Discovering the linux world through jupyter

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The objectives

Run your own analysis using jupyter book and Linux !

After this course, you will able to :

- Know the main Linux commands
- Move into the Linux file tree : `pwd` , `ls` , `cd` , mkdir`
- Work with text files: `head` , `tail` , `wc` , `grep`
- Chain and combine commands
- Run programs from the command line

What is Linux ?

An operating system well known for :

- its security and stability
- its frequent updates
- its (no) fees and openSource (mostly) softwares

Created in 1991 by Linus Torvalds

Linux source code **opensource** and **free** : copy, modify, redistribute

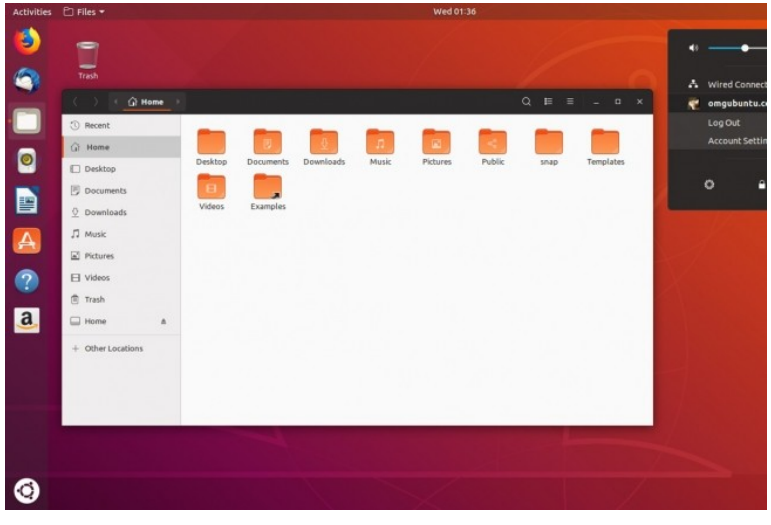
What is Linux ?

- ***Robust et multi-plateform OS*** : computer, server, android…
- ***Multi-users system*** : Several users can work simultaneously
- ***Multi-tasking system (processes/programs)*** Every user can run several programs at the same time

How to use Linux ?

- 2 classical ways :

  Graphical User Interface



How to use Linux ?

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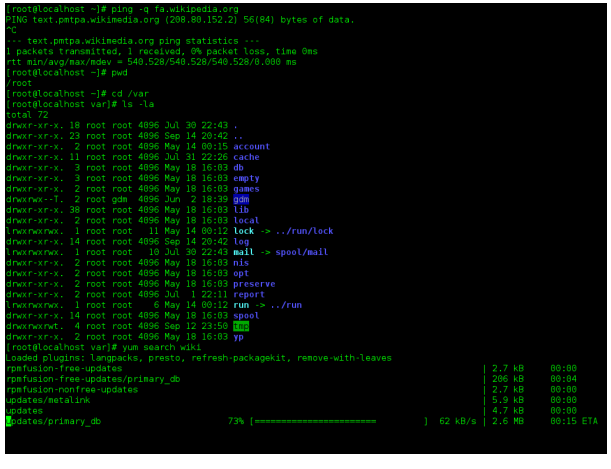
  Graphical User Interface

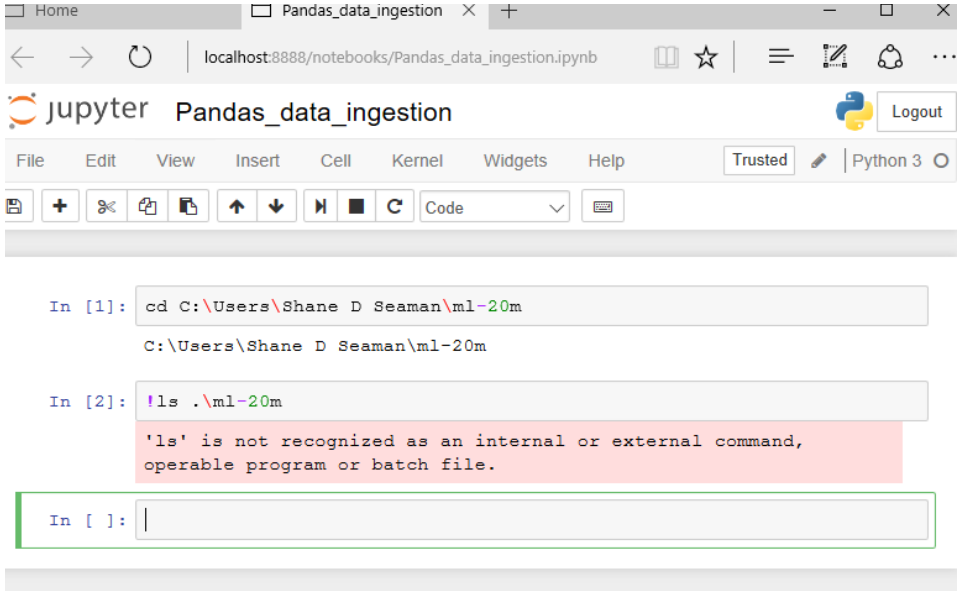
  Command-Line Interface through a terminal

