

# Practical Bioinformatics

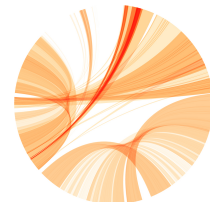
Basic Linux

Part 1

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# Why Linux?

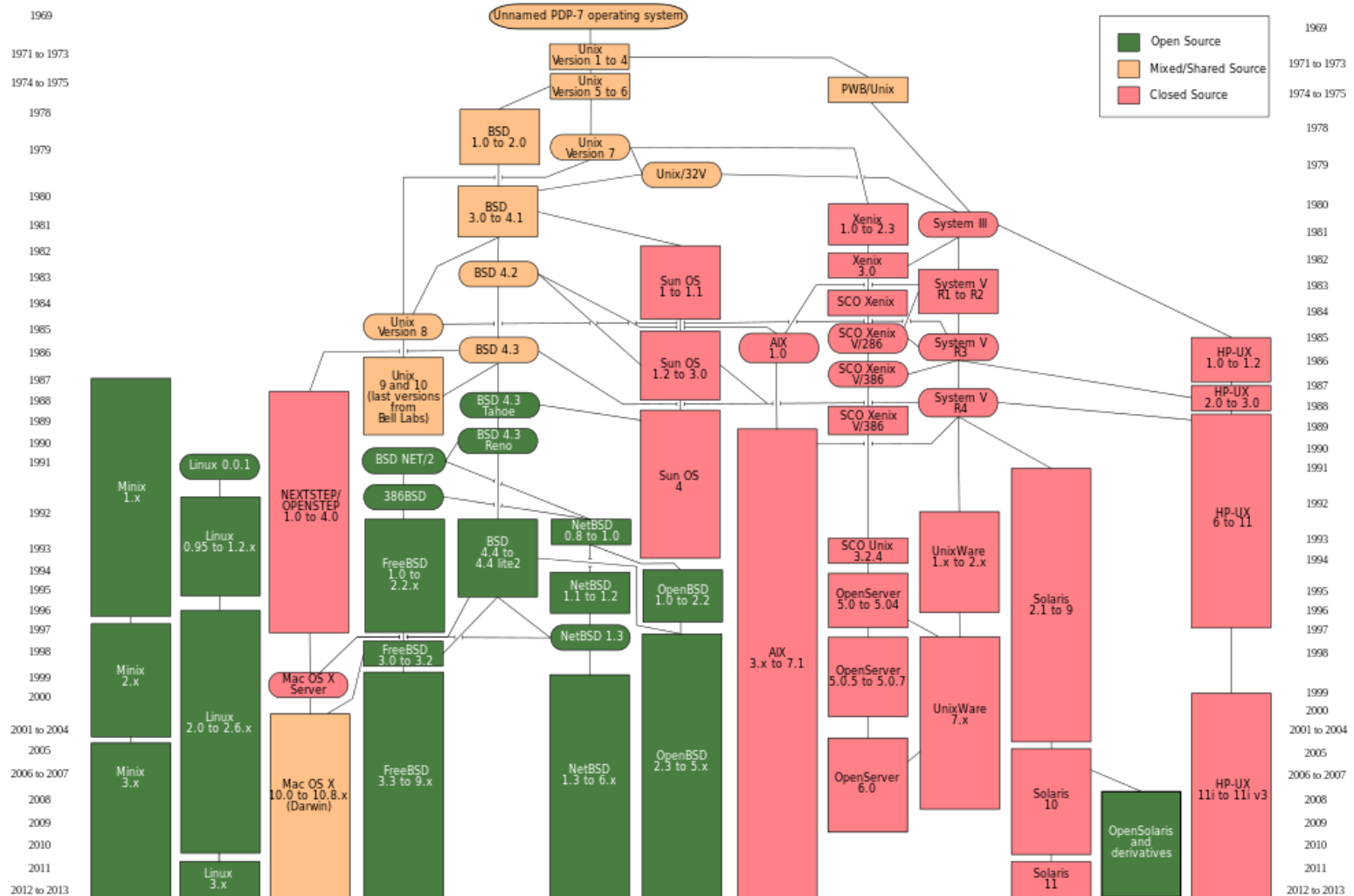
## **In Bioinformatics**

- Many bioinformatics and genomics tools are command-line only and are optimized to run on Linux.
- Very powerful with text files, even large (GBs)

## **In general**

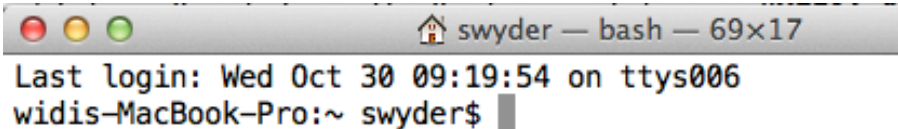
- Experienced Linux users can do more with less effort and much faster
- Multi-user
- Lots of control and customization possibilities
- 0\$
- ....

