Introduction to Linux

iCB2 – Introduction to Computational Biology and Bioinformatics
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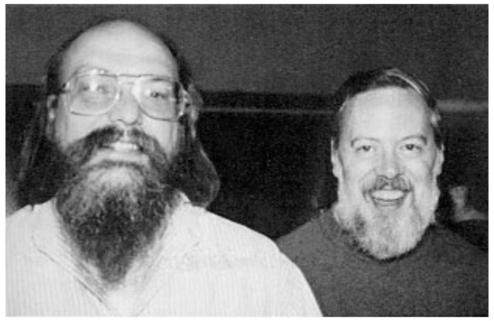
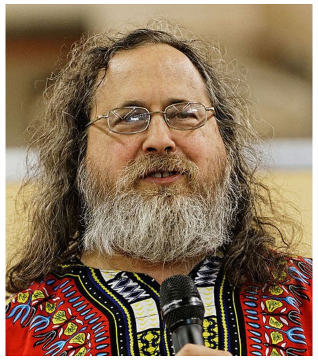
Brief history

In 1969 a team of Bell Lab researchers led by Thompson and Ritchie developed a new operating system that was named UNIX in 1970.



In 1985, Richard Stallman at MIT created Free Software Foundation (FSF). The dream was to create a “free” operating system. By 1990, he had almost everything except the kernel. This software stack is called GNU (GNU is Not Unix).



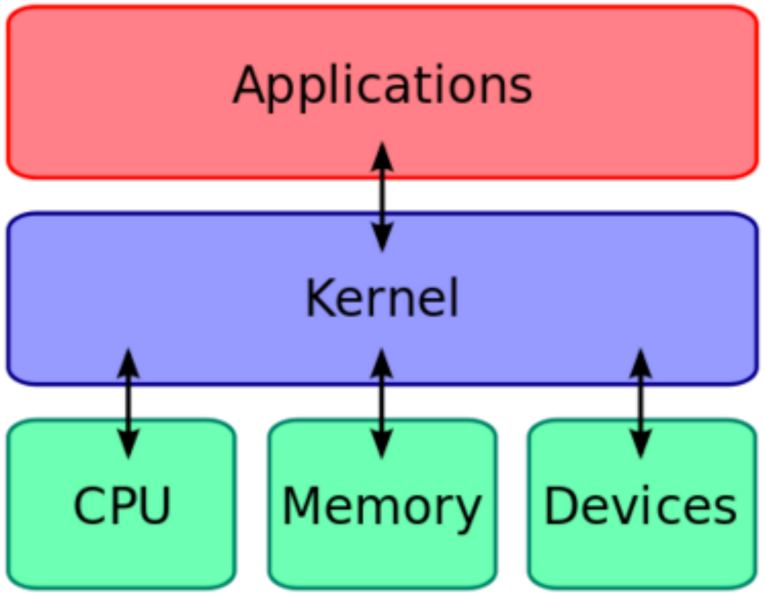
In 1991 Linus Torvalds developed Linux, a unix-like kernel, that was made free in 1992.

Another Unix like operating system is BSD which is included in OSX. Even on Windows has a Unix like system called CygWin.

Linux distribution

A Linux distribution includes

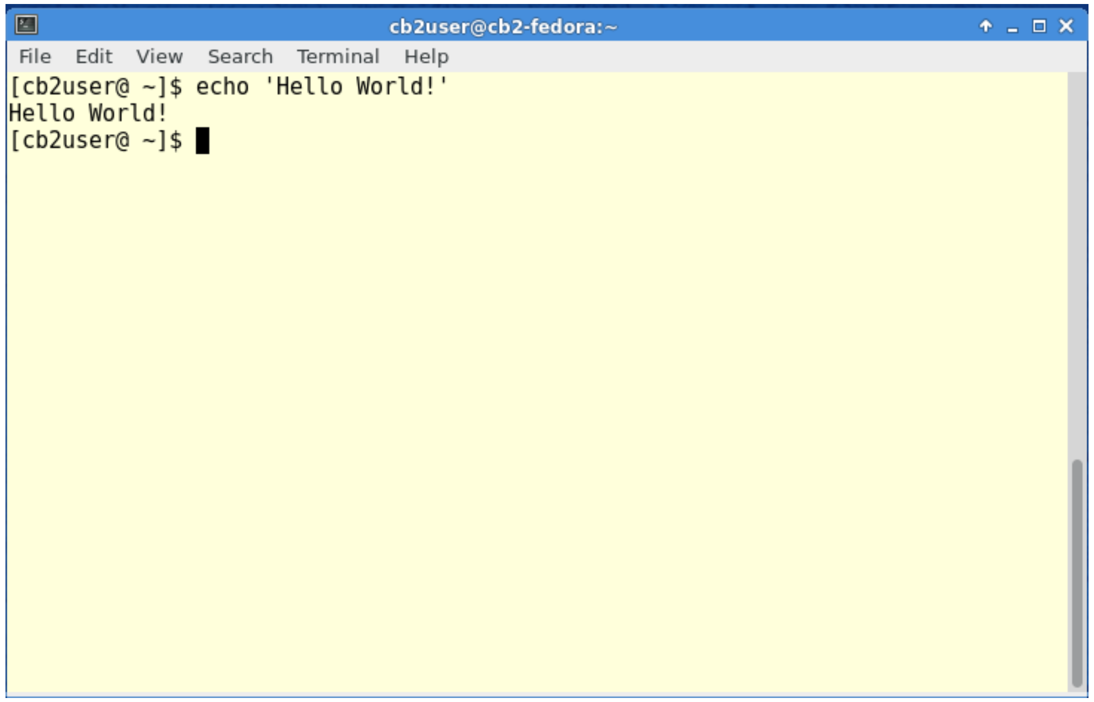
- The Kernel (Linux)
- An install system for the distribution
- Drivers
    - How the system can manage specific hardware
- A package manager
    - To install and update software
    - Usually different from one distribution to the other