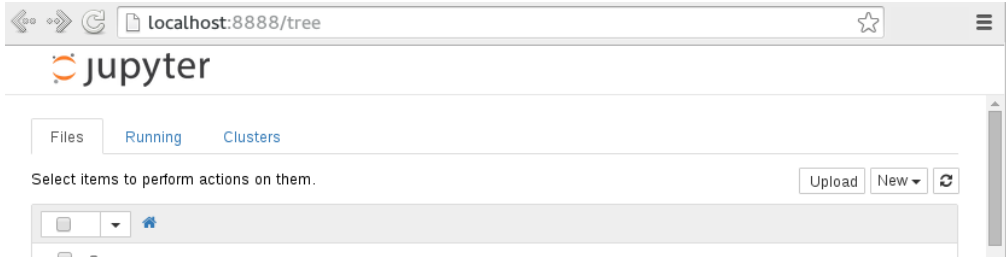


How to use Linux ?

- a new and alternative ways :

jupyter book





figures
Tutorial_Evoked_Responses_In_The_Visual_Cortex.ipynb
anatomy_of_a_region_simulation.ipynb
anatomy_of_a_surface_simulation.ipynb
connectivity_normalisation_modes.ipynb
corrcoeff_analyse_view_region.ipynb
display_sensors_locations.ipynb
display_subject_dataset.ipynb
display_surface_local_connectivity.ipynb

Why using Linux ?

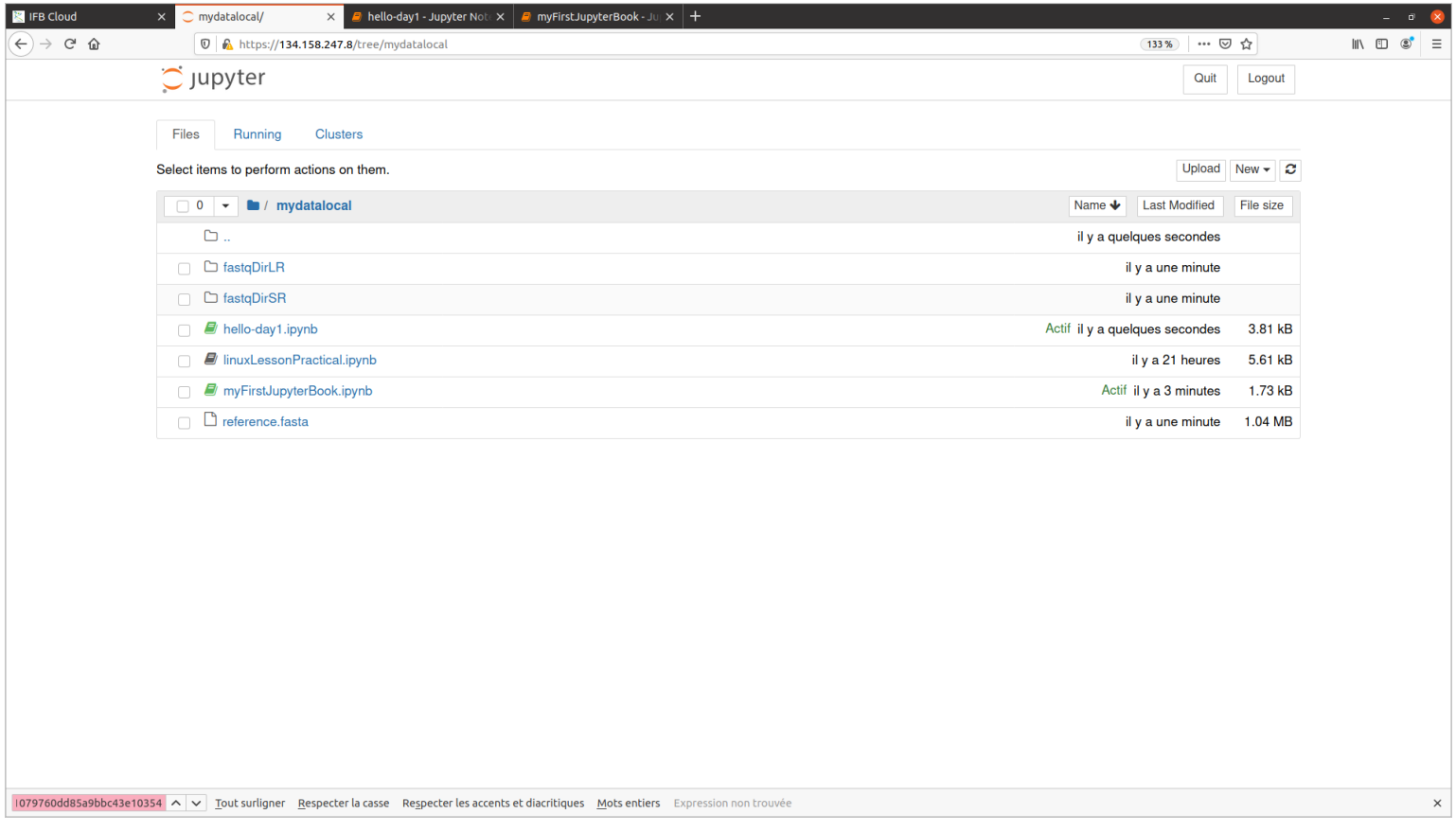
- Numerous fast and powerful programs
- Easy to link commands and programs (workflow)
- Numerous bioinformatics softwares available
- 90% of servers on Linux