# History



# Why command line?

- to run bioinformatics software
- you can automate tasks more easily
- to interact with high-performance (high-memory) servers
- offers handy tools to work with text files

A screenshot of a macOS terminal window. The title bar at the top shows three colored window control buttons (red, yellow, green) on the left, a home icon followed by the text 'swyder — bash — 69x17' in the center, and a close button on the right. The main content area of the terminal displays the text 'Last login: Wed Oct 30 09:19:54 on ttys006' on the first line, and 'widis-MacBook-Pro:~ swyder\$' on the second line, with a small black cursor block at the end of the second line.

```
swyder — bash — 69x17
Last login: Wed Oct 30 09:19:54 on ttys006
widis-MacBook-Pro:~ swyder$
```

- The shell is an interactive interpreter: it reads commands, finds the corresponding programs, runs them, and displays output
- Today we use the **Bash shell** (default shell of most Linux distributions and Mac OS X)

# The prompt

Prompt

```
eiger-uzh:~ swyder$
```

Hostname

User

Normal user

```
eiger-uzh:~ swyder$
```

Current path  
(abbreviated)



# Commands

- The tools philosophy was to have small programs to accomplish a particular task instead of trying to develop large monolithic programs to do a large number of tasks.
- "Designed to operate together"  
To accomplish more complex tasks, tools can simply be connected together.
- The shell comprises hundreds of commands, but if you know 25 you can achieve many things
- Commands are abbreviations to type less (ls:list, cp:copy, mv:move)
- Common structure:  
**Command** -**Option(s)** **Parameter(s)**  
ls -l /home/swyder/tmp

# Setting options

Command -Option(s) Parameter(s)

ls -l

ls -l -r -h

ls -l -r -h

ls -rlh

ls --reverse --human-readable      long options !only GNU tools!

The order of options does not matter  
unless they override each other (e.g. sorting)

# Options, grep as an example

- `$ grep apple fruitlist.txt`  
apple  
pineapple
- `$ grep -w apple fruitlist.txt` (or `grep -x`)  
apple
- `$ grep apple *.txt`  
fruitlist.txt:apple  
fruitlist.txt:pineapple  
recipeFruitSalad.txt:1 pineapple  
recipePinaColada.txt:2oz fresh pineapple juice
- `$ grep -v apple fruitlist.txt`  
banana  
pear  
peach
- `$ grep apple fruitlist.txt recipeFruitSalad.txt`  
fruitlist.txt:apple  
fruitlist.txt:pineapple  
recipeFruitSalad.txt:1 pineapple

Also options to color, to show context, search with compl patterns



# Getting help

**man** <command>

man cp

CP(1) BSD General Commands Manual CP(1)

NAME

cp -- copy files

SYNOPSIS

cp [-R [-H | -L | -P]] [-fi | -n] [-apvX] source\_file target\_file  
cp [-R [-H | -L | -P]] [-fi | -n] [-apvX] source\_file ... target\_directory

DESCRIPTION

In the first synopsis form, the cp utility copies the contents of the source\_file to the target\_file. In the second synopsis form, the contents of each named source\_file is copied to the destination target\_directory. The name of the source\_file must not be the same as the name of the target\_directory. If cp detects an attempt to copy a file to itself, the copy will fail.

The following options are available:

- a Same as -pPR options. Preserves structure and attributes of files but not directory structure.
- f If the destination file cannot be opened, remove it and create a new file, without preserving permissions. (The -f option overrides any previous -n option.)

...

space: scroll down a page

b: scroll up

q: quit man

<command> **--help**

cp --help

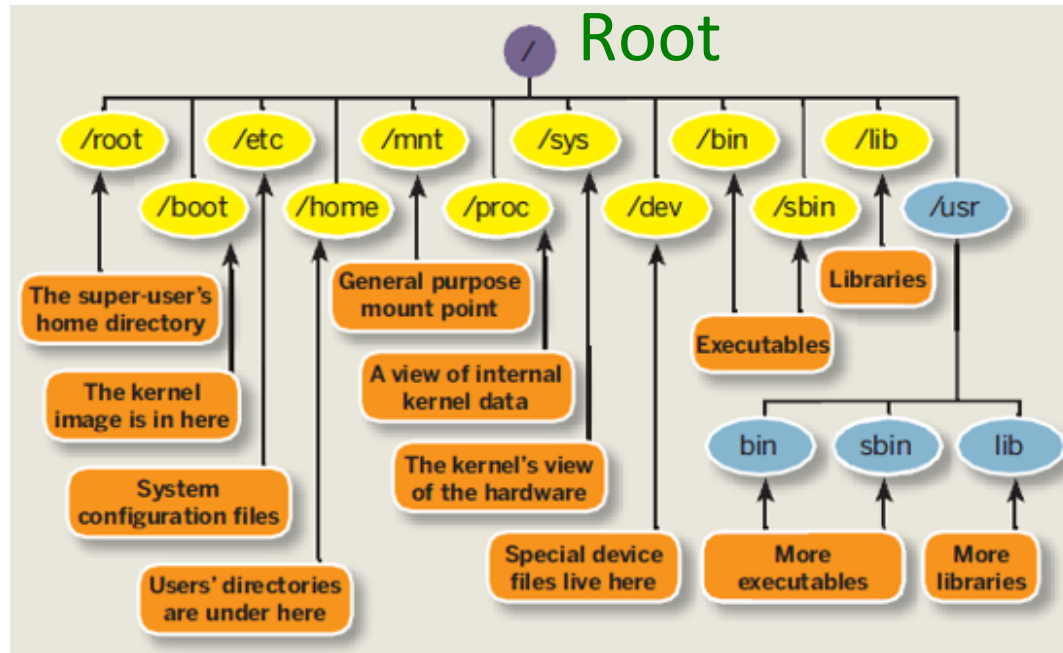
a less verbose help  
(not working on Mac OS)