More detailed lecture from Giuseppe Profiti
http://profiti.web.cs.unibo.it/res/linux-intro.pdf

Shell

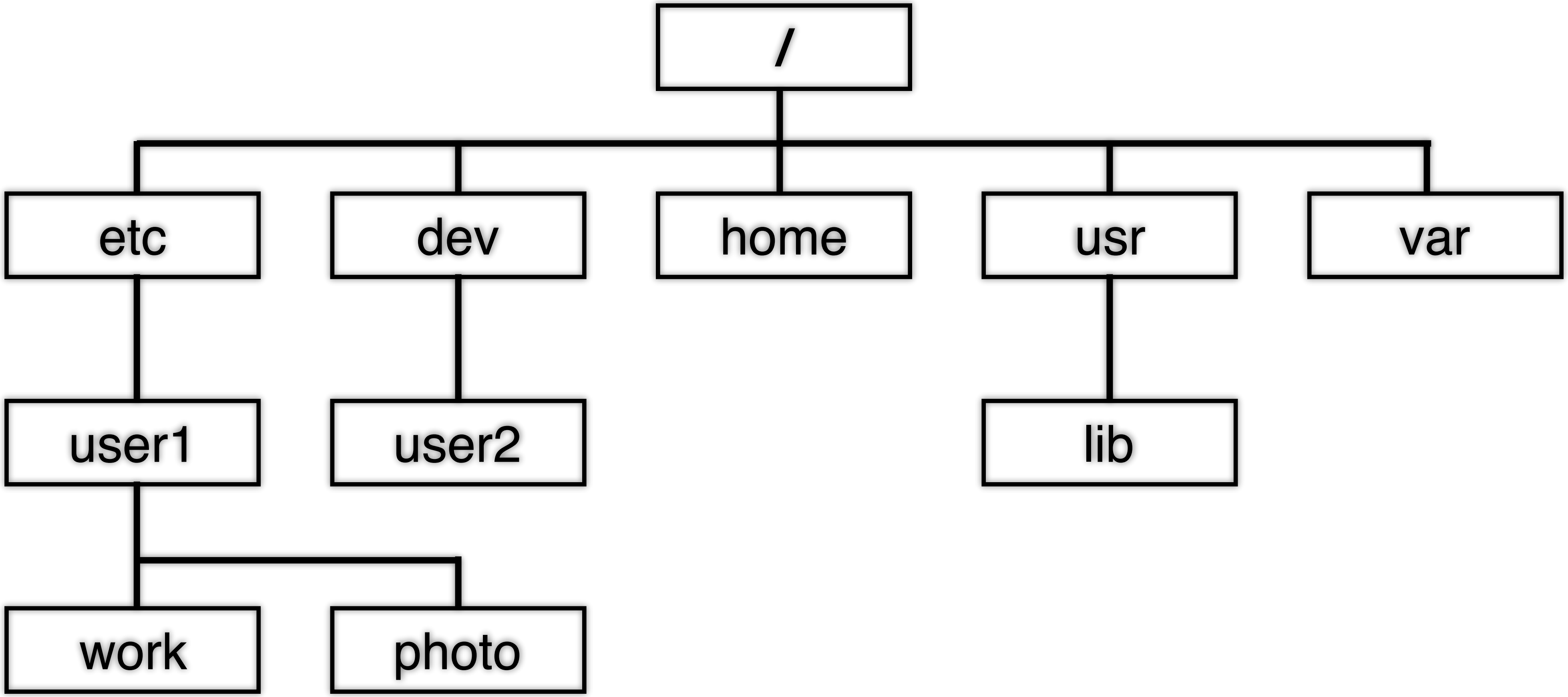
- It is the main interface with the system
- Can be used to:
  - Navigate the file system
  - Execute tools
  - Install software
  - Connect to other machines
  - Edit files
  - … everything the system can do
- Also called Console, or Terminal



```
[cb2user@ ~]$ echo 'Hello World!'
Hello World!
[cb2user@ ~]$ 
```

Filesystem

The filesystem has a hierarchical structure that allows to store files and directories



Basic Commands

- man commandname - will show you help about a particular command.
- ls dirname - shows a directory listing.
- cd dirname - changes directory
- mkdir dirname - creates dir
- cp path1 path2 - copies dir or files
- mv path1 path2 - renames or moves a file/dir.
- rm namefile - removes a file.