Why using Linux ?

Need to practice!!!

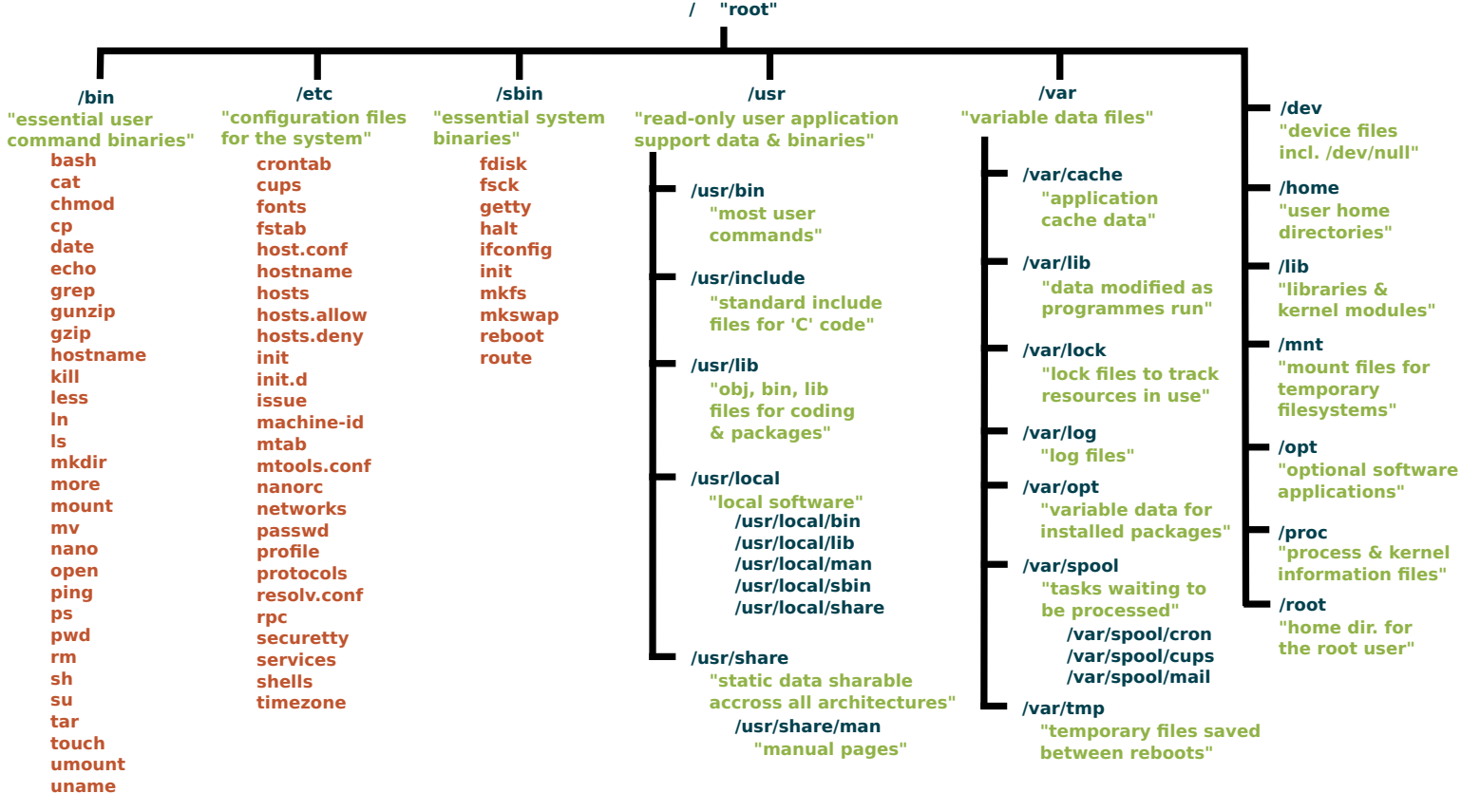
Important investissments to have good results !!!

