

## Brief Unix tutorial

### What' s UNIX/Linux?

- An operating system run on many servers/workstations
- Invented by [AT&T](#) Bell Labs in late 60' s
- Command line system
- Modular
- Currently there are different versions and variants of UNIX such as SunOS, Linux, Solaris, BSD, Mac OS X (sorta), Android (sorta) ...

## Introduction: Why Unix/Linux?

- Linux is **free**
- It's fully **customizable**
- It's **stable** (i.e. it almost never crashes)
- These characteristics make it an ideal OS for programmers and scientists

## Basic Linux

- Most functionality is accessed through the prompt.
  - Text based, like MS-DOS
- Mastery of Linux comes from being familiar with different commands
  - We will cover some of the basic commands in this class
  - You will gain mastery through TIME and PRACTICE

Recommended: If you are unfamiliar with Linux, work through (one of may) an online tutorial:

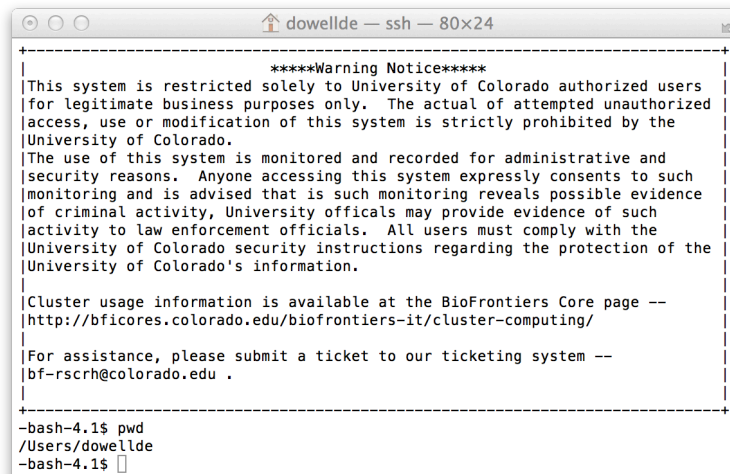
<http://www.ee.surrey.ac.uk/Teaching/Unix/>

## Today we'll quickly go over the basics.

- Getting help while on the system
- The shell
- Working with files & directories
- Wild card characters
- Security
- I/O redirection
- pipes
- process and job control commands (next week)

## Connecting to a Unix/Linux system

Open up a terminal:



```
dowelldc — ssh — 80x24
+-----+
|*****Warning Notice*****|
|This system is restricted solely to University of Colorado authorized users|
|for legitimate business purposes only. The actual of attempted unauthorized|
|access, use or modification of this system is strictly prohibited by the|
|University of Colorado.        |
|The use of this system is monitored and recorded for administrative and|
|security reasons. Anyone accessing this system expressly consents to such|
|monitoring and is advised that is such monitoring reveals possible evidence|
|of criminal activity, University officials may provide evidence of such|
|activity to law enforcement officials. All users must comply with the|
|University of Colorado security instructions regarding the protection of the|
|University of Colorado's information.  |
|Cluster usage information is available at the BioFrontiers Core page --|
|http://bficores.colorado.edu/biofrontiers-it/cluster-computing/|
|For assistance, please submit a ticket to our ticketing system --|
|bf-rscrh@colorado.edu .        |
+-----+
-bash-4.1$ pwd
/Users/dowelldc
-bash-4.1$
```

## Logging in

- To login  
**ssh <identikey>@fiji.colorado.edu**
- To logout  
**logout** or **exit**

**Note: all Unix commands are case sensitive**

## What exactly is a “shell”?

- After logging in, Linux/Unix starts another program called the **shell**
- The shell interprets commands the user types and manages their execution
  - The shell communicates with the internal part of the operating system called the **kernel**
  - The most popular shells are: tcsh, csh, korn, and bash
  - The differences are most times subtle
  - For this tutorial, we are using bash
- Shell commands are **CASE SENSITIVE!**

## General command format

### Command -options arguments

- options/flags generally identify some optional capabilities
- some parts of a command are optional. These are indicated in the man pages with [ ]
- case sensitive

## Getting Help from the System

- All Unix commands are described online in a collection of files called “man pages”

**man** command

Note that the man pages uses an ancient method of viewing content:

- For help on some topic  
**man -k keyword**
- For more information on using the man pages  
**man man**

