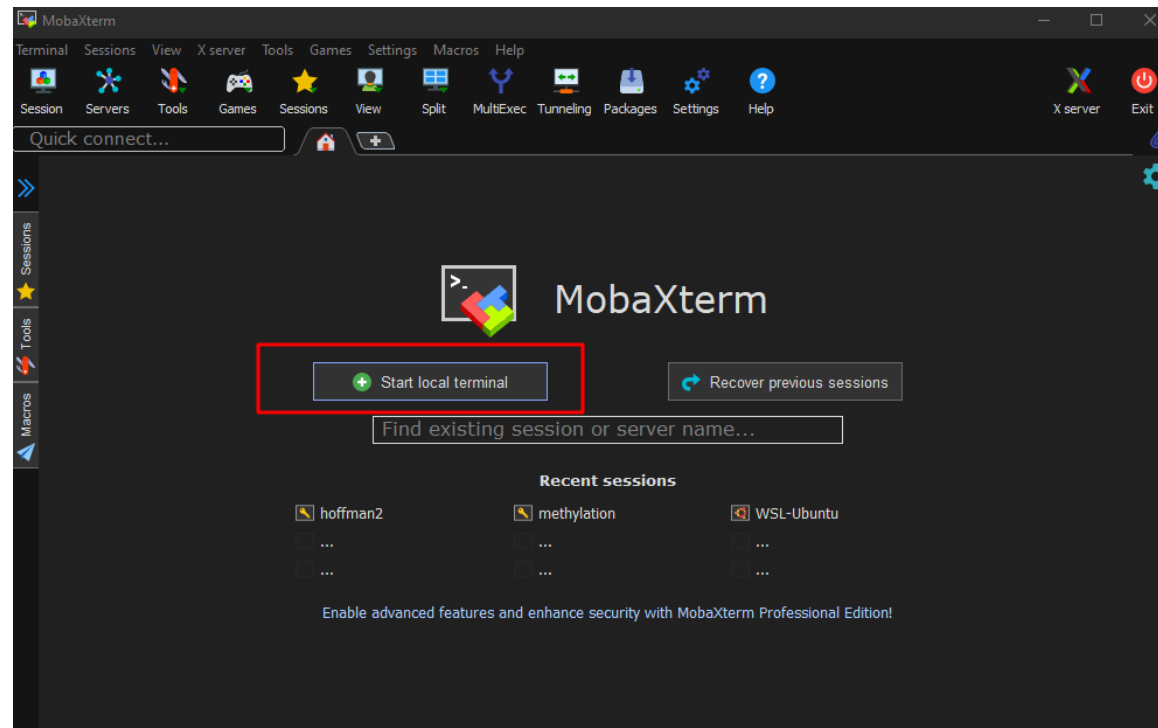
Your Answer:

Project Description:

If you have any other questions, please contact the IDRE Account Administrator at [accounts@idre.ucla.edu](mailto:accounts@idre.ucla.edu)

# Step 2: Get your computer ready!

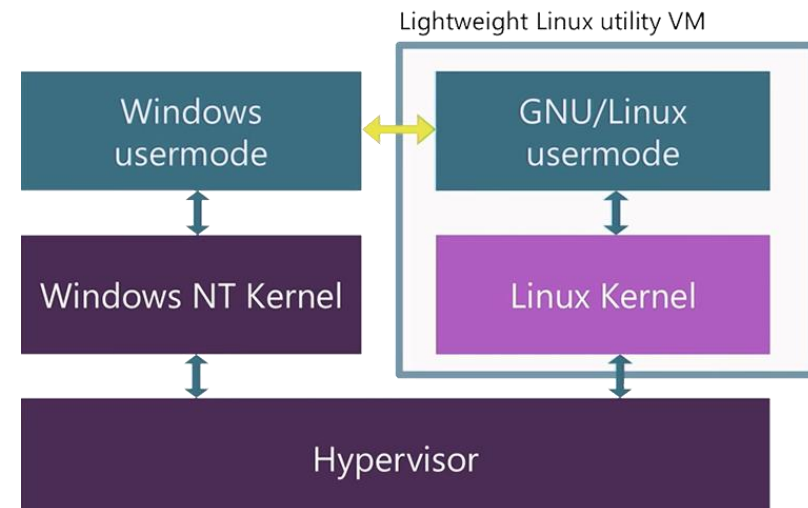
- If you are a **Windows** user
  - Option 1: Install **MobaXterm**
    - Download the free software <https://mobaxterm.mobatek.net/download.html>
    - Install and start local **terminal**





# Step 2: Get your computer ready!

- If you are a **Windows** user
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    - Install and start local **terminal**
  - Option 2: Install **Windows Subsystem Linux (WSL)**
    - Follow this [official instructions](#)
    - Open the **terminal**



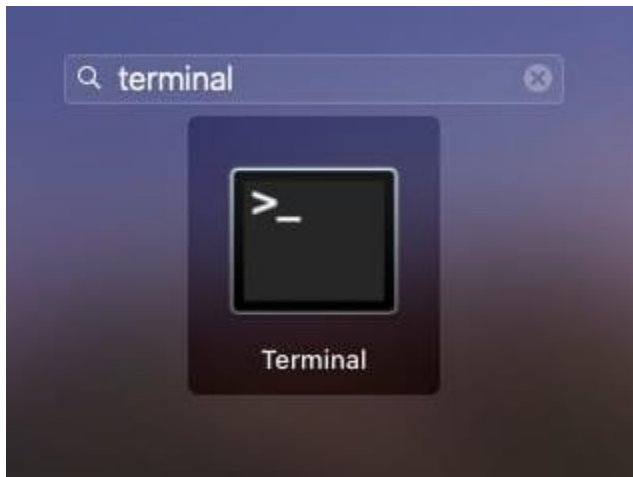
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    - Install and start local **terminal**
  - Option 2: Install **Windows Subsystem Linux (WSL)**
    - Follow this [official instructions](#)
    - Open the **terminal**
  - Option N: Other command line tools like [Cygwin](#), [GitBash](#), [Xshell](#), etc.



# Step 2: Get your computer ready!

- If you are a macOS or Linux user
  - Just open the Terminal



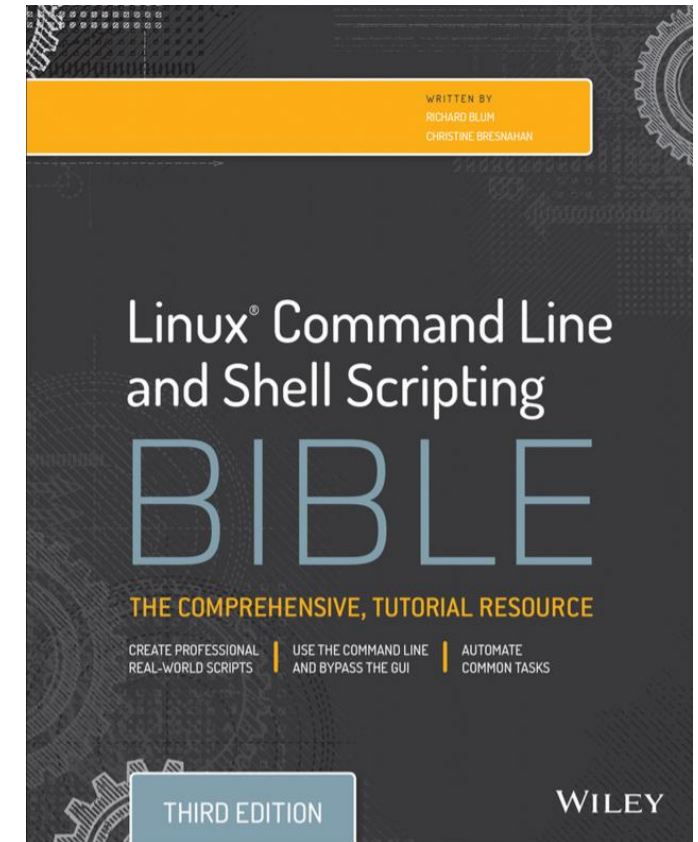
macOS



ubuntu

# Questions and references

- Write down questions at this [Google doc](#)
- Reference book is freely available [online](#)



# Day 1: Introduction to **Unix command line**

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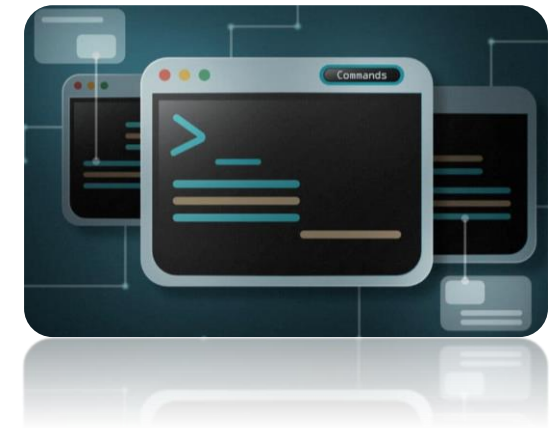
# Overview

## Time

- 3-hour workshop (45min + 45min + 30min + practice/Q&A)

## Topics

- ☐ Unix/Linux and Command line interface
  - What's that?
  - Why do we learn?
- ☐ Log into Hoffman2 cluster
- ☐ File system and file path
- ☐ Basic Command lines
  - Navigating through file system
  - Manipulating files and directories



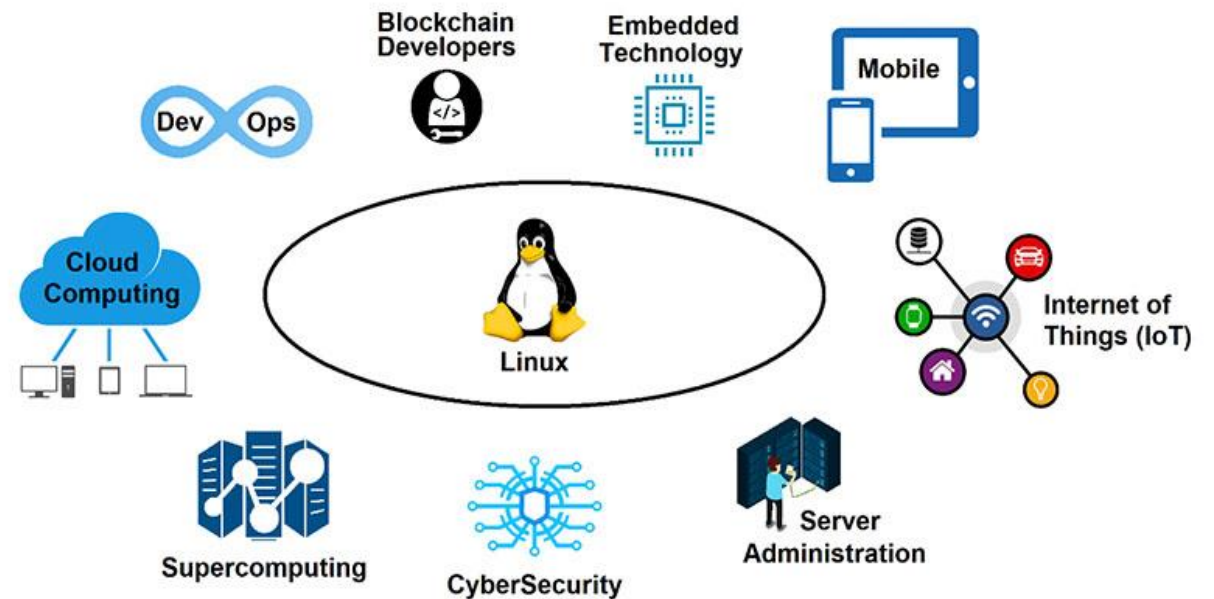
# What is Unix/Linux?

- **Unix** is a family of **multitasking**, **multiuser** computer operating systems, developed in the 1970s at the Bell Labs
- **Linux** is a **open-source**, **Unix-like** system

## Advantages:

- Secure
- Stable
- Efficient
- Flexible
- Programmer-friendly

...

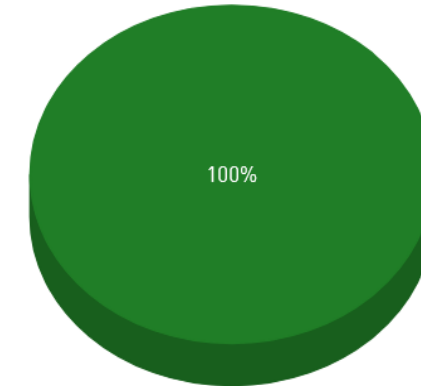


Unix/Linux is widely used in academia and industry!

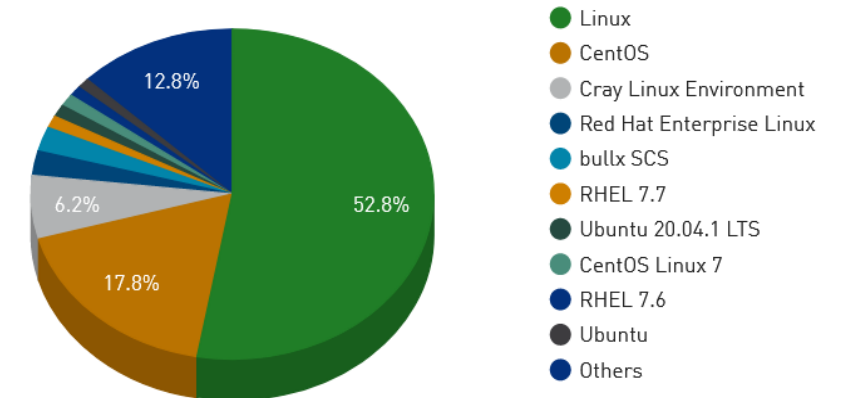
# Why Unix/Linux?

- Unix/Linux rules servers and supercomputers
  - Hoffman2 runs on CentOS

Operating system Family System Share



Operating System System Share



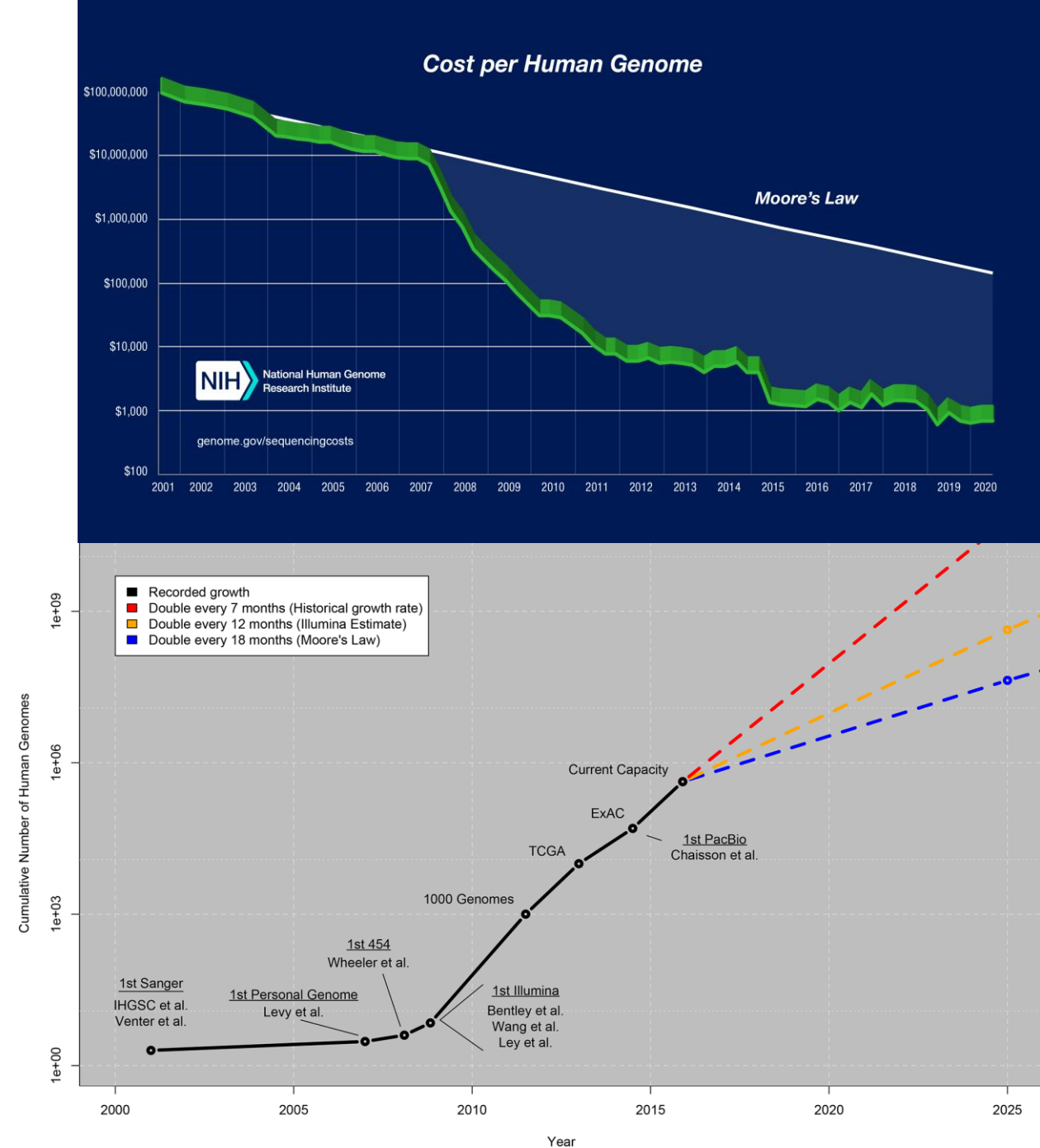


# Why Unix/Linux?

- Unix/Linux rules servers and supercomputers
- Data accumulate rapidly in Bioscience
  - Bioinformatics tools are usually developed in Unix/Linux environment
  - We process data in Unix/Linux environment

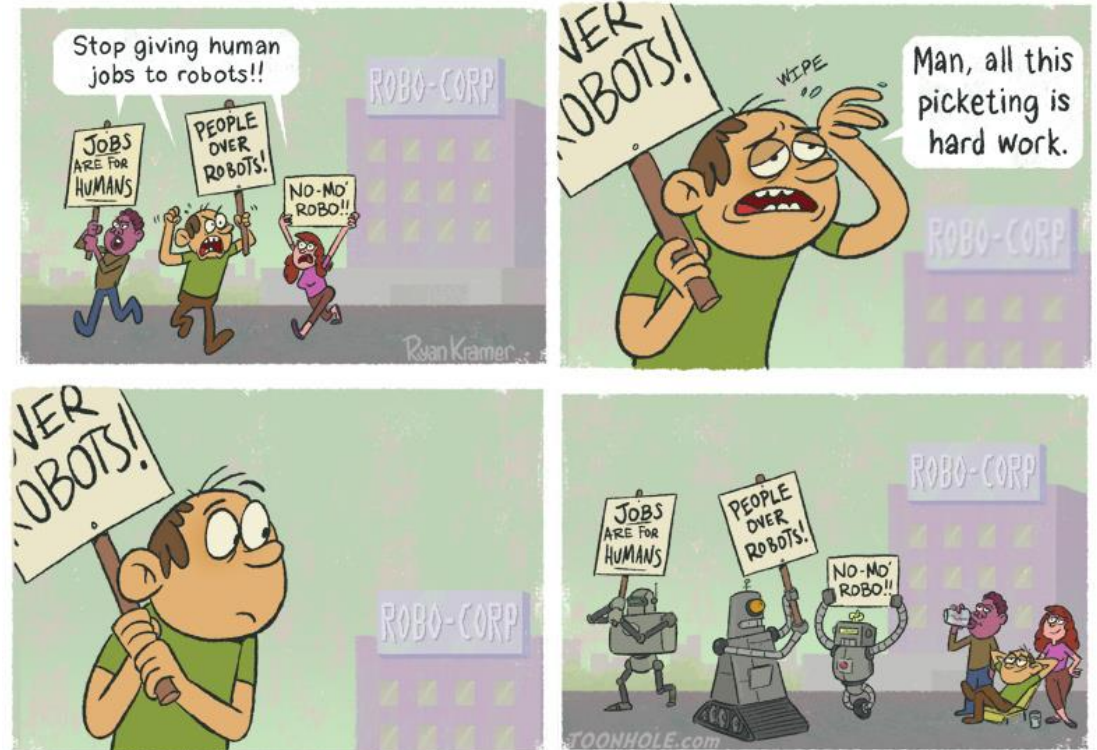
Moore's law: the number of transistors in microchip **doubles every 18 months**

NIH; Stephens ZD et al. (2015) *Plos Biology*



# Why Unix/Linux?

- Unix/Linux rules servers and supercomputers
- Data accumulate rapidly in Bioscience
- Unix/Linux is good at repetitive and tedious work
  - It can free your hand and mind
  - It's good for **reproducible** science

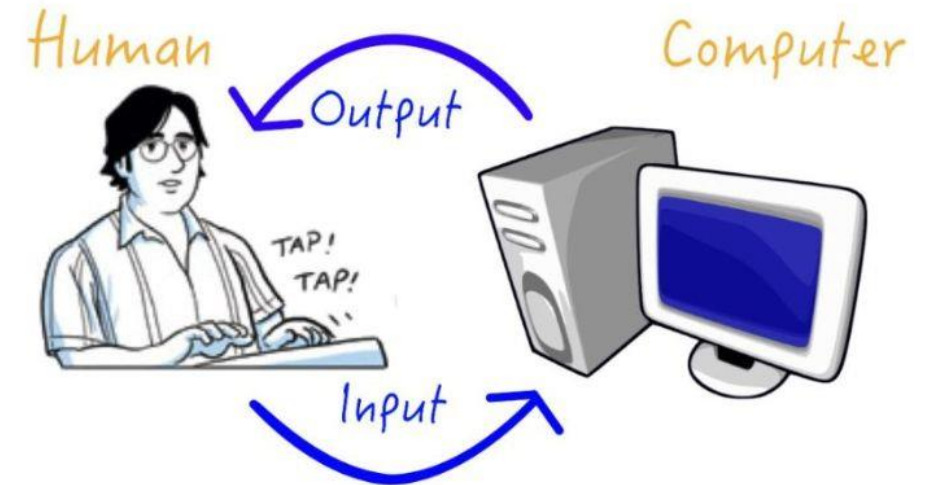


# How to give orders to the machine?

**Ideal** human-computer interaction



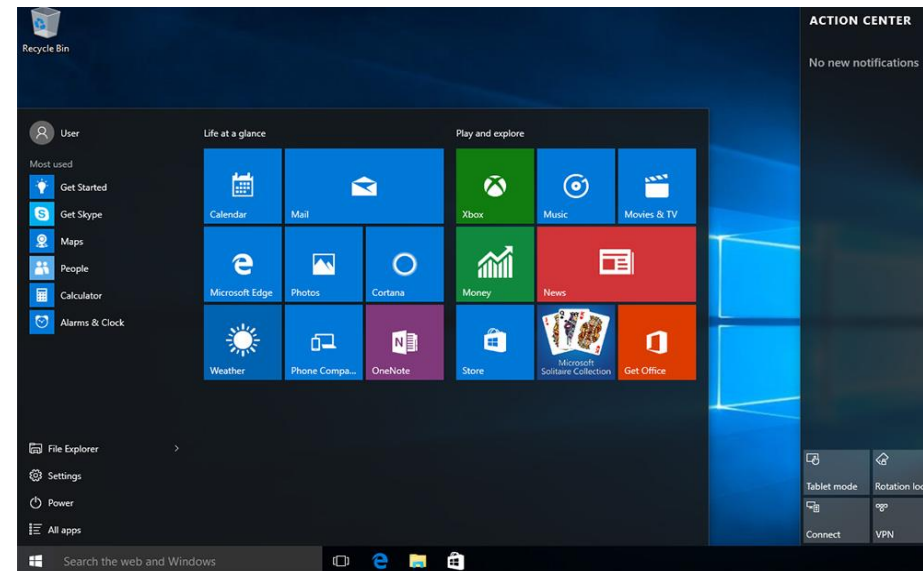
**Actual** human-computer interaction



Use Command Line!

# Command Line Interface vs Graphical User Interface

```
vincent@JARVIS: ~  
vincent@JARVIS:~$ ls  
apps code project  
vincent@JARVIS:~$ |
```



# Command Line Interface vs Graphical User Interface

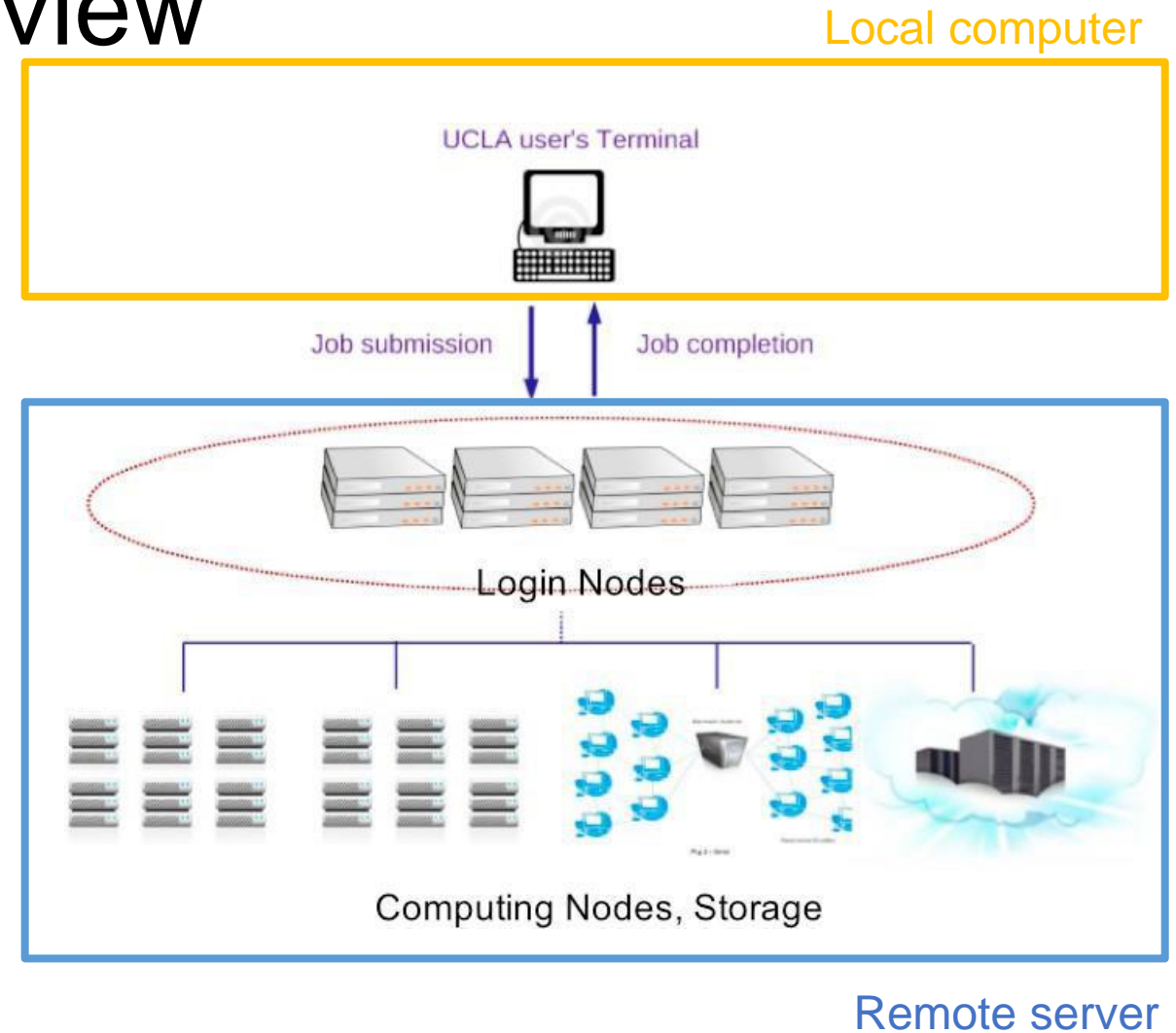
	<b>CLI: Command Line Interface</b>	<b>GUI: Graphical User Interface</b>
<b>Ease</b>	Higher degree of memorization and familiarity required	More visually intuitive
<b>Control</b>	More control over files	Advance tasks still may need to require command-line
<b>Resources</b>	Requires less system resources	Requires more system resources
<b>Speed / Strain</b>	Keyboard is utilized	Keyboard + mouse utilized
<b>Scripting</b>	Can create scripts for a sequence of commands	Much less flexible for writing programs
<b>Diversity</b>	Original commands remain the same	Interface can change with new versions



# Hoffman2 cluster overview

- Over 1,300 nodes (64-bit)
- Over 20,000 cores
- Over 50 TB aggregated memory
- 2.5 PB storage and 2PB backup

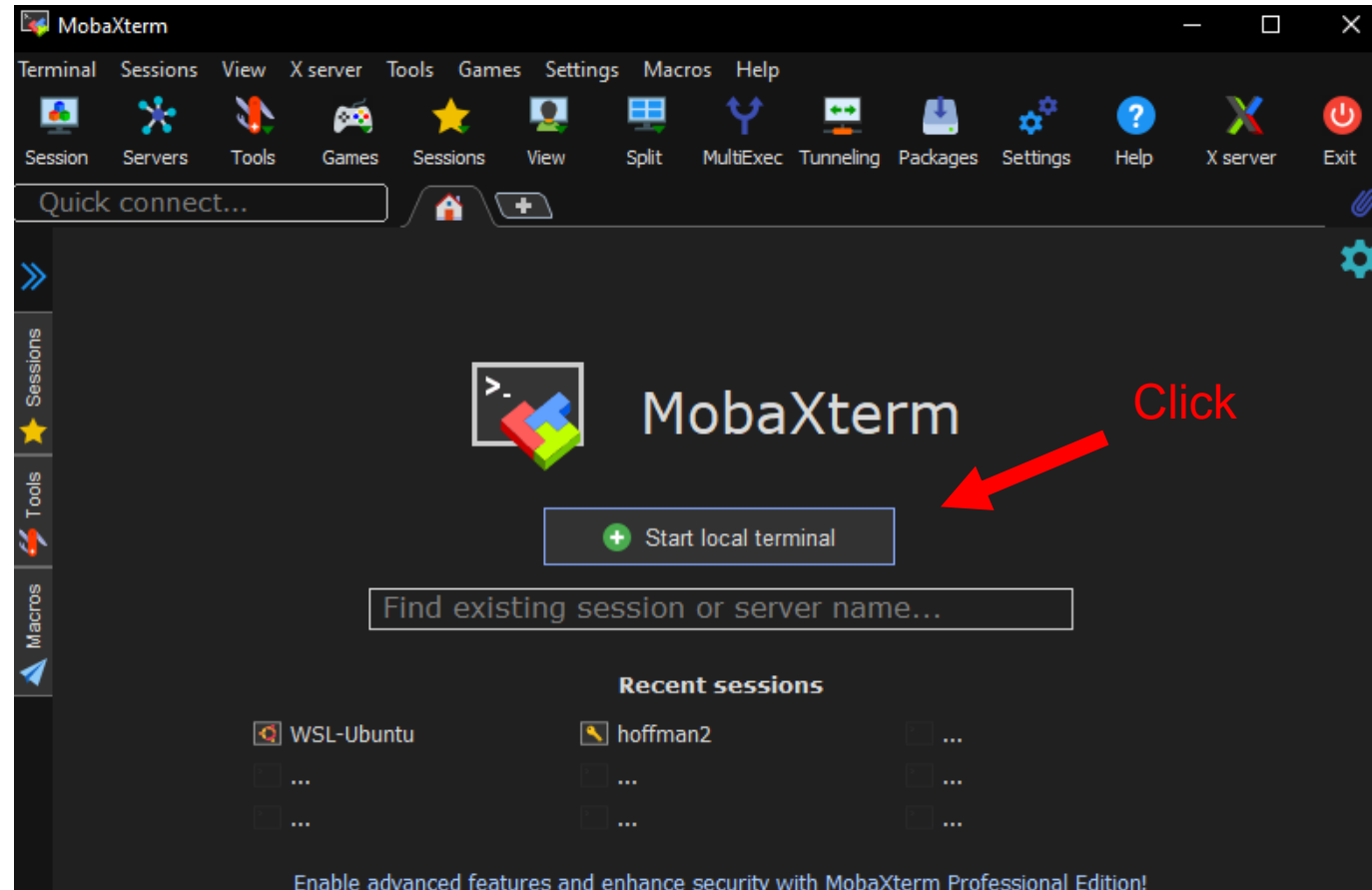
*Hoffman2 is currently **the largest and most powerful shared cluster** in the University of California system.*



Let's login to hoffman2 from **command line interface** (CLI)!

# Access hoffman2 (Windows user)

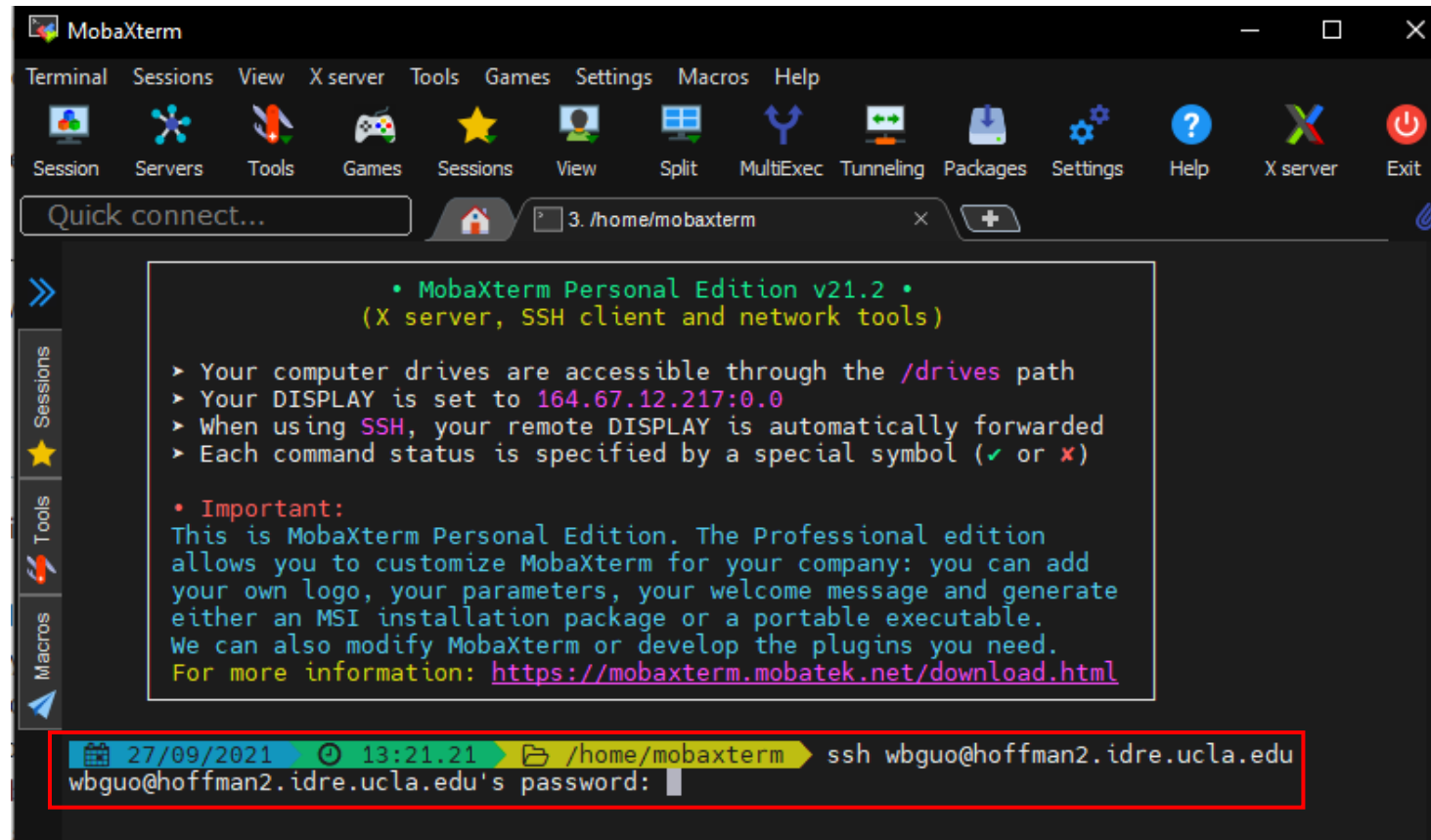
Start local **terminal**:



# Access hoffman2 (Windows user)

Type in the following commands to your computer **terminal**:

- `ssh username@hoffman2.idre.ucla.edu`  
(replace `username` with your `hoffman2` username, e.g. `wbguo`)



Note:

- Command line is **case-sensitive**
- For security reason, when you type in password, **nothing shows up** on the screen



# Access hoffman2 (Windows user)

Type in the following commands to your computer **terminal**:

- `ssh username@hoffman2.idre.ucla.edu`  
(replace `username` with your hoffman2 username, e.g. `wbguo`)

```
27/09/2021 13:30.53 /home/mobaxterm ssh wbguo@hoffman2.idre.ucla.edu
wbguo@hoffman2.idre.ucla.edu's password:
Last login: Mon Sep 27 13:22:15 2021 from 164.67.12.217
Welcome to the Hoffman2 Cluster!

Hoffman2 Home Page: http://www.hoffman2.idre.ucla.edu
Consulting: https://support.idre.ucla.edu/helpdesk

All login nodes should be accessed via "hoffman2.idre.ucla.edu".

Please do NOT compute on the login nodes.

Processes running on the login nodes which seriously degrade others'
use of the system may be terminated without warning. Use qcrsh to obtain
an interactive shell on a compute node for CPU or I/O intensive tasks.

The following news items are currently posted:

Hoffman2 Cluster OS upgrade status UPDATE
Jupyter notebooks download a fresh copy of h2jupyter
Hoffman2 Cluster OS upgrade status UPDATE.bak
Q Chem version 5.4.1 now available
How to change the time request on pending jobs
Nodes available on the next version of the OS
GPU nodes available
IDRE Workshops and Training Sessions

Enter shownews to read the full text of a news item.
Attention (2021-09-27): If you have ~/.julia_rh7, you may want to move it to ~/.julia
(For more details, see https://docs.julialang.org/en/v1/manual/environment-variables/#JULIA
DEPOT_PATH)
Loading R/4.1.0-BIO
Loading requirement: curl/7.70.0 R/4.1.0 R/4.1.0-DS
[wbguo@login1 ~]$
```

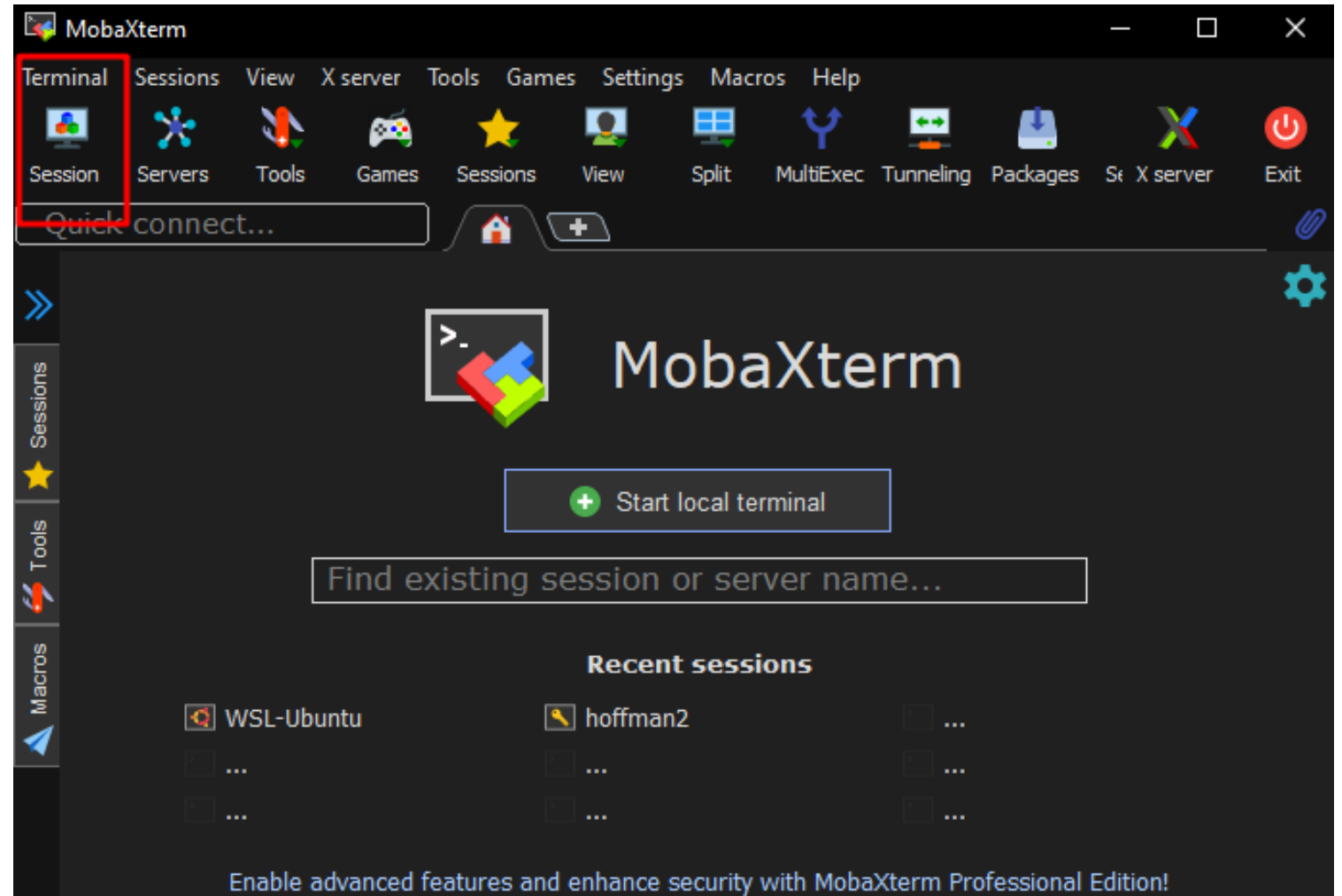
Notice

News

# Access hoffman2 (Windows user)

## Another option

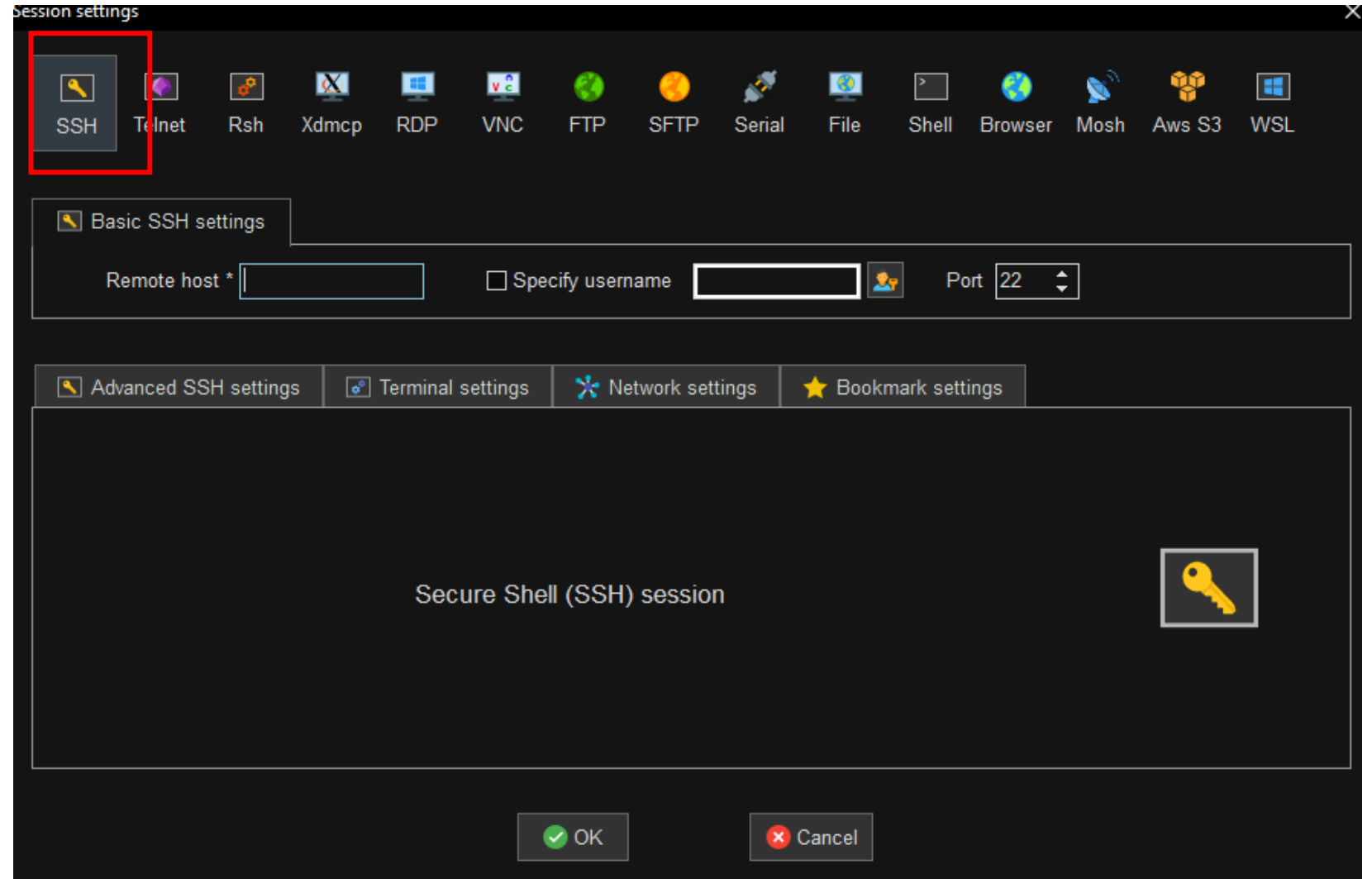
- Click Session



# Access hoffman2 (Windows user)

## Another option

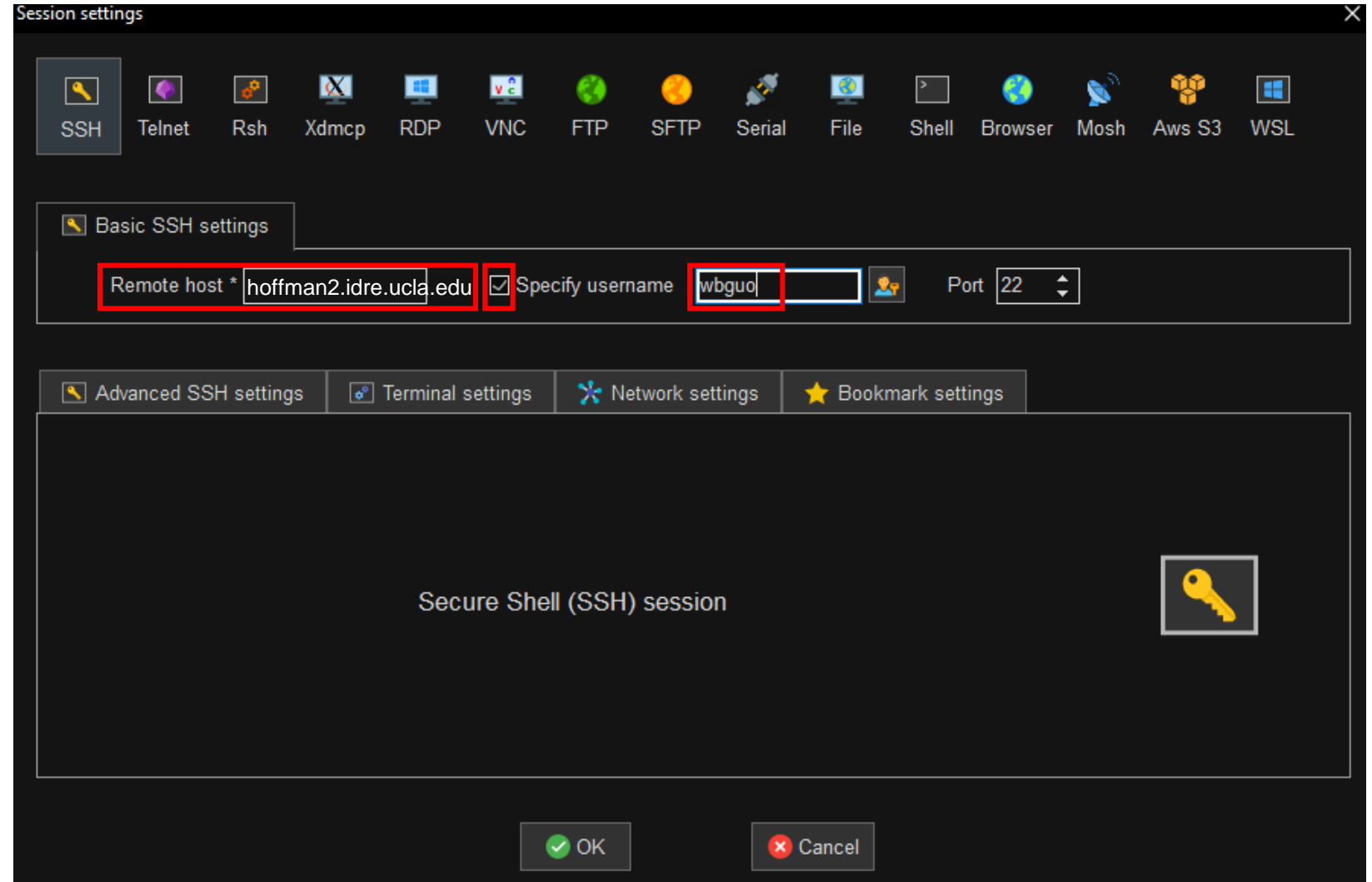
- Click Session
- Click SSH



# Access hoffman2 (Windows user)

## Another option

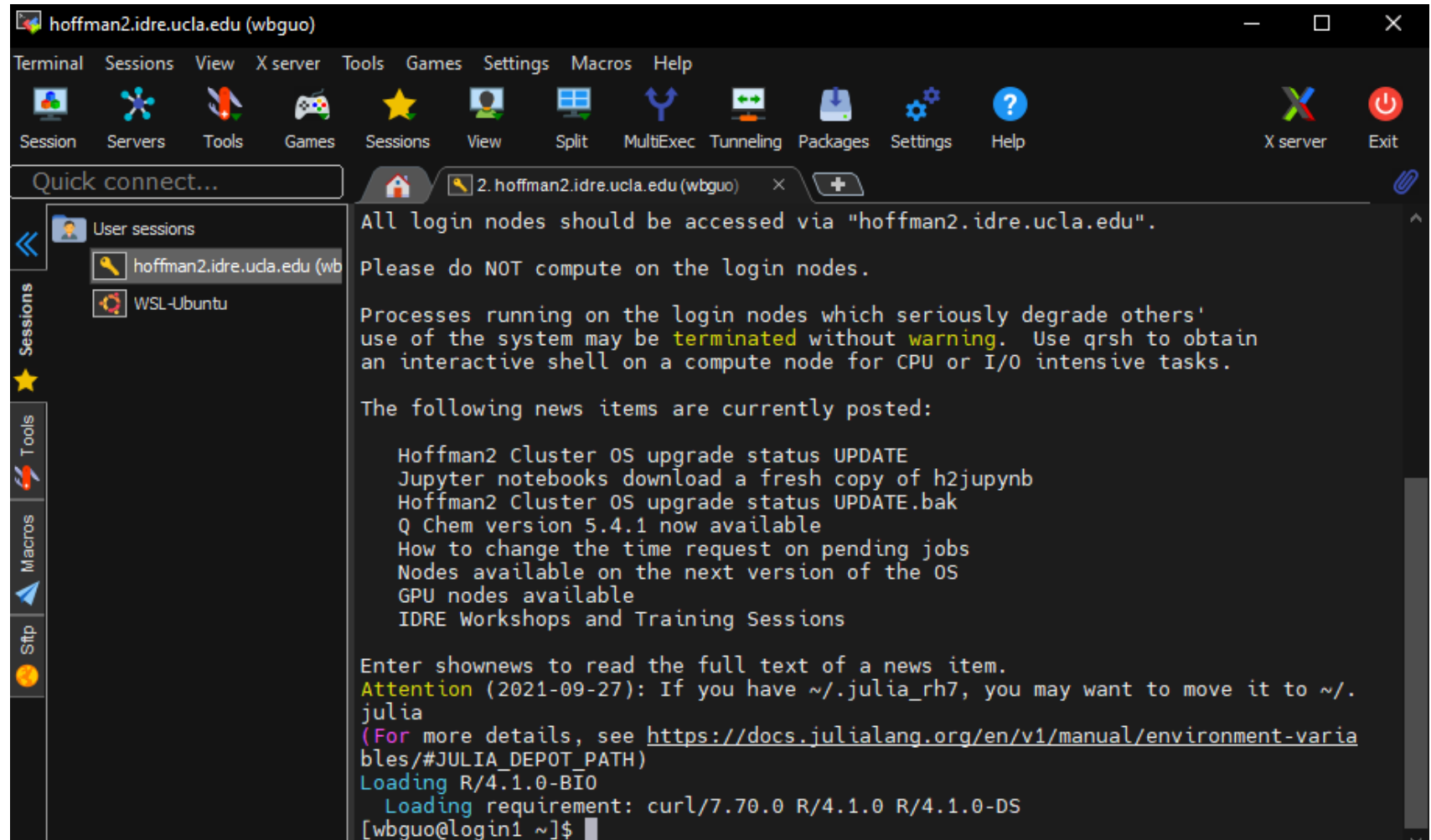
- Click Session
- Click SSH
- Fill in the blank
- Click OK



# Access hoffman2 (Windows user)

## Another option

- Click Session
- Click SSH
- Fill in the blank
- Click OK



The screenshot shows a terminal window titled "hoffman2.idre.ucla.edu (wbguo)". The window has a menu bar with options: Terminal, Sessions, View, X server, Tools, Games, Settings, Macros, Help. Below the menu bar is a toolbar with icons for Session, Servers, Tools, Games, Sessions, View, Split, MultiExec, Tunneling, Packages, Settings, Help, X server, and Exit. The main content area displays the following text:

```
Quick connect... 2. hoffman2.idre.ucla.edu (wbguo) x +
```

User sessions

- hoffman2.idre.ucla.edu (wbguo)
- WSL-Ubuntu

All login nodes should be accessed via "hoffman2.idre.ucla.edu".

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**Attention** (2021-09-27): If you have ~/.julia\_rh7, you may want to move it to ~/.julia

(For more details, see [https://docs.julialang.org/en/v1/manual/environment-variables/#JULIA\\_DEPOT\\_PATH](https://docs.julialang.org/en/v1/manual/environment-variables/#JULIA_DEPOT_PATH))

Loading R/4.1.0-BIO

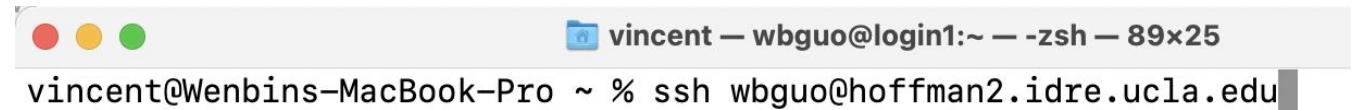
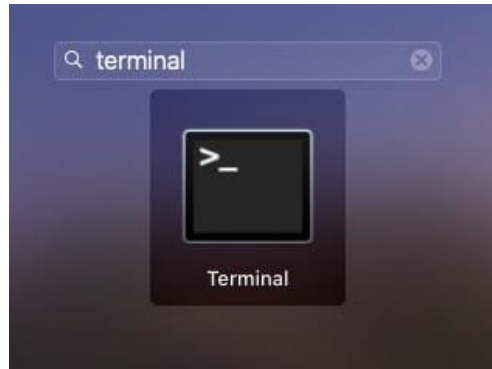
Loading requirement: curl/7.70.0 R/4.1.0 R/4.1.0-DS

[wbguo@login1 ~]\$

# Access hoffman2 (macOS or Linux user)

Type in the following commands to your computer **terminal**:

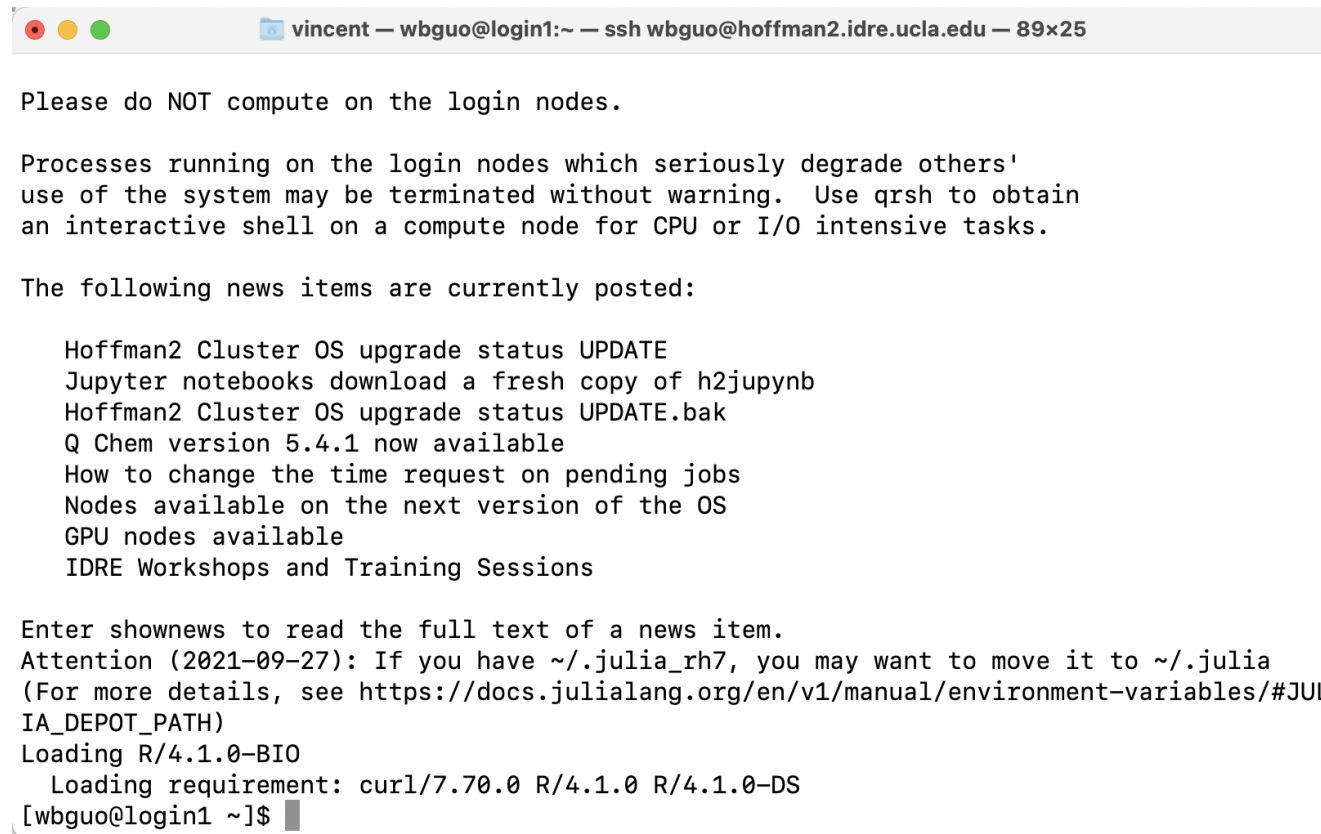
- `ssh username@hoffman2.idre.ucla.edu`  
(replace `username` with your *hoffman2* username, e.g. *wbguo*)



# Access hoffman2 (macOS or Linux user)

Type in the following commands to your computer **terminal**:

- `ssh username@hoffman2.idre.ucla.edu`  
(replace `username` with your *hoffman2* username, e.g. *wbguo*)

A terminal window titled 'vincent — wbguo@login1:~ — ssh wbguo@hoffman2.idre.ucla.edu — 89x25'. The window displays a series of messages from the remote host, including a warning not to compute on login nodes, a list of news items, and instructions on how to read news items. The prompt '[wbguo@login1 ~]\$' is visible at the bottom.

```
vincent — wbguo@login1:~ — ssh wbguo@hoffman2.idre.ucla.edu — 89x25

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IA_DEPOT_PATH)
Loading R/4.1.0-BIO
Loading requirement: curl/7.70.0 R/4.1.0 R/4.1.0-DS
[wbguo@login1 ~]$
```

# Unix Shell

[wbguo@login1 ~]\$  → Command to type-in

↙ ↘ ↘

User name      Server name      Folder name

- A **Shell** provides you with an interface to Unix/Linux system
- It waits for your command and will execute it after you press **enter** key
- After finishing, it will return output/error message to the terminal
- If no error message is displayed, it usually means the command was finished successfully (No message is good message)



# Practice: login to Hoffman2 and say Hello!



- After login, try

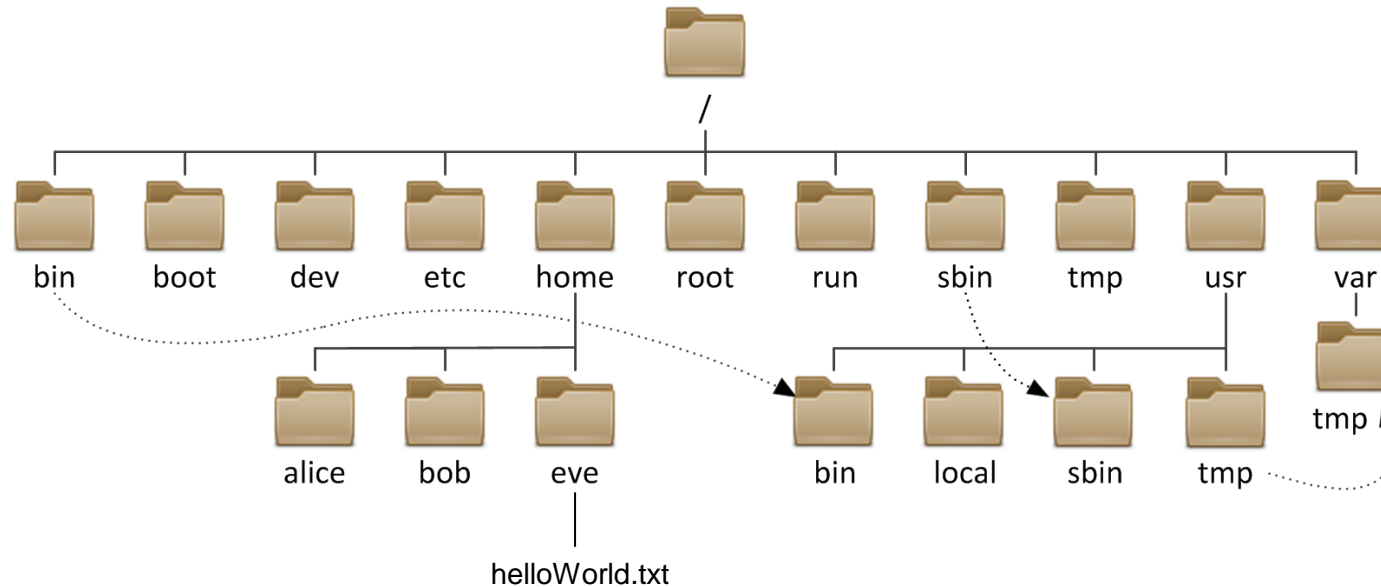
- `echo 'Hello world!'`

```
vincent — wbguo@login2:~  
[wbguo@login2 ~]$ echo 'Hello world!'  
Hello world!  
[wbguo@login2 ~]$
```

- `git clone https://github.com/wbvguo/qcbio-intro2Unix.git`

# File system

- Appears as hierarchical **tree** structure
- Consists of files, directories, and symbolic links



**Parent folder:** the folder that is **one level up** from the current directory

# Path to a file/directory

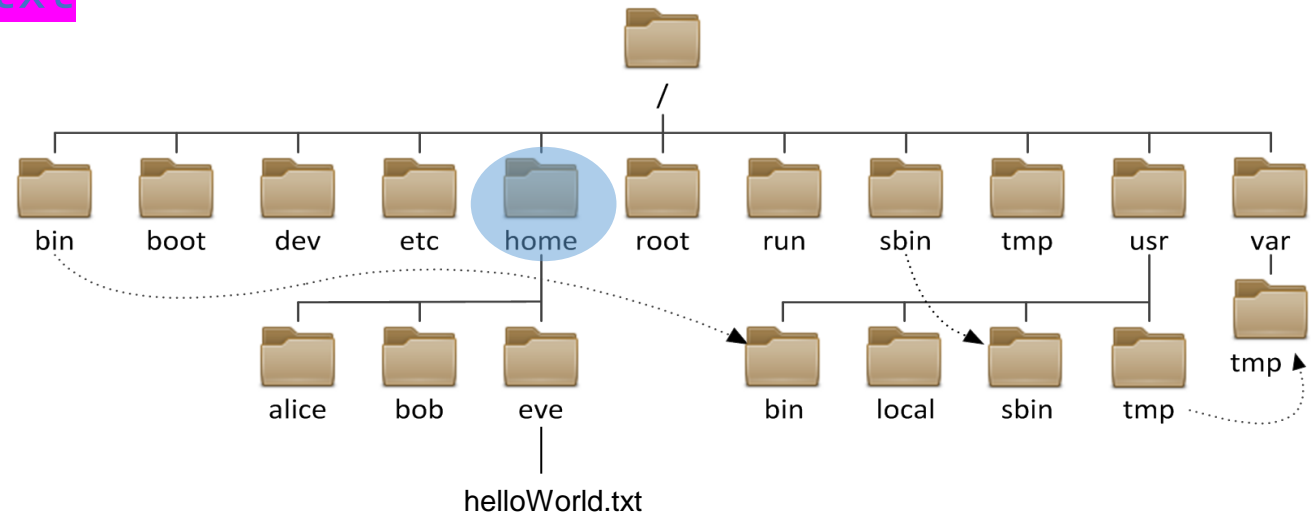
You can refer to a file/directory using **absolute path** or **relative path**

- **Absolute path**: the full path from the root to the file/directory

e.g. absolute path: `/home/eve/helloWorld.txt`

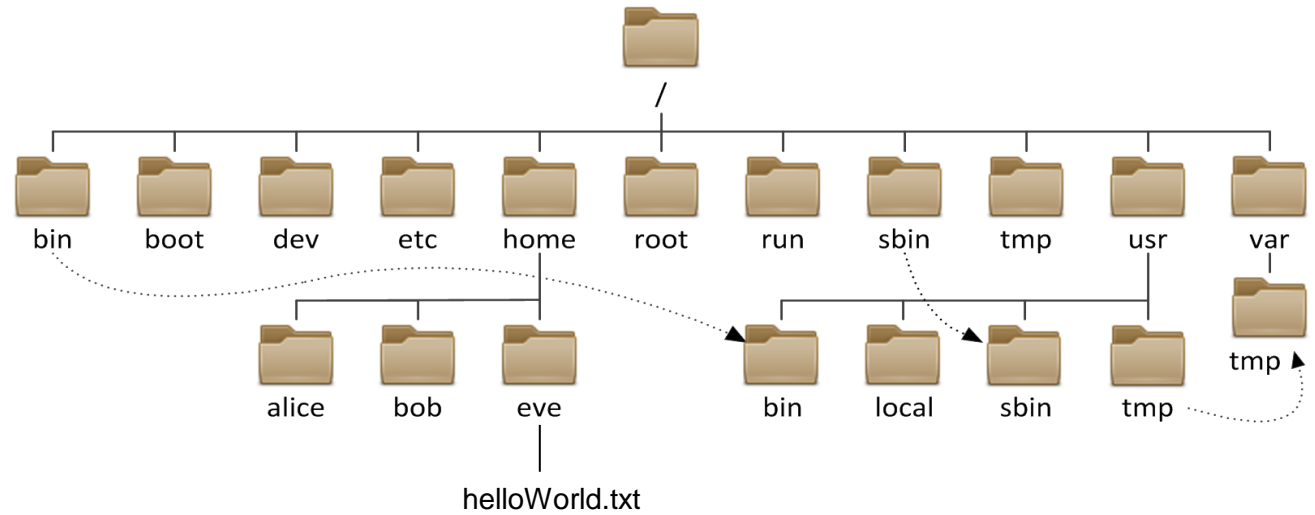
- **Relative path**: relative to your current location

e.g. relative path: `eve/helloWorld.txt`  
(assume you are in folder `/home`)



# Navigate through the file system

- pwd
- cd
- ls



# Command pwd

- **pwd**: **p**rint **w**orking **d**irectory (show the absolute path of current directory)
- Syntax: pwd

```
[wbguo@login1 ~]$ pwd  
/u/home/w/wbguo
```

**Note:** When you open a shell, you start in your home directory ~

# Command cd

- **cd**: **c**hange **d**irectory (go to another directory)
- Syntax: `cd <directory path>`

```
[wbguo@login1 ~]$ cd qcbio-intro2Unix/  
[wbguo@login1 qcbio-intro2Unix]$ pwd  
/u/home/w/wbguo/qcbio-intro2Unix
```

If you don't have a folder called qcbio-intro2Unix, run

➤ `git clone https://github.com/wbvguo/qcbio-intro2Unix.git`

# Command cd

- `~` is the home directory

```
[wbguo@login1 ~]$ pwd  
/u/home/w/wbguo
```

- `.` is the current directory

```
[wbguo@login1 ~]$ cd qcbio-intro2Unix/  
[wbguo@login1 qcbio-intro2Unix]$ cd .  
[wbguo@login1 qcbio-intro2Unix]$
```

- `..` is the **parent folder** of the current directory

```
[wbguo@login1 qcbio-intro2Unix]$ pwd  
/u/home/w/wbguo/qcbio-intro2Unix  
[wbguo@login1 qcbio-intro2Unix]$ cd ..  
[wbguo@login1 ~]$ pwd  
/u/home/w/wbguo
```

# Practice

- Print absolute path of your home directory
- Go to the [qcbio-intro2Unix](#) folder





# Command `ls`

- **ls**: **list** (list the information of files/folders in a directory)
- Syntax: `ls -<flag> <file_name/directory>`

```
[wbguo@login1 ~]$ cd qcbio-intro2Unix/
```

```
[wbguo@login1 qcbio-intro2Unix]$ ls
```

```
README.md  day1  day2  day3
```

```
[wbguo@login1 qcbio-intro2Unix]$ ls ~
```

```
R      iproject  project-collab  project-msehl      qrsh4h8g  run_kde_sim.sh  test
apps  perl5      project-mcdb    qcbio-intro2Unix  qsubJN    sample_list     ttest
```

# Command ls

## flag options:

- **-l**: long list

```
[wbguo@login1 qcbio-intro2Unix]$ ls -l
```

```
total 12
```

```
-rw-r--r--. 1 wbguo matteop  19 Jan  3 22:19 README.md
drwxr-xr-x. 2 wbguo matteop 4096 Jan  3 22:19 day1
drwxr-xr-x. 2 wbguo matteop 4096 Jan  3 22:19 day2
drwxr-xr-x. 3 wbguo matteop 4096 Jan  3 22:19 day3
```

- 1<sup>st</sup> column: permission
- 2<sup>nd</sup> column: the number of hard links to the file
- 3<sup>rd</sup> column: owner
- 4<sup>th</sup> column: group
- 5<sup>th</sup> column: size
- 6<sup>th</sup> -8<sup>th</sup> column: modified time
- 9<sup>th</sup> column: name

# Command ls

## flag options:

- **-a**: all files/folders

```
[wbguo@login1 qcbio-intro2Unix]$ ls -la
```

```
total 28
```

```
drwxr-xr-x.  6 wbguo matteop 4096 Jan  3 22:19 .  
drwx----- 17 wbguo matteop 8192 Jan  3 22:31 ..  
drwxr-xr-x.  8 wbguo matteop 4096 Jan  3 22:19 .git  
-rw-r--r--.  1 wbguo matteop   19 Jan  3 22:19 README.md  
drwxr-xr-x.  2 wbguo matteop 4096 Jan  3 22:19 day1  
drwxr-xr-x.  2 wbguo matteop 4096 Jan  3 22:19 day2  
drwxr-xr-x.  3 wbguo matteop 4096 Jan  3 22:19 day3
```

# Command ls

## flag options:

- **-S**: sort by size (big to small)

```
[wbguo@login1 qcbio-intro2Unix]$ ls -lS
total 12
drwxr-xr-x. 2 wbguo matteop 4096 Jan  3 22:19 day1
drwxr-xr-x. 2 wbguo matteop 4096 Jan  3 22:19 day2
drwxr-xr-x. 3 wbguo matteop 4096 Jan  3 22:19 day3
-rw-r--r--. 1 wbguo matteop  19 Jan  3 22:19 README.md
```

- **-t**: sort by time (from new to old)

```
[wbguo@login1 qcbio-intro2Unix]$ ls -lt
total 12
drwxr-xr-x. 3 wbguo matteop 4096 Jan  3 22:19 day3
drwxr-xr-x. 2 wbguo matteop 4096 Jan  3 22:19 day2
drwxr-xr-x. 2 wbguo matteop 4096 Jan  3 22:19 day1
-rw-r--r--. 1 wbguo matteop  19 Jan  3 22:19 README.md
```

# Command ls

## flag options:

- **-h**: human readable

```
[wbguo@login1 qcbio-intro2Unix]$ ls -lSh
total 12K
drwxr-xr-x. 2 wbguo matteop 4.0K Jan  3 22:19 day1
drwxr-xr-x. 2 wbguo matteop 4.0K Jan  3 22:19 day2
drwxr-xr-x. 3 wbguo matteop 4.0K Jan  3 22:19 day3
-rw-r--r--. 1 wbguo matteop  19 Jan  3 22:19 README.md
```

- **-r**: reverse order

```
[wbguo@login1 qcbio-intro2Unix]$ ls -lShr
total 12K
-rw-r--r--. 1 wbguo matteop  19 Jan  3 22:19 README.md
drwxr-xr-x. 3 wbguo matteop 4.0K Jan  3 22:19 day3
drwxr-xr-x. 2 wbguo matteop 4.0K Jan  3 22:19 day2
drwxr-xr-x. 2 wbguo matteop 4.0K Jan  3 22:19 day1
```

# Tips

- Go back to previous command, use up and down arrows
- Use Tab key for auto completion
- Use history to see your command history
- Use clear to clean screen



# Practice



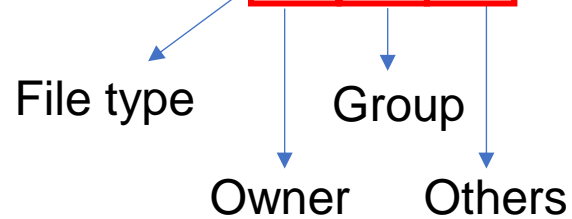
- Print absolute path of your home directory
- Go to the qcbio-intro2Unix folder
- List the files/folder in long form, sorted by size in human-readable mode
- Go back to home directory
- Clean terminal screen
- Try up and down arrow key and Tab auto-completion

# File permission

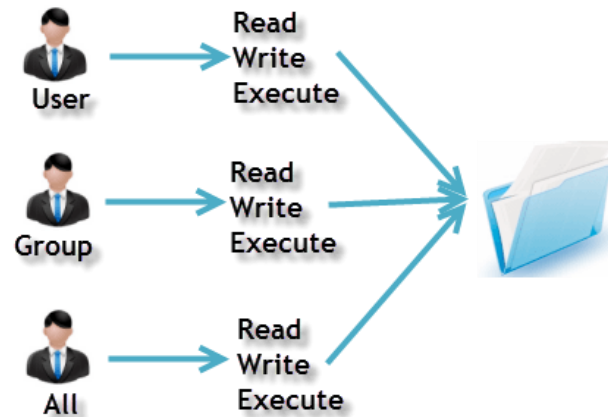
```
[wbguo@login1 qcbio-intro2Unix]$ ls -l
```

```
total 12
```

```
-rw-r--r--. 1 wbguo matteop 19 Jan 3 22:19 README.md  
drwxr-xr-x. 2 wbguo matteop 4096 Jan 3 22:19 day1
```



Owners assigned Permission On Every File and Directory



Unix/Linux classified users into 3 types, each can have different permission on the file, which creates a secure environment

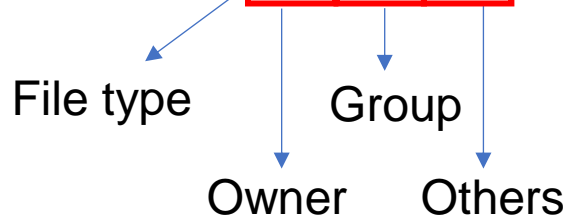


# File permission

```
[wbguo@login1 qcbio-intro2Unix]$ ls -l
```

```
total 12
```

```
-rw-r--r--. 1 wbguo matteop 19 Jan 3 22:19 README.md  
drwxr-xr-x. 2 wbguo matteop 4096 Jan 3 22:19 day1
```



- File type: **d** (directory), **l** (link), **-** (file)
- User type: **Owner** (you), **Group** (users in the same group), **Others** (the rest of people on the server system)
- Permission type: **r** (read, encode as **4**), **w** (write, encode as **2**), **x** (execute, encode as **1**)
- **rwxr--r--** is equal to 744, meaning Owner/Group/Others can read, but only Owner can write and execute

# Change file permission

- **chmod**: **ch**ange **mo**de (modify file permission)
- Syntax
  - chmod [**u**ser/**g**roup/**o**thers/**a**ll] [**+****-**] [permission] <file/directory name>

Add permission

Remove permission

Assign executive permission to owner

- chmod 744 README.md
- chmod u+x README.md

```
[wbguo@login1 qcbio-intro2Unix]$ ls -lh
total 12K
-rw-r--r--. 1 wbguo matteop  19 Jan  3 22:19 README.md
drwxr-xr-x. 2 wbguo matteop 4.0K Jan  3 22:19 day1
drwxr-xr-x. 2 wbguo matteop 4.0K Jan  3 22:19 day2
drwxr-xr-x. 3 wbguo matteop 4.0K Jan  3 22:19 day3
[wbguo@login1 qcbio-intro2Unix]$ chmod u+x README.md
[wbguo@login1 qcbio-intro2Unix]$ ls -lh
total 12K
-rwxr--r--. 1 wbguo matteop  19 Jan  3 22:19 README.md
drwxr-xr-x. 2 wbguo matteop 4.0K Jan  3 22:19 day1
drwxr-xr-x. 2 wbguo matteop 4.0K Jan  3 22:19 day2
drwxr-xr-x. 3 wbguo matteop 4.0K Jan  3 22:19 day3
[wbguo@login1 qcbio-intro2Unix]$
```

# Practice

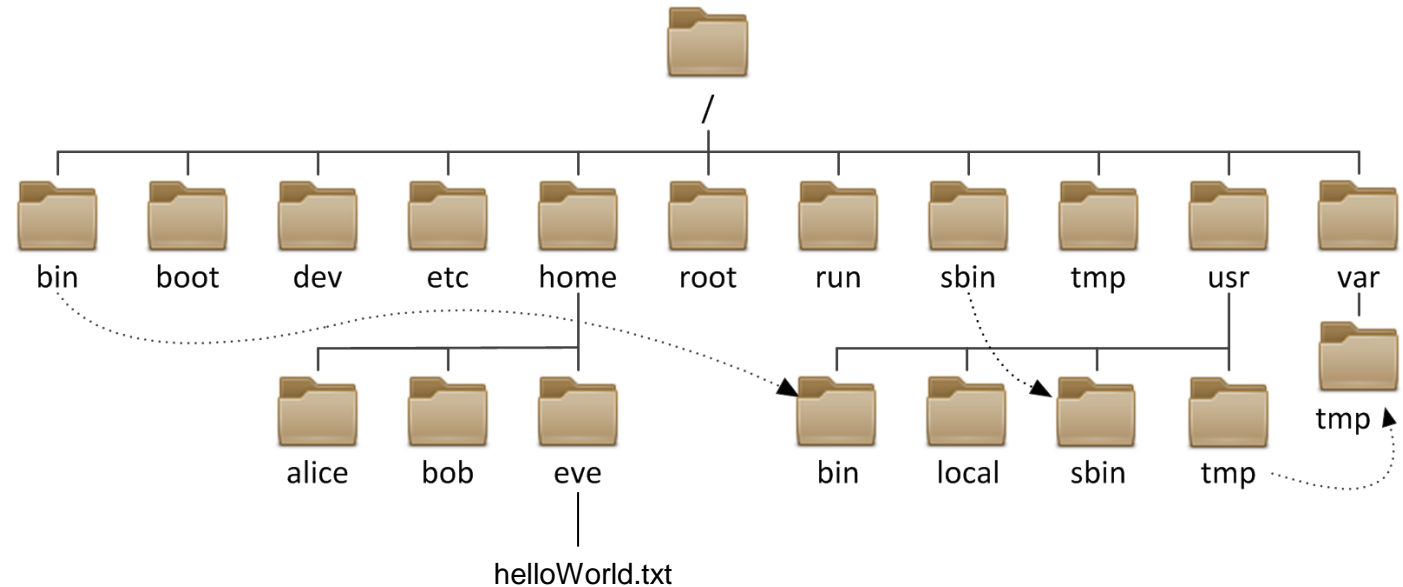


- Give README.md execution permission
- Convert day1 to a private folder (group/others users cannot read/write/execute)

# Manipulating files and directories

## Operations

- Create/Delete
- Copy/Move
- View/Modify
- Compress/Decompress
- Download/Upload



General syntax:

command -<flags> <file/directory>

e.g. `ls -lah helloWorld.txt`

# Create (mkdir, touch)

- Directory
  - **mkdir**: make directory
  - Syntax: mkdir <directory path>
- File
  - **touch**
  - Syntax: touch <file\_name>

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3
[wbguo@login1 qcbio-intro2Unix]$ mkdir myFolder
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  myFolder
[wbguo@login1 qcbio-intro2Unix]$ touch myFile.txt
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  myFile.txt  myFolder
```

# Create (mkdir, touch)

- Directory
  - **mkdir**: make directory
  - Syntax: `mkdir <directory path>`
- File
  - **touch**
  - Syntax: `touch <file_name>`
- When file/directory already exists

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 myFile.txt myFolder
[wbguo@login1 qcbio-intro2Unix]$ mkdir myFolder
mkdir: cannot create directory 'myFolder': File exists
[wbguo@login1 qcbio-intro2Unix]$ touch myFile.txt
```

touch will change the file's modified time when the file exists

# Delete (rm)

- **rm**: remove
- Syntax: `rm -<flag> <directory path>`
- Flag options:
  - **-r**: recursively  
Remove directory and their contents
  - **-i**: interactively  
Ask to confirm before every removal
  - **-v**: verbose  
Explain what is being done
  - **-f**: force  
Remove without asking

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  myFile.txt  myFolder
[wbguo@login1 qcbio-intro2Unix]$ rm -r myFolder/
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  myFile.txt
[wbguo@login1 qcbio-intro2Unix]$ rm myFile.txt
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3
```

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  myFile.txt  myFolder
[wbguo@login1 qcbio-intro2Unix]$ rm -ir myFolder/
rm: remove directory 'myFolder/'? y
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  myFile.txt
[wbguo@login1 qcbio-intro2Unix]$ rm -i myFile.txt
rm: remove regular empty file 'myFile.txt'? n
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  myFile.txt
```



# Delete (rm)

- Be cautious with delete!
  - Usually **cannot be undone** if there is no back-up (no trash folder!)
  - If you accidentally delete files on hoffman2, check out this [hoffman2 recover option](#) or contact [IDRE hoffman2 support](#)
- Back up your important files
  - Google Drive has unlimited capacity for edu users
- Change file to read-only file with chmod
  - `chmod 444 <file name>`



# Practice

- Create a folder named `myFolder`, a file named `myFile.txt`
- remove both the folder and file in interactive mode



# Copy (cp)

- **cp**: copy
- Syntax: `cp -<flag> <source> <destination>`
- Flag options:
  - **-r**: recursively  
Copy directories and their contents
  - **-i**: interactively  
Ask to confirm before overwrite
  - **-v**: verbose  
Explain what is being done

# Copy (cp)

- **cp**: copy
- Syntax: `cp -<flag> <source> <destination>`

- Copy a file

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3
[wbguo@login1 qcbio-intro2Unix]$ cp README.md readme_copy.md
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 readme_copy.md
```

- Copy a directory

```
[wbguo@login1 qcbio-intro2Unix]$ cp -r day1/ day1_backup
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day1_backup day2 day3 readme_copy.md
```

- Copy a file into directory

```
[wbguo@login1 qcbio-intro2Unix]$ ls day1_backup/
test
[wbguo@login1 qcbio-intro2Unix]$ cp README.md day1_backup/
[wbguo@login1 qcbio-intro2Unix]$ ls day1_backup/
README.md test
```

# Move (mv)

- **mv**: move
- Syntax: `mv <source> <destination>`

- Rename a file/folder

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day1_backup day2 day3 readme_copy.md
[wbguo@login1 qcbio-intro2Unix]$ mv readme_copy.md tmp.md
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day1_backup day2 day3 tmp.md
[wbguo@login1 qcbio-intro2Unix]$ mv day1_backup/ tmp
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 tmp tmp.md
```

- Move a file to folder

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 tmp tmp.md
[wbguo@login1 qcbio-intro2Unix]$ ls tmp
README.md test
[wbguo@login1 qcbio-intro2Unix]$ mv tmp.md tmp
[wbguo@login1 qcbio-intro2Unix]$ ls tmp/
README.md test tmp.md
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 tmp
```

# Practice




- Copy *day1* to *day1\_backup*
- Copy *README.md* to *readme\_copy.md*, and move it to *day1\_backup*
- Rename *readme\_copy.md* as *tmp.md*

# View (cat)

- **cat**: concatenate files and print on standard output
- Syntax: `cat <file name>`

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 tmp
[wbguo@login1 qcbio-intro2Unix]$ ls day1/
test
[wbguo@login1 qcbio-intro2Unix]$ cat day1/test
hello world
```

## Modify (vi)

- **vi**: Visual Editor (default text editor for Unix-like system)
  - **vim**: **vi** **im**proved (an improved text editor tool)
  - Syntax: `vi <file name>`
- 

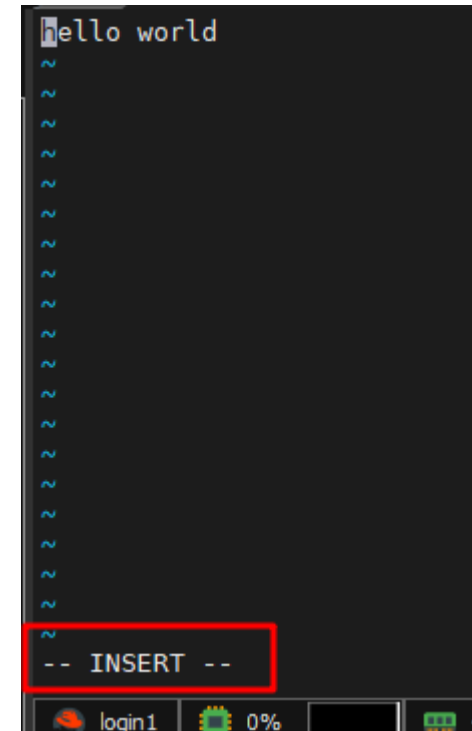
```
[wbguo@login1 qcbio-intro2Unix]$ cd day1/
[wbguo@login1 day1]$ ls
test
[wbguo@login1 day1]$ vi test
```

[illegible]

# Modify (vi)

Once inside the file

- Press "**i**" to type in new text (**i**nsertion mode)
- Press "**Esc**" to jump out the insertion mode





# Modify (vi)

Once inside the file

- Press "**i**" to type in new text (**i**nsertion mode)
- Press "**Esc**" to jump out the insertion mode
- Enter
  - **:w** (**w**rite)
  - **:q** (**q**uit)
  - **:wq** (**w**rite and **q**uit)
  - **:q!** (force **q**uit – the modification will not be saved)

A screenshot of a terminal window with a dark background. The first two lines of the file are "hello world" and "Command line is cool!". Below these are several lines of blue tilde (~) characters representing spaces. At the bottom of the window, the command ":wq" is entered, followed by a cursor. The terminal window has a thin border and a title bar at the top.

# Modify (vi)

Once inside the file

- Press "**i**" to type in new text (**i**nsertion mode)
- Press "**Esc**" to jump out the insertion mode

- Enter
  - **:w** (**w**rite)
  - **:q** (**q**uit)
  - **:wq** (**w**rite and **q**uit)
  - **:q!** (force **q**uit – the modification will not be saved)

```
[wbguo@login1 day1]$ vi test
[wbguo@login1 day1]$ cat test
hello world
Command line is cool!
```

- Note: if the file exists, then vi editing can **modify** the file, if the file does not exist, vi editing can **create** the file

# Practice



- Append a line “UCLA QCB wrokshop” to the end of *test* file in *day1* directory
- Use `cat` to display the modified file
- Create a new file using `vi`, with contents “Less is more”

# Compress and decompress (gzip)

## File

- **gzip**: **GNU zip**
- Syntax:
  - Compress: `gzip <file name>`
  - Decompress: `gzip -d <file name>.gz`
- Option:
  - **-d**: decompress

```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 tmp
[wbguo@login1 qcbio-intro2Unix]$ chmod u-x README.md
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 tmp
[wbguo@login1 qcbio-intro2Unix]$ gzip README.md
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md.gz day1 day2 day3 tmp
[wbguo@login1 qcbio-intro2Unix]$ gzip -d README.md.gz
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md day1 day2 day3 tmp
```

# Compress and decompress (tar)

## Directory

- **tar**: tape **a**rchive (create a compressed archive)
- Syntax:
  - Compress: `tar -czvf <file name>.tar.gz <file name>`
  - Decompress: `tar -xzvf <file name>.tar.gz`
- Options
  - **-c**: **c**reate a new archive
  - **-x**: **e**xtract from archive
  - **-v**: **v**erbose, list the processed files
  - **-f**: use archive **f**ile
  - **-z**: compress/extract using **g**zip

# Compress and decompress (tar)

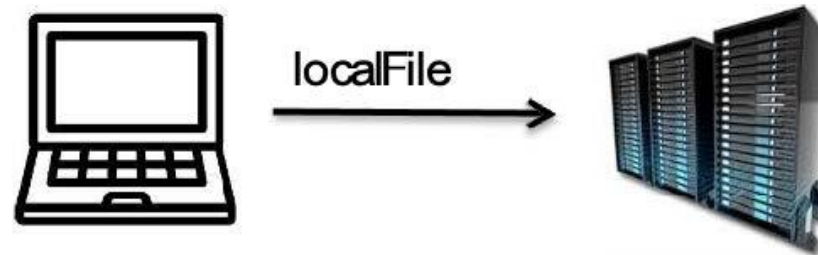
## Directory

- **tar**: tape **a**rchive (create a compressed archive)
- Syntax:
  - Compress: `tar -czvf <file name>.tar.gz <file name>`
  - Decompress: `tar -xzvf <file name>.tar.gz`

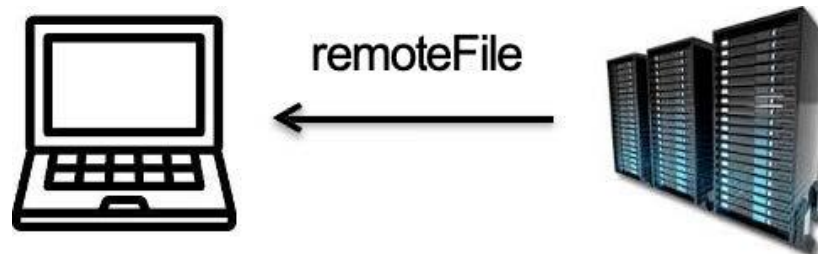
```
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  tmp
[wbguo@login1 qcbio-intro2Unix]$ tar -czvf tmp.tar.gz tmp/
tmp/
tmp/test
tmp/README.md
tmp/tmp.md
[wbguo@login1 qcbio-intro2Unix]$ ls
README.md  day1  day2  day3  tmp  tmp.tar.gz
```

# Download & upload (scp)

- **scp**: openssh **s**ecure file **c**opy
- Syntax (**on local computer terminal**):
  - Upload: `scp <local file> username@hoffman2.idre.ucla.edu:<path>`



- Download: `scp username@hoffman2.idre.ucla.edu:<path> .`



# Download & upload (scp)

- **scp**: openssh **s**ecure file **c**opy

- Upload

```
vincent@Wenbins-MacBook-Pro ~ % ls
Applications Downloads Movies Pictures gDrive
Desktop Dropbox Music Public opt
Documents Library OneDrive Zotero readme
vincent@Wenbins-MacBook-Pro ~ % cat readme
this is a local file
vincent@Wenbins-MacBook-Pro ~ % scp readme wbguo@hoffman2.idre.ucla.edu:qcbio-intro2Unix/
readme
100% 21 4.9KB/s 00:00
vincent@Wenbins-MacBook-Pro ~ %
```

- Download

```
vincent@Wenbins-MacBook-Pro ~ % ls
Applications Downloads Movies Pictures gDrive
Desktop Dropbox Music Public opt
Documents Library OneDrive Zotero readme
vincent@Wenbins-MacBook-Pro ~ % scp wbguo@hoffman2.idre.ucla.edu:qcbio-intro2Unix/day1/test .
test
100% 34 9.6KB/s 00:00
vincent@Wenbins-MacBook-Pro ~ % ls
Applications Downloads Movies Pictures gDrive test
Desktop Dropbox Music Public opt
Documents Library OneDrive Zotero readme
vincent@Wenbins-MacBook-Pro ~ % cat test
hello world
Command line is cool!
vincent@Wenbins-MacBook-Pro ~ %
```



# Download & upload (sftp)

- **sftp**: (ssh file transfer protocol)
- Syntax (from local computer terminal):
  - `sftp username@hoffman2.idre.ucla.edu`

- List remote files: **ls**

```
sftp> ls
R                apps                iproject
perl5            project-collab  project-mcdb
project-msehl    qcbio-intro2Unix run_kde_sim.sh
test             test.RDS        ttest
sftp>
```

- Change remote directory: **cd**

```
sftp> pwd
Remote working directory: /u/home/w/wbguo
sftp> cd qcbio-intro2Unix
sftp> pwd
Remote working directory: /u/home/w/wbguo/qcbio-intro2Unix
sftp>
```

- List local files: **lls**

```
sftp> lls
Applications      Dropbox           OneDrive          gDrive
Desktop           Library           Pictures          opt
Documents         Movies           Public            readme
Downloads         Music            Zotero            test
sftp>
```

- Change local directory: **lcd**

```
sftp> lpwd
Local working directory: /Users/vincent
sftp> lcd Downloads
sftp> lpwd
Local working directory: /Users/vincent/Downloads
sftp>
```

# Download & upload (sftp)

- **sftp**: (ssh file transfer protocol)
- Syntax (from local computer terminal):
  - `sftp username@hoffman2.idre.ucla.edu`

- Download file to local computer: **get <file name>**

```
sftp> get README.md
Fetching /u/home/w/wbguo/qcbio-intro2Unix/README.md to README.md
/u/home/w/wbguo/qcbio-intro2Unix 100% 19 2.3KB/s 00:00
sftp> ll
Applications Library Public readme
Desktop Movies README.md test
Documents Music Zotero
Downloads OneDrive gDrive
Dropbox Pictures ont
```

- Upload file to remote server: **put <file name>**

```
sftp> ls
README.md day1 readme tmp
sftp> put test
Uploading test to /u/home/w/wbguo/qcbio-intro2Unix/test
test 100% 34 7.0KB/s 00:00
sftp> ls
README.md day1 readme test tmp
sftp> bye
vincent@Wenbins-MacBook-Pro ~ %
```

- Terminate sftp connection: **bye**

# Download & upload (GUI tools option)

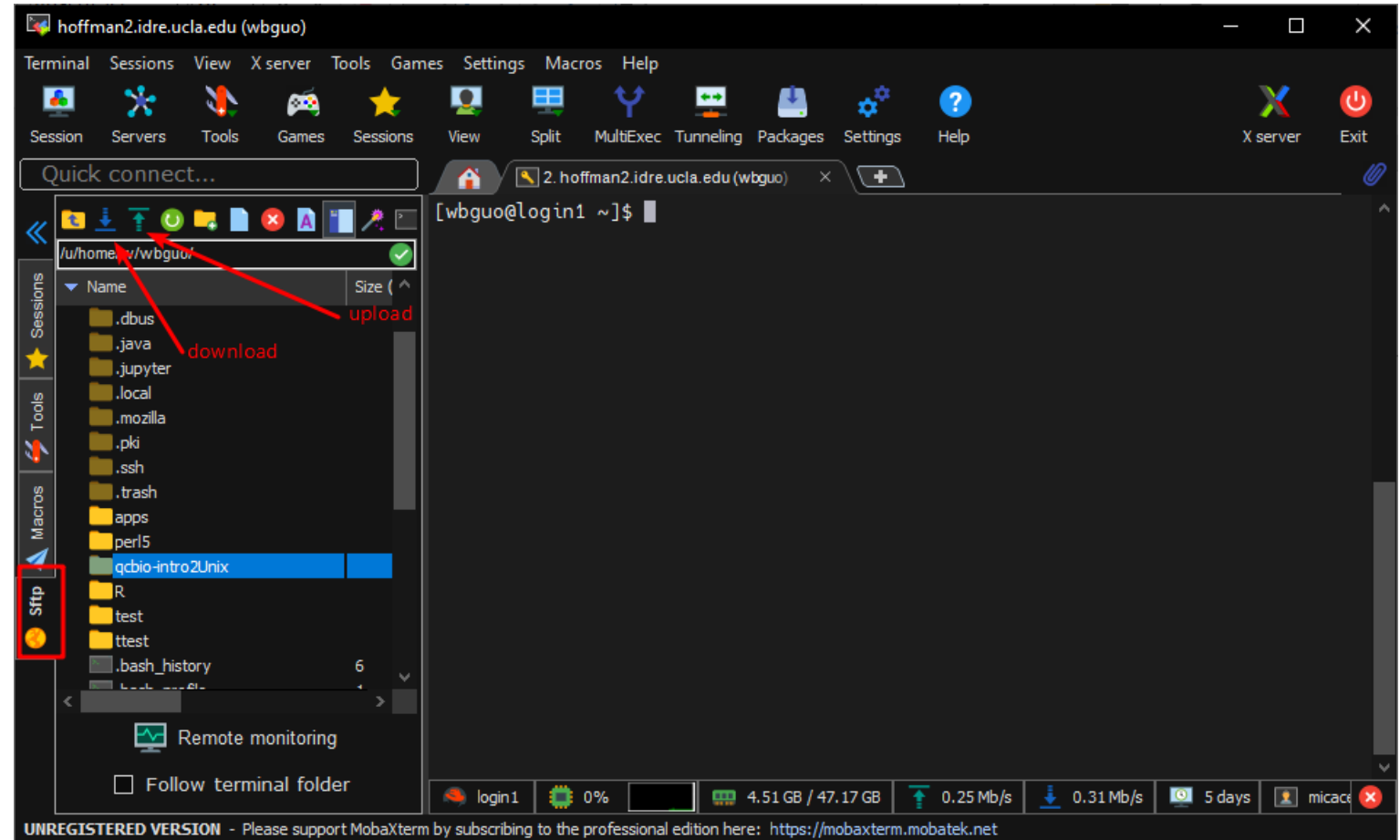
Windows user

- MobaXterm



Other tools:

- WinSCP
- FileZilla



# Download & upload (GUI tools option)

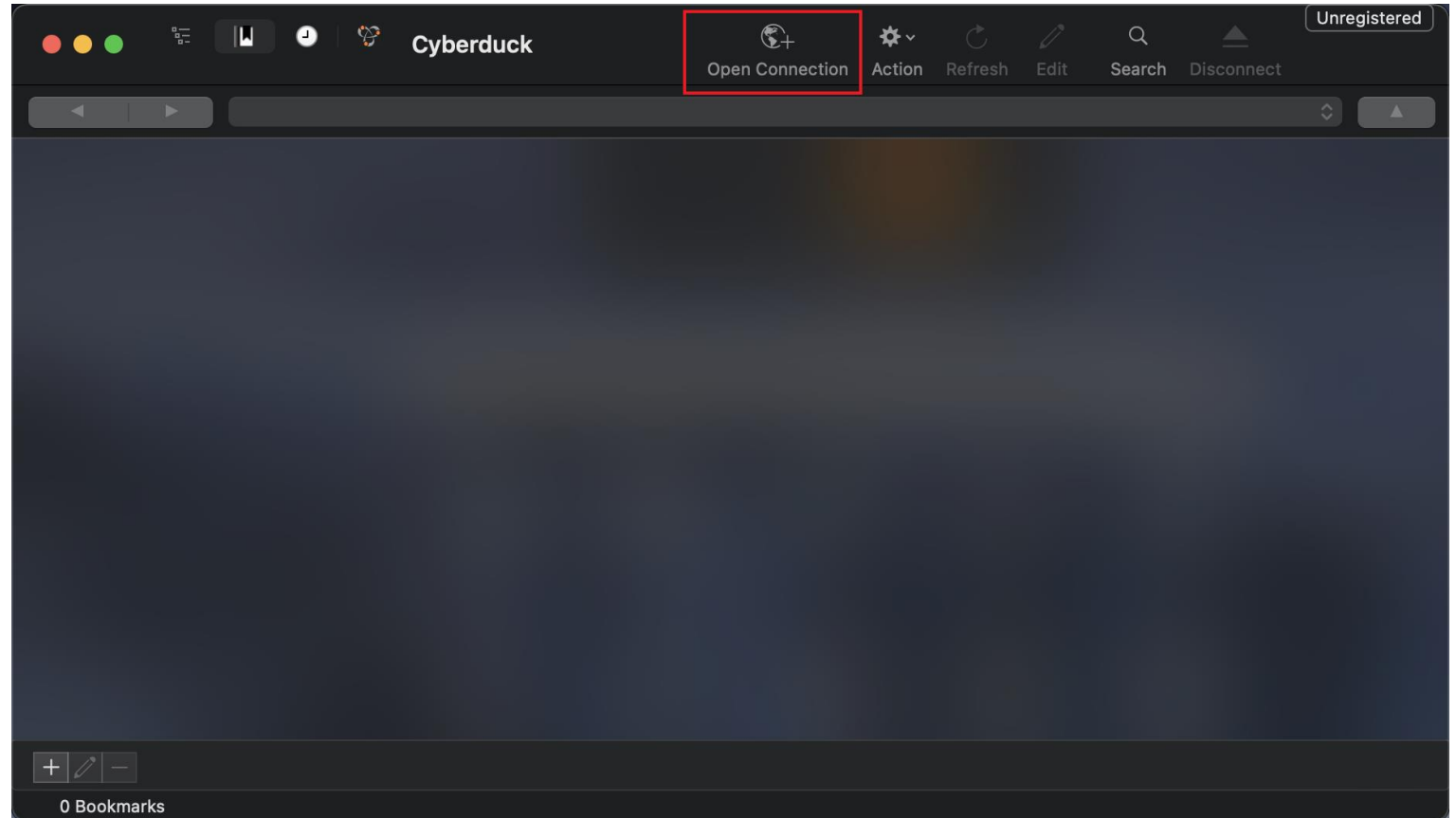
macOS user

- Cyberduck



Other tools:

- FileZilla



# Download & upload (GUI tools option)

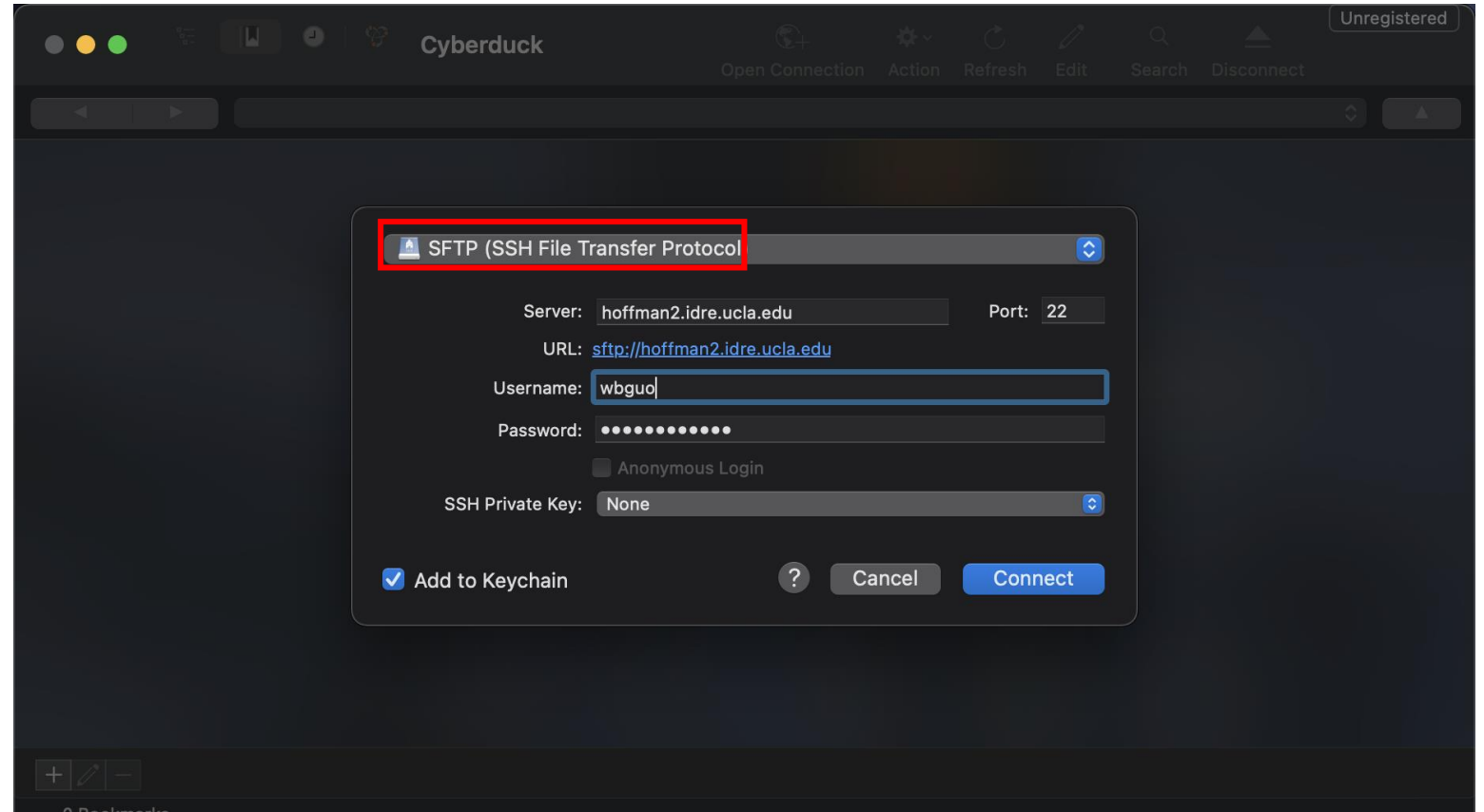
macOS user

- Cyberduck



Other tools:

- FileZilla



# Download & upload (GUI tools option)

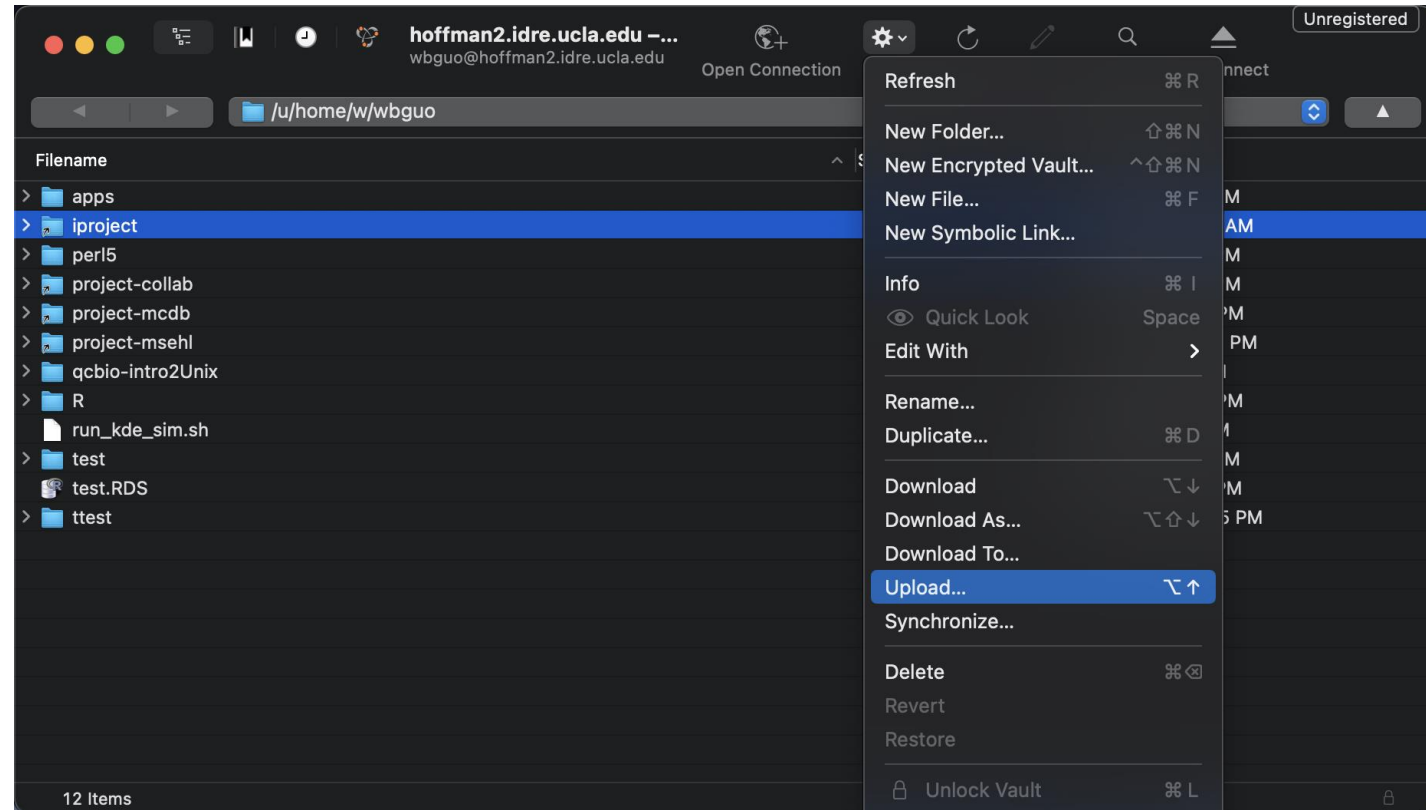
macOS user

- Cyberduck



Other tools:

- FileZilla



# Practice



- Compress the day1 folder into a tar.gz file
- Transfer the file from hoffman2 to your local computer using scp and an GUI application

# Close connection to hoffman2

- **exit**: close ssh connection



# Cannot remember so many commands?

- No problem!
- `--help`
  - Usage: command --help

```
[wbguo@login1 ~]$ ls --help
Usage: ls [OPTION]... [FILE]...
List information about the FILES (the current directory by default).
Sort entries alphabetically if none of -ctuvSUX nor --sort is specified.

Mandatory arguments to long options are mandatory for short options too.
-a, --all                do not ignore entries starting with .
-A, --almost-all        do not list implied . and ..
                        --author          with -l, print the author of each file
-b, --escape             print C-style escapes for nongraphic characters
                        --block-size=SIZE scale sizes by SIZE before printing them; e.g.,
                        ' --block-size=M' prints sizes in units of
                        1,048,576 bytes; see SIZE format below
-B, --ignore-backups     do not list implied entries ending with ~
-c                       with -lt: sort by, and show, ctime (time of last
                        modification of file status information);
                        with -l: show ctime and sort by name;
                        otherwise: sort by ctime, newest first
-C                       list entries by columns
                        --color[=WHEN]   colorize the output; WHEN can be 'never', 'auto',
                        or 'always' (the default); more info below
-d, --directory          list directories themselves, not their contents
-D, --dired              generate output designed for Emacs' dired mode
-f                       do not sort, enable -aU, disable -ls --color
-F, --classify           append indicator (one of */=@|) to entries
                        --file-type       likewise, except do not append '*'
                        --format=WORD     across -x, commas -m, horizontal -x, long -l,
                        single-column -1, verbose -l, vertical -C
                        --full-time       like -l --time-style=full-iso
-g                       like -l, but do not list owner
                        --group-directories-first
                                group directories before files;
                                can be augmented with a --sort option, but any
                                use of --sort=none (-U) disables grouping
-G, --no-group           in a long listing, don't print group names
-h, --human-readable     with -l, print sizes in human readable format
                        (e.g., 1K 234M 2G)
                        --si              likewise, but use powers of 1000 not 1024
-H, --dereference-command-line
                        follow symbolic links listed on the command line
                        --dereference-command-line-symlink-to-dir
                                follow each command line symbolic link
                                that points to a directory
--hide=PATTERN           do not list implied entries matching shell PATTERN
                        (overridden by -a or -A)
--indicator-style=WORD  append indicator with style WORD to entry names:
                        none (default), slash (-p),
                        file-type (--file-type), classify (-F)

-i, --inode              print the index number of each file
-I, --ignore=PATTERN     do not list implied entries matching shell PATTERN
-k, --kibibytes          default to 1024-byte blocks for disk usage
-l                       use a long listing format
```

# Cannot remember so many commands?

- No problem!
- **--help**
  - Usage: command --help
- **man: manual**
  - Usage: man command

Use up/down arrow to scroll line by line  
Use PgDn/PgUp to scroll page by page  
Press q for exit

```
LS(1)                                User Commands                                LS(1)

NAME
    ls - list directory contents

SYNOPSIS
    ls [OPTION]... [FILE]...

DESCRIPTION
    List information about the FILEs (the current directory by default). Sort
    entries alphabetically if none of -cftuvSUX nor --sort is specified.

    Mandatory arguments to long options are mandatory for short options too.

    -a, --all
        do not ignore entries starting with .

    -A, --almost-all
        do not list implied . and ..

    --author
        with -l, print the author of each file

    -b, --escape
        print C-style escapes for nongraphic characters

    --block-size=SIZE
        scale sizes by SIZE before printing them; e.g., '--block-size=M'
        prints sizes in units of 1,048,576 bytes; see SIZE format below

    -B, --ignore-backups
        do not list implied entries ending with ~

    -c
        with -lt: sort by, and show, ctime (time of last modification of file
        status information); with -l: show ctime and sort by name; otherwise:
        sort by ctime, newest first

    -C
        list entries by columns

    --color[=WHEN]
        Manual page ls(1) line 1 (press h for help or q to quit)
```

# Where to get help?

- <https://www.google.com>
- <https://stackoverflow.com>
- <https://unix.stackexchange.com>
- [https://www.tutorialspoint.com/unix/shell\\_scripting.htm](https://www.tutorialspoint.com/unix/shell_scripting.htm)



# Q&A

[Google doc](#)