Let’s go through jupyter



First steps on Linux

Commands for *moving around the file system* and *manipulating files/folders*



Linux command syntax

command [-options] [arguments]

Your first command *pwd*

pwd print the name of the current directory (the full path)

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In [ ]:
```
pwd
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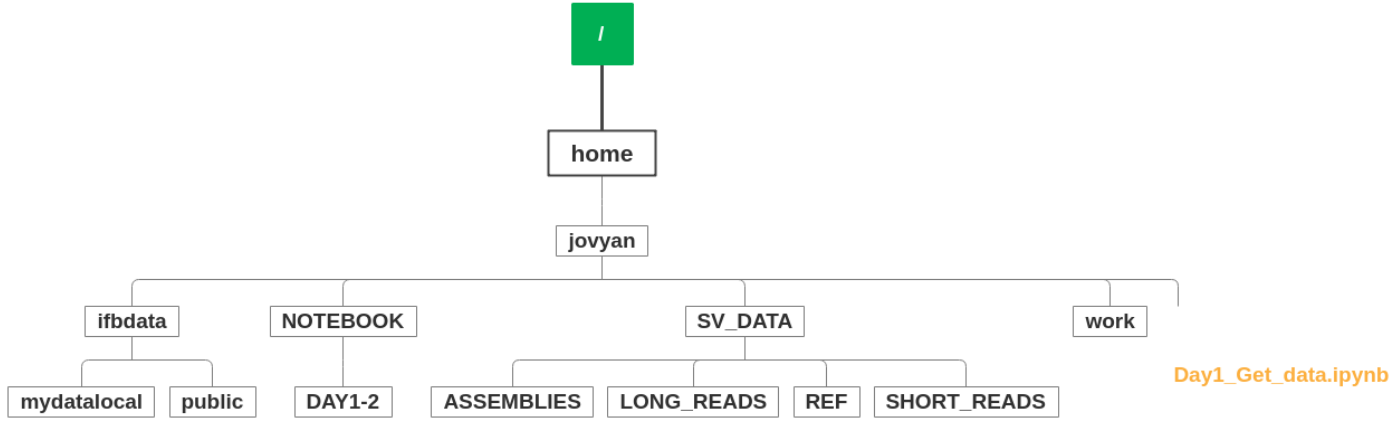


2nd command *ls*

- without argument : list all the files in the current directory (by default)

2nd command */s*

- without argument : list all the files in the current directory (by default)

In [ ]:
```
ls
```

ls + option -l

ls -l : *list files with more information about each file* (long)

ls + option -l

ls -l : *list files with more information about each file* (long)