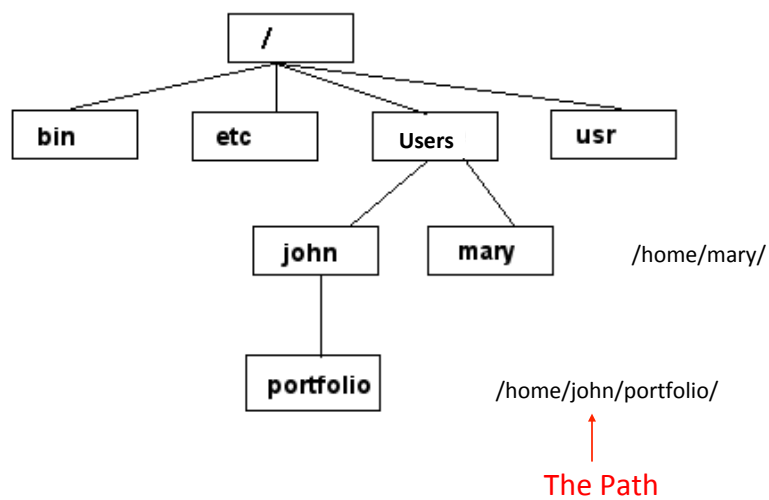
- <spacebar> to go down a page
- Arrow keys *\*should\** work to review already seen segments.
- <q> to quit the man pages

## Files and Directories

- Home directory:
  - The actual path of your home directory may be something like:  
**/Users/identikey**
  - Note the forward slashes

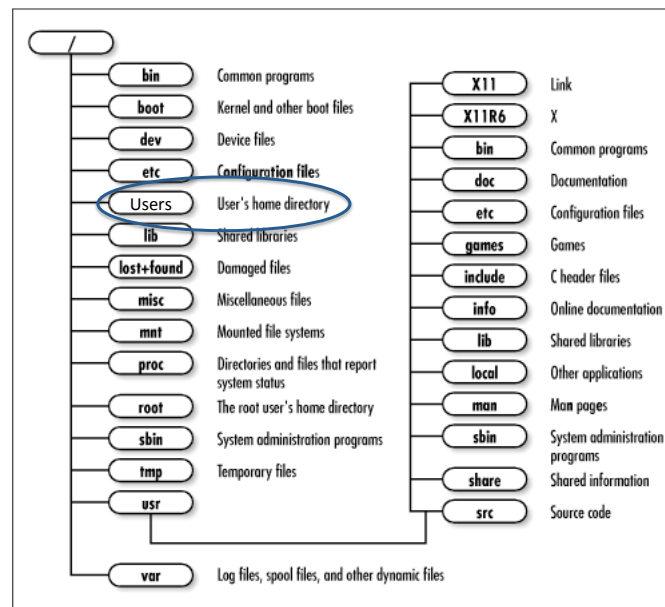
## Unix/Linux File System

NOTE: Unix file names are **CASE SENSITIVE!**



# Linux Directory Structure

- Files are grouped in the directory structure. The file-system is arranged like hierarchical tree structure.
- The top of the tree is called “root” which usually contains several sub-directories.
  - “/”(forward slash) is used to present the “root”.



## Pathnames

- **pwd (print working directory)**

```
-bash-4.1$ pwd  
/Users/dowellde
```

## Listing contents of a directory

- ls (list files and directories)**

**ls**

- The ls command lists the contents of your current working directory.



## Listing contents of a directory

- To generate a detailed listing

```
ls -l
```

- To display all files (including hidden)

```
ls -a
```

- To make information “human readable”

```
ls -h
```

## Command: ls

- ls has many options
  - -l long list (displays lots of info)
  - -t sort by modification time
  - -S sort by size
  - -h list file sizes in human readable format
  - -r reverse the order
- “man ls” for more options
- Options can be combined: “ls -alhr”

## Listing contents of a directory

- To generate listing of a specific directory

**ls -alh pathname**

where **pathname** is the path of intended directory.

**pathname** may be full path or relative path.

- “.”: points to the current directory
- “..”: points to the parent directory of the current working directory
- “~”: points to your home directory

## Pathnames

- Absolute Pathnames

\$ /Users/dowellde/4521/FASTQ/file1

- Relative pathnames

- If you are already in the /Users/dowellde directory, the relative pathname for file1 is:  
4521/FASTQ/file1

## Wildcards

- `~`: a tilde at the beginning of a word expands to the name of your home directory.

e.g: `ls ~`  
`cat ~/proj1.cc`

- if you append `~` to a user name, it refers to that user's home directory.

e.g: `ls ~smith`  
 lists all files in home directory of user smith

## Wildcards

- The characters `*` will match against one or more characters in a file or directory name.