Note: rm -rf is a special command that will remove everything from the current directory without prompting.

If you accidentally execute this command in "/", it will try to wipe out everything from your computer.

Special Characters

The following characters have special meanings

- * - represent “one or more” characters
- ? - represents one character
- > - redirect the output to a file
- | (pipe) - redirect the output to the standard input (STDIN)
- 2> - redirect to standard error (STDERR)

To redirect the list of files and directories in your current location to the file names.txt

```
> ls > names.txt
```

Handling Files

- cat - dumps the content of the file to output.
- less or more - show an input page by page.
- wc - count the lines, words, and characters. head
- head - shows the first few lines of a file.
- tail - displays the last lines of the file.

The option “-n number_of_lines” for “head” and “tail” allows to specify the number of lines to shows. If you want to skip the first 2 lines of a file,

```
> tail -n+3 <filename>
```

File Path

The path indicates the location of a resource in the filesystem.

- pwd - current path
- "." - current directory.
- ".." - parent directory

Exercise

What is the absolute path of your home? Using a relative path, go up all the way to root and come back again in the same directory

Environment variables

An environment variable is defined in bash as follows:

```
> export foo=bar
```

To run a command (or program), the location of the program has to be in a particular environment variable called PATH. You can add to the existing $PATH by adding to it like this:

```
> export PATH=$PATH:/some_dir/of/my/choice
```

You may add line like this in your .bashrc or .bash_profile. You can also run a program by calling it by absolute path.

You can find the absolute path of a command by using “which command_name”.

File permissions

There are three kind of permissions: read, write, and execute. A file need to have executable permission in Linux to run.

You can change the permission of a file that you own by the command chmod.

You can check the permission of a file by “ls -l”. chmod is run like this:

```
> chmod a+wrx filename
```

Exercise

Change the permission of a file that you own to executable by everyone.

Important Commands (I)

- cut - extracts the columns from a text file. The default field separator is tab. To extract 2nd column for a tab-delimited text file

```
> cat foo.txt | cut -f 2
```

- sort - sort the line of a input in alphabetical order.

```
> cat foo.txt | sort
```

- uniq - Removes duplicate lines if the are consecutive. You have to use sort to use uniq correctly.

```
> cat foo.txt | sort | uniq
```

- wget - is a swiss-army-knife of web downloader. wget URL

Important Commands (II)

- grep - searches for a pattern in file or input.

```
> grep ‘string’ filename
```

- tr - “translates” one or more character in a string to another. Import option “-d string“ for deleting strings.

```
> echo 'emidio' | tr '[a-z]' '[A-Z]'
```

- find - searches files recursively going into a directory hierarchy

```
> find dirname -name filename
```

Exercise

Download the file of the human proteome from
ftp://ftp.uniprot.org/pub/databases/uniprot/current_release/knowledgebase/reference_proteomes/Eukaryota/UP000005640_9606.fasta.gz
using wget and find how many sequences are contained.

Compression and Archiving

The two most common compression programs are gzip and bzip2. Traditionally they take .gz and .bz2 extensions, respectively. If you just type gzip file, the compressed file will be automatically named file.gz and original file will be replaced.

```
> echo "Hello there." | gzip -c >hello.gz
  and unzip with
> gunzip hello.gz
```

To compress many files (including directories) you need to use “tar” first then use gzip/bzip2.

```
> tar -c Downloads/ | gzip -c >downloads.tar.gz
  or
> tar -czvf downloads.tar.gz Downloads/
```

For uncompress use the option “-xzvf”. For bzip2 “-czvf” is replaced with “-cvbf"

Program Compilation

There is a standard way to compile a C program in Linux. Almost all the software are distributed as .tar.gz files. These are source codes. You should compile and install the software like this:

```
> tar -xvzf foo.tar.gz
> cd foo
> ./configure
> make
> make install
```

The last install step may require you switch to “root”.

Exercise

HMMER is a software for sequence analysis using profile hidden Markov model. Download HMMER source code from http://selab.janelia.org/software/hmmer3/3.1b1/hmmer-3.1b1.tar.gz then install the software in your machine.

Problem Set

- Problem 1
  PFAM is a database of domains. It also provides pre-calculated domains for all proteomes. The current version can be found here ftp://ftp.sanger.ac.uk/pub/databases/Pfam/current_release/proteomes/.
  Each file is a proteome identified by its taxonomic ID. Human has the ID 9606.
  Each of these files is tab-delimited and the 6th column is the domain ID.
  Download the human proteome file using wget. After downloading write just a single line of bash to find how many domain types (unique domains) are there in human genome.

- Problem 2
  E. coli MG1655 is the standard reference strain of E. coli. The protein FASTA file for this strain can be downloaded from ftp://ftp.ncbi.nlm.nih.gov/genomes/Bacteria/Escherichia_coli_K_12_substr__MG1655_uid57779/NC_000913.faa.
  Using just bash commands can you find out what is the average length of protein in this strain?