In [ ]:
```
ls -l
```

2nd command + argument

/s

with directory path as argument

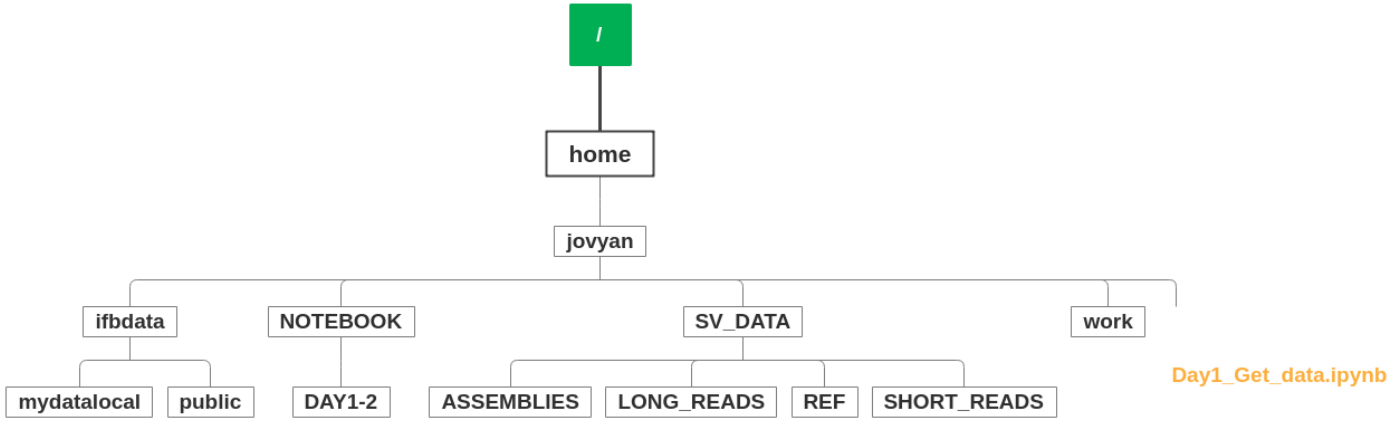
2nd command + argument

ls

with directory path as argument

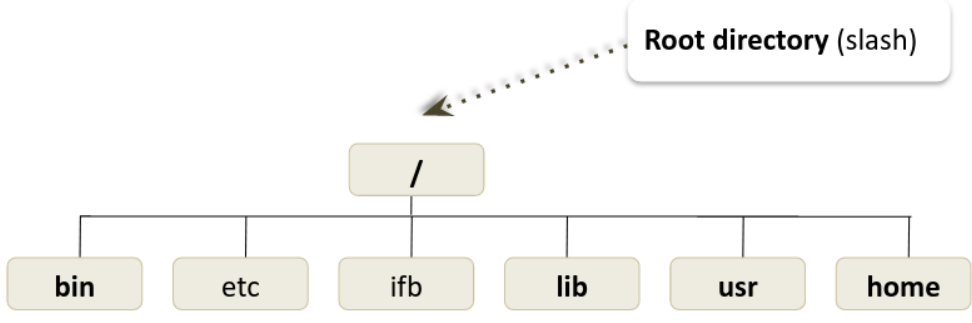
In [ ]:
```
ls /home/jovyan/SV_DATA/REF
```

- What is a file tree for Linux?

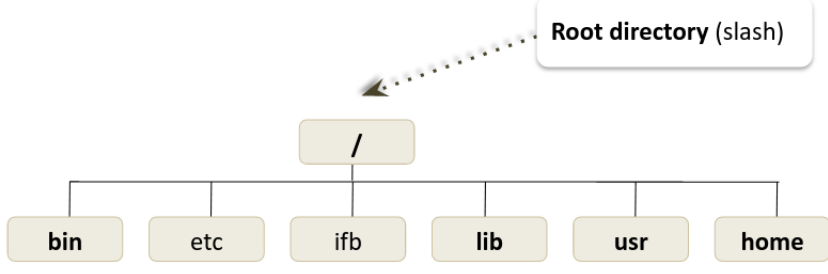


The file tree - file system

- Directory structure starts at the root directory called “/” (slash)



The file tree - Main directories



/bin	**Main commands, shell, programs**
/usr, /opt	**Applications and user librairies**
/usr/bin	**Other commands**
/home	**User directory (one per user, name= login)**

Path of a file

- Path = location to a file/directory in the file system
- On linux filetree, you can use absolute or relative path
- What is the difference between the absolute and relative path ?

What is an absolute path of a file or a directory ?

- Path = location to a file/directory in the file system

ABSOLUTE
Complete path of a file starting from the root directory /
starts always with /
always good wherever user is working

What is a relative path of a file or a directory ?

- Path = location to a file/directory in the file system

RELATIVE
Path related to the present working directory (where the user is working)
Never starts with /
Depends on where the user is working

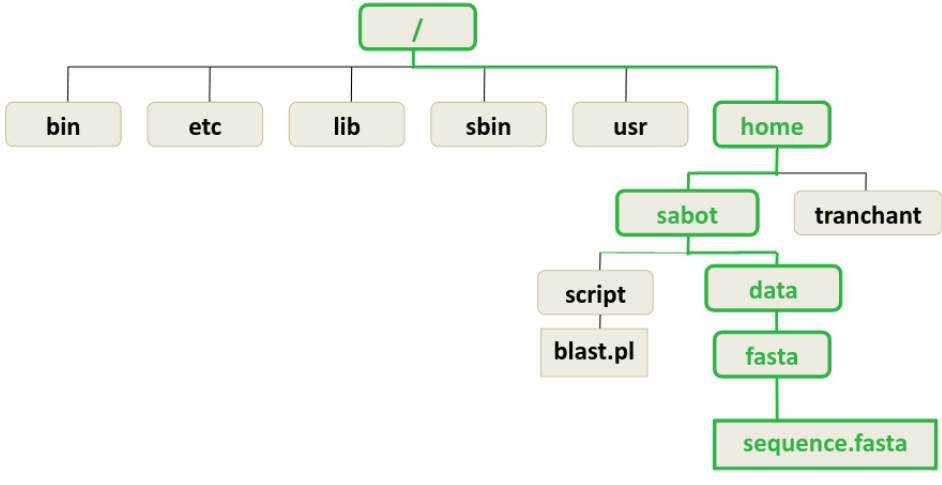
In brief

- Path = location to a file/directory in the file system

ABSOLUTE	**RELATIVE**
Complete path of a file starting from the root directory /	Path related to the present working directory (where the user is working)