**The web**

<http://linuxconfig.org/linux-commands>

# **Working with files and directories**

# Directory structure



<http://www.tuxradar.com/>

- Everything the system uses is located somewhere under root '/'.
- Every user has his home directory, e.g. /home/swyder
- Do your work in your home directory
- The system folders can only be modified by the administrator

# File and Directory names

- Upper- and lower-case matter
- up to 256 characters long
- Every character except / is allowed. But by convention special characters like \$äéÜ are not used.
- Don't use white spaces. Use underscores (\_), hashes (-) and dots (.) to separate words  
Oct2013\_RNAseq  
~~Oct2013\RNAseq~~

# Main commands

Command	Meaning
ls	Content of current directory
cd <i>dir_name</i>	Change to directory
cd	Change to home directory
cd ~	Change to home directory
mkdir	Make a directory
cp	Copy a file/directory
rm	Delete a file/directory

# **Working with text files**

# Main text commands

UNIX has an extensive toolkit for text extraction, reporting and manipulation

Task	Commands
Show	<b>less</b> , more, head, tail, cat
Search/Extract	<b>grep</b> , <b>cut</b> , awk, uniq
Manipulate	<b>sort</b> , tr, sed, join, paste
Replace	<b>tr</b> , sed
Count	<b>wc</b> , <b>uniq -c</b>
Compare	comm, diff



# Piping



# Piping

## Philosophy

"filters": simple programs which only do 1 thing  
the output of a filter is the input of the next

```
grep "mRNA" test.gff | less
```

```
grep -w "gene" test.gff | cut -f 1 | sort | uniq -c
```

# Redirection

> Writing the output to a file

>> Appending the output to a file

```
ls > output.txt
```

```
grep -w "gene" test.gff | cut -f 1 | sort | uniq -c > output.txt
```

```
ls >> output.txt
```

< Reading from file

```
wc < hello.txt > hello_counts.txt
```

# **Differences in the Shell**

## **Linux - Mac**

# Differences Linux - Mac

- Mac line breaks are '\r\n' (and Windows: '\r') instead of the standard Linux '\n'  
When working in the command line make sure the files have the right format  
`perl -pi -e 's/\r\n?/\n/g' <filename>`  
which you could alias and put in the .bashrc
- Mac has no GNU tools by default  
less options – less powerful  
for installation install homebrew  
then: `brew install coreutils`  
All GNU commands are then installed with the prefix 'g': `gls`, `gcp`, `gsed`,...
- Mac has non-standard folder structure  
e.g. home (~) is `/Users/swyder`

# What next?

## **Part 2 of the tutorial**

- Running scripts
- Permissions
- Installing software (rpm, compiling)
- File/Dir Compression&Extraction
- Automatizing tasks (scripting)
- Connecting with Unix/Linux servers
- (Search Patterns, Regular Expressions)
- Backup (rsync)

# Sources & Links

## Acknowledgements

- Some exercises are from von Mering group (IMLS, UZH)

## Material

- SIB course <http://edu.isb-sib.ch/course/view.php?id=41>
- O'reilly Books <http://oreilly.com/linux/>
- Video tutorials (~100 min) <http://software-carpentry.org/v4/shell/index.html>
- Cheatsheet <http://www.embnet.org/sites/default/files/quickguides/guideUNIX.pdf>

# Intro

- Unix has been developed in the late 60's
- Linux (specifically:the Linux kernel) was created in 1991 by Linus Torvalds. Together with the GNU tools and libraries, this established a freely available Unix on regular PC hardware



- For the sake of simplicity I use Linux even when Unix would be more appropriate from now on
- Over time, graphical user interfaces have been added making Linux easier to use.

# Many Linux Distributions



Ubuntu, Debian, CentOS, RedHat, Fedora, Slackware, SuSE, Darwin  
Main differences are the graphical system (KDE vs Gnome, support durance