`ls proj*`

- The character `?` Will match against any single character
- `[ ]`: the brackets enclose a set of characters any one of which may match a single character in that position.

e.g `cat proj[125]`  
`cat proj[1-7]`

## Some tips

- “tab” is used for auto-complete.
  - If a file/directory name was partly typed in, tab will auto-complete it.
  - If there are multiple options, tab will auto-complete up to the point where the options branch and show you a list of possible options
- “\*” is used as a wild card.
  - “rm *blah\**” removes all files which start with *blah*, so *blah1*, *blah2*, and *blahblah* would all be removed
  - Using “cp public/\* private/” copies all files in your public directory into your private directory, and keeps all file names intact.

## Making Directories

### **mkdir (make directory)**

**mkdir    name**

- creates a subdirectory in current working directory

**mkdir    somepath/name**

- creates a subdirectory in directory **somepath**

## Changing to a different directory

### **cd (change directory)**

**cd pathname**

- change current working directory to **pathname**.
- **cd** by itself will make your home directory the current working directory.
- **cd ..** : cd to parent of current directory
- **cd ~** : cd to home directory

## Copying files

### **cp (copy)**

**cp file1 file2**

- makes a copy of file1 and calls it file2. File1 and file2 are both in current working directory.

**cp pathname1/file1 pathname2**

- copies file1 to pathname2

e.g **cp ~/tutorial/science.txt .**

## Moving files

**mv** (move)

```
mv file1 file2
```

- moves (or renames) file1 to file2
- use the -i option to prevent an existing file from being destroyed

```
mv -i file1 file2
```

- if **file2** already exist, **mv** will ask if you really want to overwrite it.

## Removing files and directories

**rm** (remove)

```
rm file1 [file2]...
```

- Use the -i option for interactive remove:

```
rm -i proj*.*
```

Be very careful,  
deletions are  
permanent in  
Unix/Linux

## Removing files and directories

**rmdir** (remove directory)

**rmdir path**

- will not remove your current working directory
- will not remove a directory that is not empty
- To remove a directory and any files and subdirectories it contains use -r (recursively)

**rmdir -r path**

**rmdir -ir path**

## Displaying the contents of a file on the screen

**cat** (concatenate)

**cat myfile**

displays the contents of myfile on monitor

**cat file1 file2 file3**

**more** (**less**)

displays a file on the screen one page at a time. Use space bar to display to next page.

**Head** -- displays first 10 lines

**tail** -- displays last 10 lines

## A brief segue: Sequence Files (fasta and fastq)

### Simple fasta format

- **FASTA format:** A sequence record in a FASTA format consists of a single-line description (sequence name), followed by line(s) of sequence data. The first character of the description line is a greater-than (">") symbol.

[https://en.wikipedia.org/wiki/FASTA\\_format](https://en.wikipedia.org/wiki/FASTA_format)