starts always with /	Never starts with /
always good wherever user is working	Depends on where the user is working

Absolute Path

- Always start with / (root directory)
- Always works wherever user is working on the server or vm



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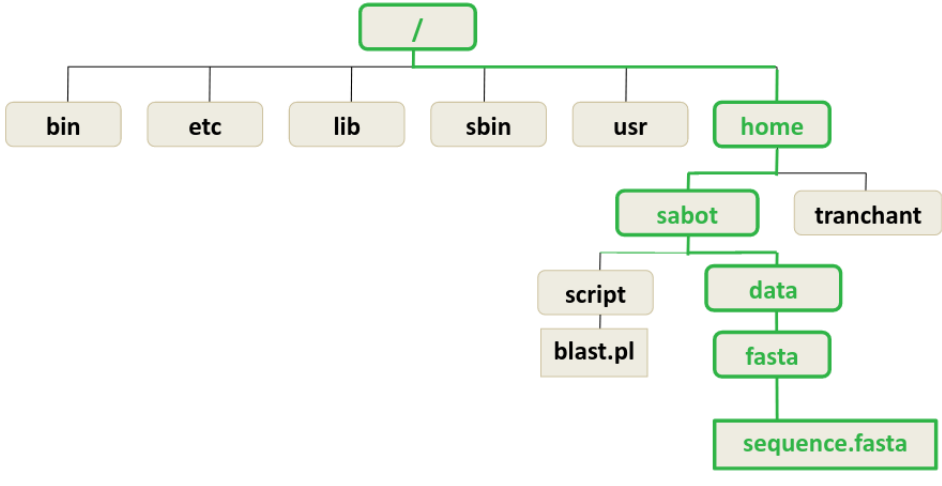

- What is the absolute path of the file sequence.fasta ?

Absolute Path

- Always start with / (root directory)
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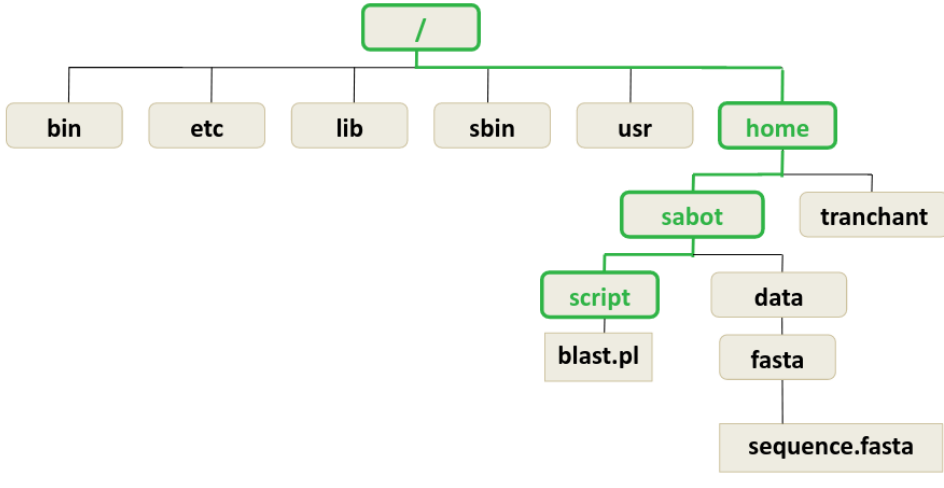

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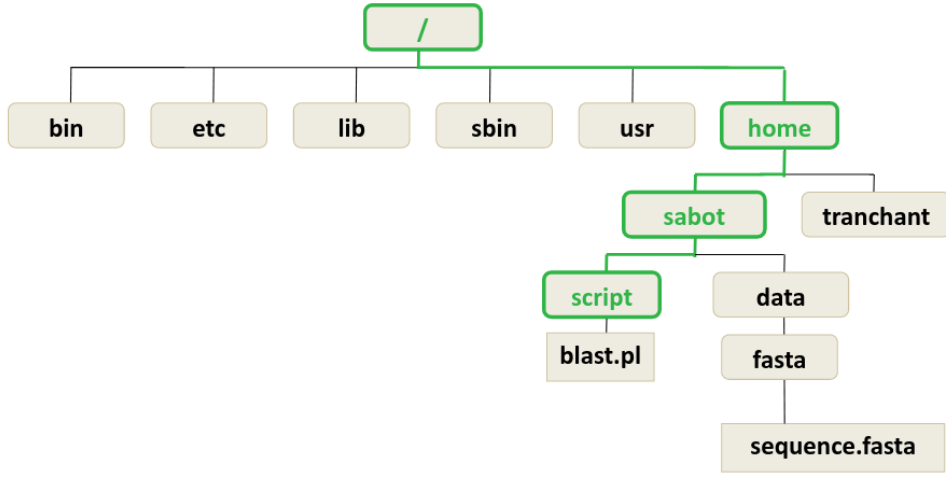
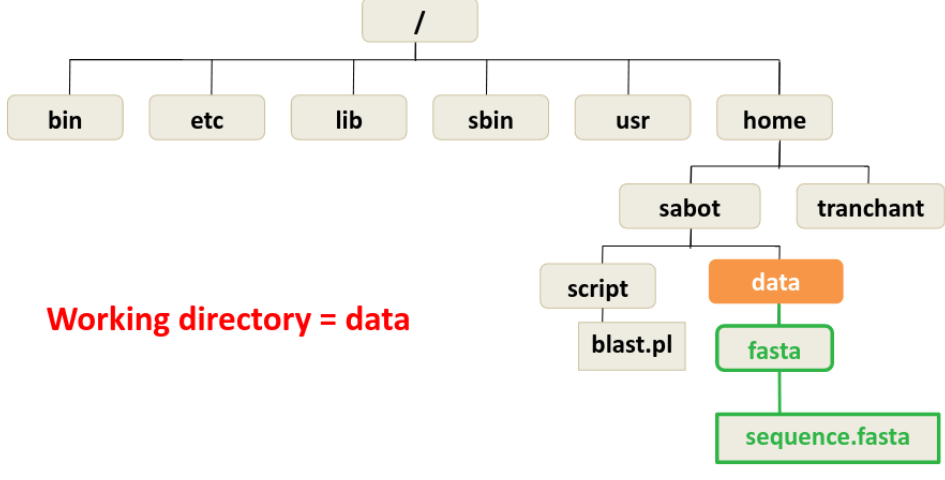


- What is the absolute path of the directory script ?

Relative Path

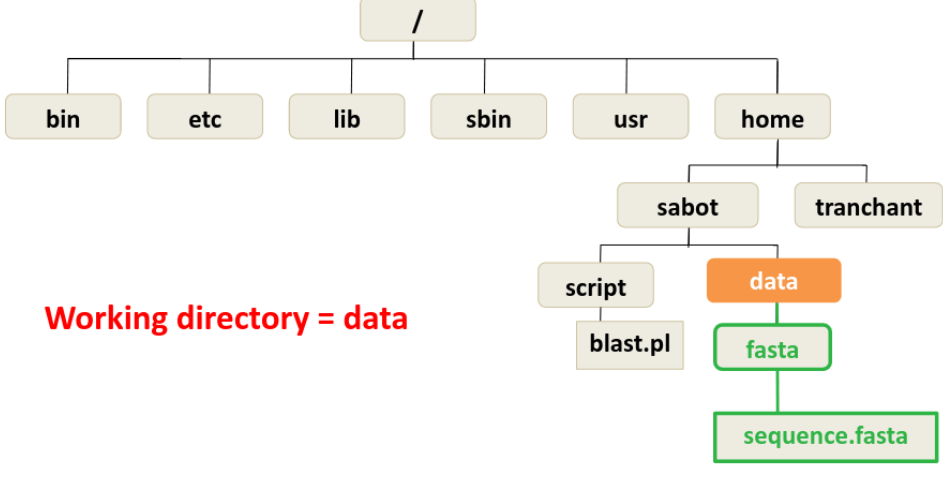
- Path related to the present working directory
- Never starts with /



Working directory = data

Relative Path

- Path related to the present working directory
- Never starts with /

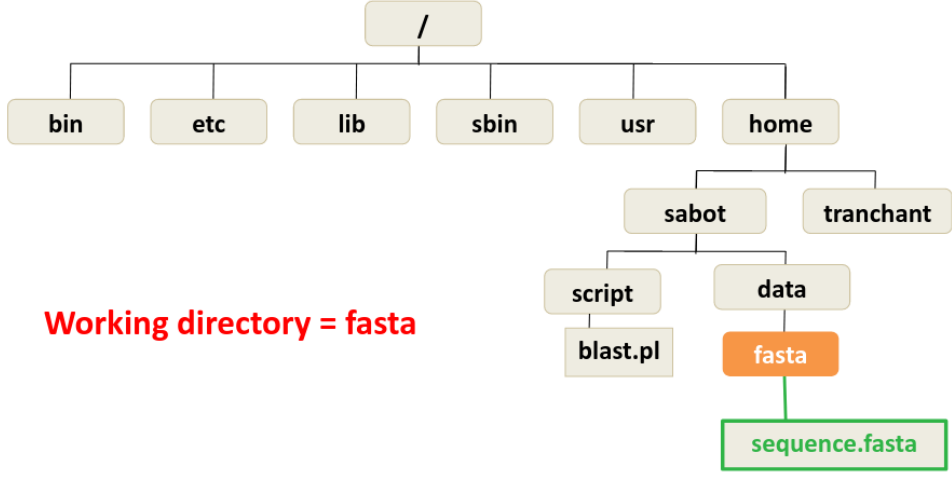


Working directory = data

- What is the relative path of the file sequence.fasta ?

Relative Path

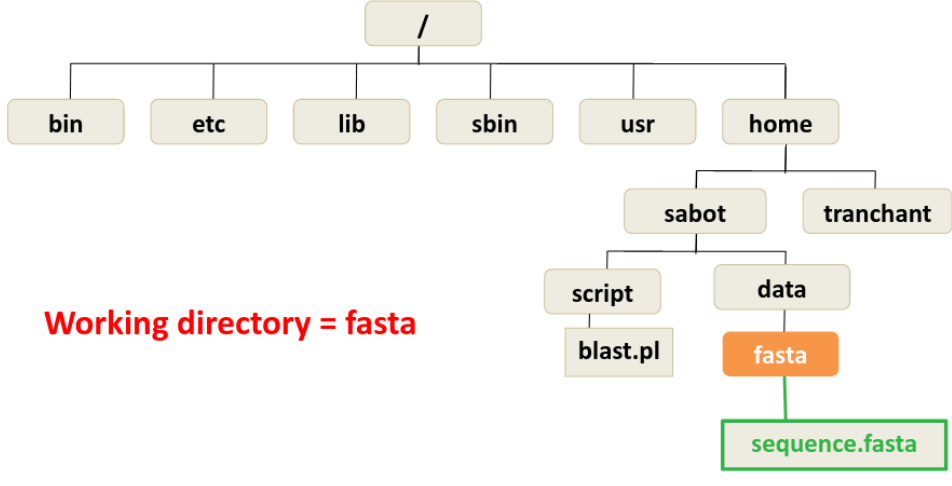
- Path related to the present working directory
- Never starts with /



Working directory = fasta

Relative Path

- Path related to the present working directory
- Never starts with /



Working directory = fasta

- What is the relative path of the directory fasta ?

Rules for naming file and directory names

- linux is case sensitive

```
  Sequence.fasta    SEQUENCE.fasta
sequence.fasta
```

Rules for naming file and directory names

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- