

Introduction to Linux



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About Linux



- An **operating system (OS)** that manages a computer's resource – like MacOS and Windows.
- Derived from UNIX operating system (and so it is called **UNIX-like OS**).
- Developed by Linus Torvald, hence the name: Linux = Linus + Unix.
- A family of operating systems based on Linux as the center (**kernel**) is known as **Linux distribution or distro**.
 - For example: Debian, Ubuntu, CentOS, Fedora, Arch Linux, etc.
 - Each distribution has their own specification – i.e. RedHat is more suitable to be run in server while Ubuntu is more suitable for desktop.



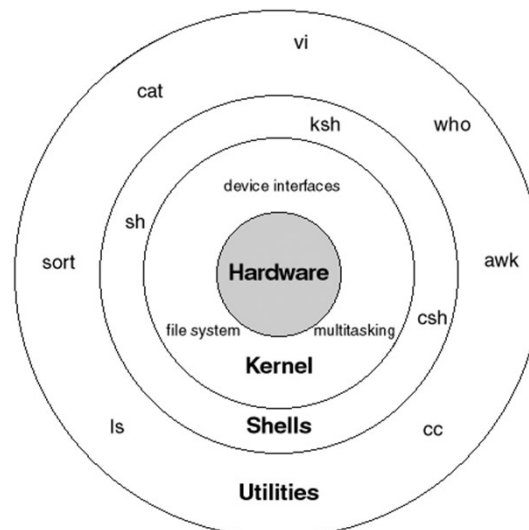
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Linux comes in many flavors



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The Linux system



Layers of Linux

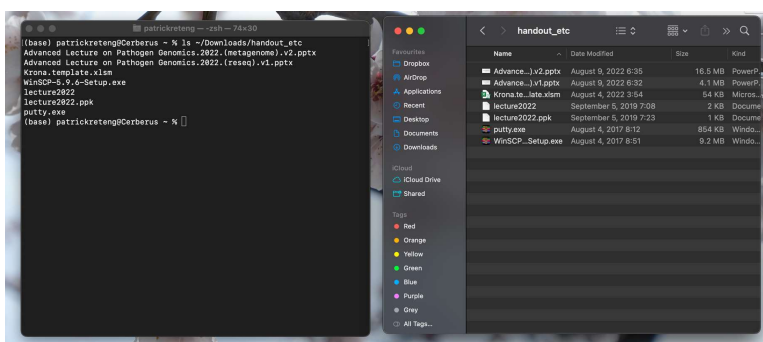
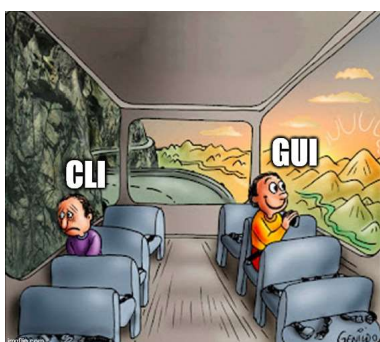
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Linux and Bioinformatics

- Bioinformatics is the application of tools of computation and analysis to the capture and interpretation of biological data.
- Why Linux become the natural environment for bioinformatician?
 - Open source – free.
 - Linux gives freedom to control hardwares – i.e. memory allocation.
 - Most developers working on Linux.

GUI or CLI?

- Command line interface (CLI) or graphical user interface (GUI).



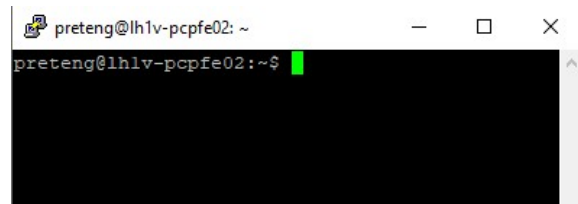
- Viewing files inside the folder requires knowledge of command and path.
- Viewing files inside the folder is as easy as opening the folder.

GUI or CLI?

- Why CLI?
 - Repetition: easier to repeat task with CLI. More input – more reason to use CLI.
 - Reproducibility: with good script/command/code documentation.
 - Access to server or high performance computer: usually use CLI.
 - Not many utilities for genome analysis is available in GUI – need to familiarize with CLI.

The shell

- In Linux OS, shell is a program that facilitates user-computer interaction.
 - Most Linux systems use **BASH** (Bourne Again Shell).
 - Other examples: C shell, sh.
- Communication is done by typing commands into the shell – the shell translates this command and pass the prompt to the kernel.
- The general format of the default command prompt is: [username@hostname cwd]\$ (or #).

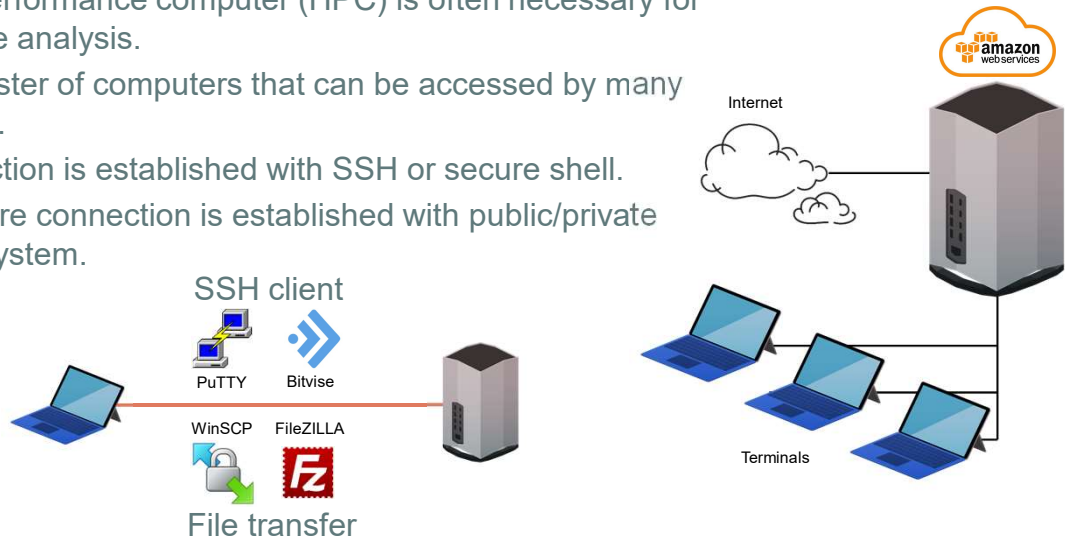


A screenshot of a terminal window. The title bar shows 'preteng@lh1v-pcpfe02: ~'. The terminal content shows the prompt 'preteng@lh1v-pcpfe02:~\$' followed by a green cursor. The window has standard Linux window controls (minimize, maximize, close) in the top right corner.

\$ = regular user
= root user

Accessing a server

- High performance computer (HPC) is often necessary for genome analysis.
 - A cluster of computers that can be accessed by many users.
- Connection is established with SSH or secure shell.
 - Secure connection is established with public/private key system.



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Commands

- The way to communicate with the computer.
- Structure or syntax:
 - Starts with either a command or a program+command.
 - Followed by options and/or arguments.

\$ls -l /path/to/a/directory/
command options argument

\$grep -A1 chr1 ref.fasta
command options argument1 argument2

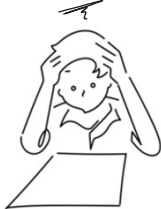
\$samtools view -bS input.bam
program command options argument

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Commands

- Computer is great at doing repetitive task.

Calculate \log_{10} of 1 to 10,000



Errors and
frustration



No complaints,
less errors

- Communicating with computer can be challenging.
- Be systematic and concise.



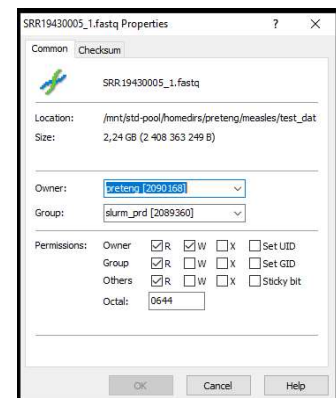
“Wear shoes”



- Locate shoes
- Locate socks
- Put left sock on
- Put right sock on
- Put right shoe on
- Put left shoe on

User and permission

- Linux OS is multiuser.
- A user will be given a full access to a directory – this is called home.
- All files and directory will be granted a certain level of permission.
- The level of permission can be freely manipulated - use `chmod` command.
 - Use `ls -l` to check file permission.
- There are special user: those with root access.
 - With great power comes great responsibility.



```
--rw-r--r-- 1 preteng slurm_prd 200343970 Jul 14 10:47 SRR19430007_1.fastq
--rw-r--r-- 1 preteng slurm_prd 367019163 Jul 14 10:27 SRR19430008_1.fastq
--rw-r--r-- 1 preteng slurm_prd 121562174 Jul 14 10:28 SRR19430009_1.fastq
--rw-r--r-- 1 preteng slurm_prd 844531777 Jul 14 10:32 SRR19430010_1.fastq
--rw-r--r-- 1 preteng slurm_prd 399631998 Jul 14 10:36 SRR19430011_1.fastq
--rw-r--r-- 1 preteng slurm_prd 401427154 Jul 14 10:35 SRR19430012_1.fastq
```

Virtual environment

- Conda, mamba, miniconda, are package manager.
- Why using package manager? Easier installation – simple commands and programs can be installed without being a root user.

Computer environment

- R v4.2
- Python v3.7

Program X:

ERROR. Requires-Python >=3.7,
R>=3.0, <4.0.

ERROR: Could not find a version that
satisfies the requirement

Virtual environment

- R v3.5

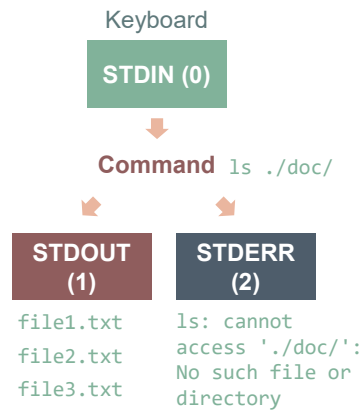
Program X:

Requirement satisfied

Path

- Path is simply the location of a file or a directory – precede by “/”
- Absolute path: no assumption on the current directory
—Example: /home/documents/file.txt
- Relative path: describe the path relative to the current directory.
—Example: ../documents/file.txt or ./documents/file.txt
- Tips
 - ~/ = home directory (/home/documents/ = ~/documents/)
 - ./ = current directory
 - ../ = one directory above the current directory
 - pwd = printing the current directory

Redirection



- The standard channels 0, 1, and 2 can be replaced with files.
- User can output the STDOUT and STDERR into a file.
 - `ls ./doc/ > filelist.txt #STDOUT` (or `>>` to append in a same file).
 - `ls ./doc/ 2> filelist.txt #STDERR`
- Or, user can input STDIN from a file.
 - `grep string < file.txt`

Piping

- Output from one command can be used as an input to the next command – this is called piping.
- The command should be joined by “|”.
- Example:
 - `cat file.txt | sort | uniq`
 - `grep string file.txt | awk '{print $1}' > output.txt`
- Useful when combining commands.

Foreground and background



- When a job is running in **foreground**, user can observe the progress directly, but **cannot run additional command**.
- When a job is running in **background**, user cannot directly observe the progress, but user **can run another command**.
- Jobs related command:
 - jobs**: showing jobs running in the background.
 - fg**: bring a job in the background to the foreground.
 - CTRL+Z**: move foreground job to the background and suspend them.
 - bg**: continue any suspended job in the background.
 - &**: running a job in the background.

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Terminating a process



- **Ctrl+C**: terminating a job running in foreground.
- **kill %<job id>**: terminating a job running in background, check job id with the **jobs** command.
- **killall -u user**: kill all job executed by a certain user – if you have root access.
- **Closing the terminal = ending any running jobs!**
- User can give up privilege to manage job by disowning (**disown**) the jobs – job will keep running in the server until it is finished or it encounters an error.

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Tips

- Use the up and down arrow keys to access previous commands.
- Autocomplete = tab button.
- “/” is not allowed to be used in a file name.
- Avoid using space or other special characters in file/directory name.

man

- `man` → Printing out the manual of a certain command.
- Similar to `-h` `-help` or `-help`.
- Example

```
$man grep
$grep --help
```
- Press “Q” to quit the manual.

Directories

- Directory = folder.
- `mkdir` → make directory, creating a new directory.
 - Usage: `$mkdir directory_name`
 - Can not create a directory with the same name.
- `cd` → change directory, move to another directory.
 - Usage: `$cd path_to_directory`
- `pwd` → print working directory, print out the current directory.

cp and mv

- These two commands are used to move files or directories around.
- `cp` → copy, create a copy.
 - Usage: `$cp original_file copy_file`
- `mv` → move.
 - Usage: `$mv original_file destination_path`
- **Be careful not to accidentally overwrite a file/directory.**
 - Use autocomplete to ensure the filename is unique.

rm

- `rm` → remove, deleting a file or a directory.
—Add the recursive option “-r” for directory.
- **No warning, no backup!**
—Once rm-ed, it is gone forever.

ls

- `ls` → list, print out the list of files present in a directory
- usage: `$ls options directory`
—Option `-l` gives full list, including permission, date created, and size.
—Use `man ls` to get the full options list or `ls -h`.

grep

- `grep` → generalized regular expression parser, find a **string** in a plain-text data.
 - Usage: `$grep options "search_term" file.txt`
 - The good practice is to always keep the **string** inside quotation marks.
 - The output is **lines** in `file.txt` that contains the `search_term`.
- Useful options:
 - “-A” and “-B” – get nth line after and before the match.
 - “-w” – match only whole words.
 - “-f” – find pattern from a file.
 - Use “`grep --help`” to get the full options.

string = a series of characters.

sort

- `sort` → sort the lines.
- Usage:
 - `$sort file`
 - `$grep chr1 file.txt | sort`
- Options to sort based on number or alphabet, reverse sort, and other options are available.
 - r: sort in reverse order.
 - n: treat the data as integer.
 - k: sort the data based on a column.

uniq

- `uniq` → unique, remove repeated lines – file needs to be sorted.
- Usage:
 - `$uniq file`
 - `$grep chr1 file.txt | sort | uniq`
- Available options:
 - `-d`: print only the redundant lines.
 - `-c`: show how many times the redundant lines appear.
 - `-i`: ignore case sensitivity.
 - `-s <INT>`: skip the first <INT> characters when making comparison.

comm

- `comm` → common, find common lines between two files.
- Usage:
 - `$comm file1 file2`
- Options:
 - `-1` print lines common for both files and lines unique to file2.
 - `-2` print lines common for both files and lines unique to file1.
 - `-3` print lines unique to file1 and file2.
 - `-12` print lines common for both files.
- Both files must be in sorted order.

WC

- `wc` → word count, print line, word, and byte count for a file.
- Usage:
 - `$wc file`
- Useful:
 - `$wc -l file.fastq` #counting lines in a fastq files
- Options
 - `-l`: count lines;
 - `-m`: count characters;
 - `-w`: count words.

cat

- `cat` → concatenate, concatenate and print files to the standard output
- Usage:
 - `$cat file1 file2`

Preview a file

- Only for text file! Binary file cannot be previewed.
- `less` → preview a file without reading the entire file.
- `more` → similar to `less` but the program reads the entire file first.
- `head` → print lines from the start of the file (default 10 lines); `head -20` = print the first 20 lines.
- `tail` → print lines from the end of the file (default 10 lines); `tail -20` = print the last 20 lines.

Loop

- Very useful for automation.
- The most common is the `for` in command:

```
$for var in A B C; do rm file${var}.txt; done
fileA.txt
fileB.txt
fileC.txt
```

 - A list name `var` is defined by the user that contains the letter A, B, and C.
 - The `rm` command will be repeated to the length of `var` (in this case three times).
 - The `${var}` part will be substituted with different letter in each repetition.

Loop

- Other useful command for loop is while read.

```
$cat list.txt
```

```
A
```

```
B
```

```
C
```

```
$while read var; do echo file${var}.txt; done < list.txt
```

```
fileA.txt
```

```
fileB.txt
```

```
fileC.txt
```

- Similar to previous, but instead of defining the variable in the command, we asked the computer to use each line in the file list.txt as the list of variable.

Sed

- sed → stream editor, for parsing and transforming text (similar to awk).

- Example:

```
—sed 's/string1/string2' file #substitute (s) string1 to string2  
in a file.
```

Awk

- awk is a domain-specific language designed for text processing and typically used as a data extraction and reporting tool.
 - awk = Aho, Weinberger, and Kernighan, its designer.
- Useful in manipulating columns of data.
- Example
 - \$ awk '{print \$5}' file
 - \$ awk awk 'NR%2==1' file
 - awk '\$3=="www"'
- More explanation: <https://www.gnu.org/software/gawk/manual/gawk.html>.

Practice time~