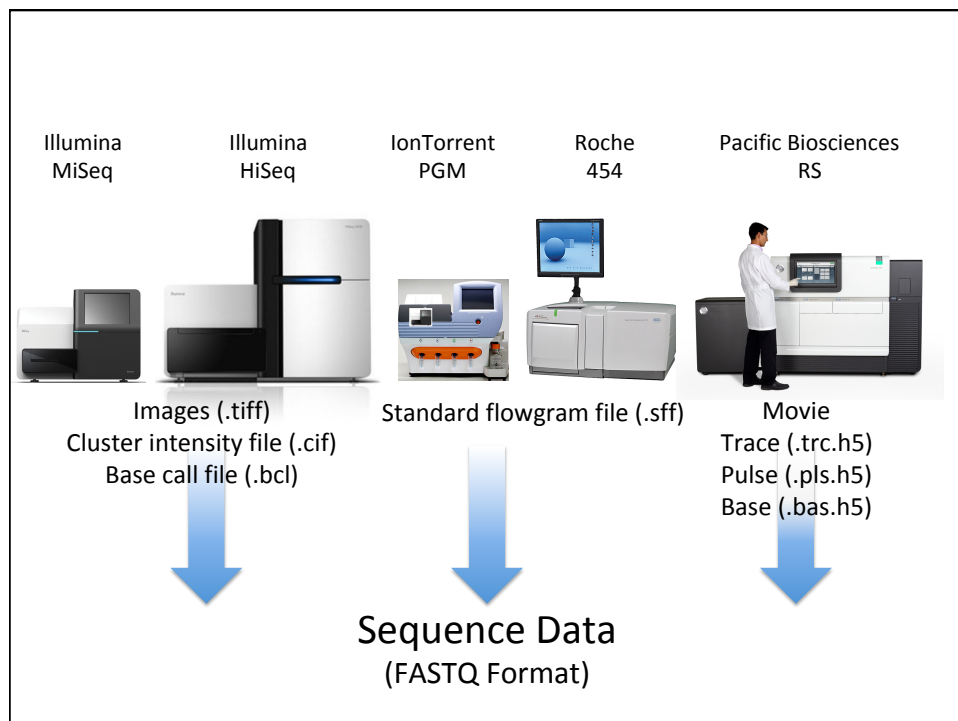


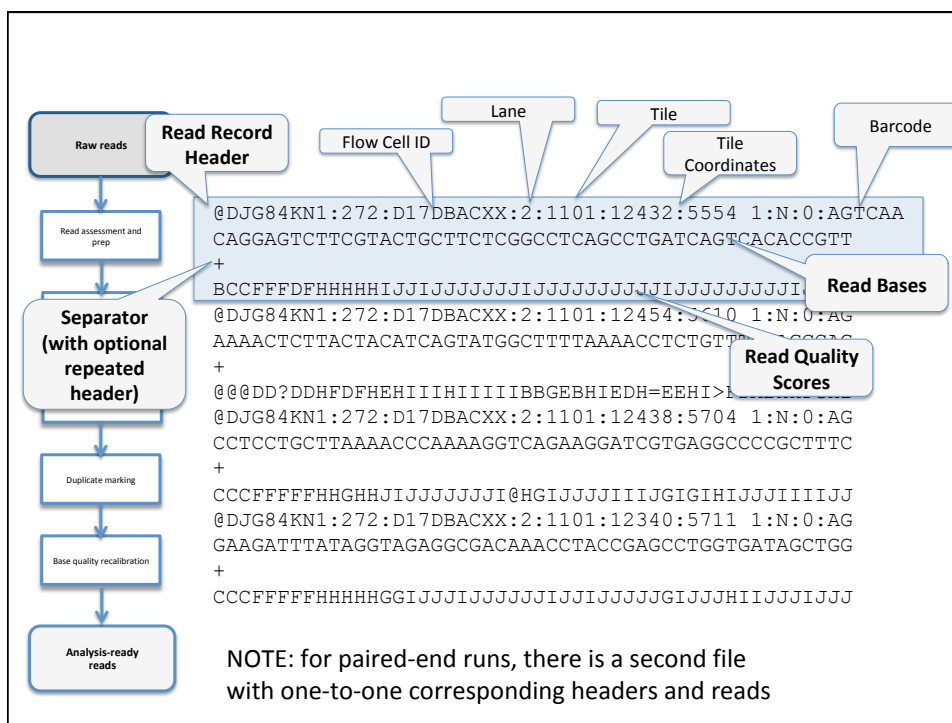
## Example FASTA file:

```

>seq0
FQTWEEFSRAAEKLYLADPMKVRVVLKYRHVDGNLCIKVTDDLVLVYRTDQAQDVKKIEKF
>seq1
KYRTWEEFTRAAEKLYQADPMKVRVVLKYRHCDGNLCIKVTDDVVCLLYRTDQAQDVKKIEKFHSQLM
RLME LKVTDNKECLKFKTDQAEAKKMEKLNNIFFTLM
>seq2
EEYQTWEEFARAAEKLYLTDPMKVRVVLKYRHCDGNLCMKVTDDAVCLQYKTDQAQDVKKVEKLHG
K
>seq3
MYQVWEEFSRAVEKLYLTDPMKVRVVLKYRHCDGNLCIKVTDNSVCLQYKTDQAQDVK
>seq4
EEFSRAVEKLYLTDPMKVRVVLKYRHCDGNLCIKVTDNSVVSYEMRLFVQKDNFALEHSL
>seq5
SWEEFAKAAEVLYLEDPMKCRMCTKYRHVDHKLVLKLTDNHTVLKYVTDMAQDVKKIEKLTTLLMR
>seq6
FTNWEEFAKAAERLHSANPEKCRFVTKNHTKGELVLKLTDDVVCLQYSTNQLQDVKKLEKLSSTLLRSI
>seq7
SWEEFVERSVQLFRGDPNATRYVMKYRHCEGKLVKVTDDRECLKFKTDQAQDAKKMEKLNNIFF
PDTRYVVKYRHCEGKLVKVTDNHECLKFKTDQAQDAKKMEK

```





Phred\* quality score  $Q$  with base-calling error probability  $P$

$$Q = -10 \log_{10} P$$

\* Name of first program to assign accurate base quality scores. From the Human Genome Project.

Q score	Probability of base error	Base confidence	Sanger-encoded (Q Score + 33) ASCII character
10	0.1	90%	"+"
20	0.01	99%	"5"
30	0.001	99.9%	"?"
40	0.0001	99.99%	"I"

[illegible]

## Searching the contents of a file

- **Searching using more**

For example, to search **myfile** for the word science, type

```
more myfile
```

then type

```
/ science
```

Type **n** to search for the next occurrence of the word

## GREP (a powerful approach)

- Searching using **grep**

```
> grep music myfile
```

- To ignore upper/lower case distinctions, use the -i option

```
> grep -i music myfile
```

- To search for a phrase or pattern, you must enclose it in single quotes. For example to search for the phrase operating systems, type

```
> grep -i 'operating systems' myfile
```

```
> grep -i 'operating systems' *
```

## Searching the contents of a file

Some of the other options of grep are:

- v display those lines that do NOT match
- n precede each matching line with the line number
- c print only the total count of matched lines

Whole books are written on using GREP.

## Other Useful Commands

### **wc (word count)**

- To do a word count on myfile, type  
**wc -w myfile**
- To find out how many lines the file has, type  
**wc -l myfile**
- To do both  
**wc myfile**

## Redirecting Input and Output

- In general, Unix commands use the standard input (keyboard) and output (screen).
- **<** : redirect input
- **> and >>** : redirect output

## Redirecting Input and Output

- An example: search for the word `mysort` in all the `c` source files in the current directory and write the output to `file1`.
- **`grep mysort *.c > file1`**

## Using redirection to concatenate files

- Examples:

```
cat file1 > file2
```

copies file1 into file2

- To concatenate files:

```
cat file1 file2 > file3
```

- or

```
cat file2 >> file1
```

## Pipes

- A pipe is a way to use the output from one command as the input to another command without having to create intermediary files.
- Example: want to see who is logged in, and you want the result displayed alphabetically:

```
who > namelist
```

```
sort namelist
```

- Using a pipe:

```
who | sort
```

## Protecting files and directories

- The `ls -l` command display detailed listing of a file, including its protection mode:

```
drwxrwxrwx  owner  size  directoryname  ....
-rwxrwxrwx  owner  size  filename  ...
```

- the first character (**d** or **-**) indicates whether it is a file or directory name.
- The following 9 character indicate the protection mode.

## Protecting files and directories

```
rwX rwX rwX
```

- Each group of three characters describes the access permission: **read , write and execute**
- the first three settings pertain to the access permission of the **owner** of the file or directory, the middle three pertain to the **group** to which the owner belongs, and the last three pertain to **everyone else**.

## Access rights on files.

- **r** (or **-**), indicates read permission, that is, the presence or absence of permission to read and copy the file
- **w** (or **-**), indicates write permission; that is, the permission to change a file
- **x** (or **-**), indicates execution permission; that is, the permission to execute a file, where appropriate

**example:**    `-rwxrw-r--`

## Access rights on directories.

- **r**: allows users to list files in the directory;
- **w**: means that users may delete files from the directory or move files into it.
  - Never give write permission to others to your home directory or any of its subdirectories.
- **x**: means the right to access files in the directory. This implies that you may read files in the directory if you have read permission on the individual files.

**example:**    `drwxrw-r--`



## Changing file access permission

### chmod (changing protection mode)

- Consider each group of three to be a 3-bit number

example: you want to set permission to

```

rwx r-- ---
111 100 000    (in binary)
7   4   0

```

**chmod 740 filename**

**chmod [user/group/others/all]+[permission] [file(s)]**

## Creating files in Unix/Linux

- Can “touch” to create an empty file, can copy an existing file, etc.
- But novel content requires using an editor
- Various Editor
  - 1) vi / vim
  - 2) emacs



### Recommended Reading:

Bill Noble's **A Quick Guide to Organizing Computational Biology Projects**

PLoS Comput Biol 5(7): e1000424. doi:10.1371/journal.pcbi.1000424

### Assignment this week:

- Practice interacting with Fiji: login, move files around, create and edit files
- Create a README file in your home directory that you will use throughout the class. Include appropriate documentation of any files/directories created today.

## Prepare for next week:

- We will be going over transferring files, process management, and submitting jobs to the cluster
  - we will run our first sequence quality analysis.
- Recommended Videos:
  - Day 3: Cluster usage
  - Day 4: Data Quality (Sequencing QC)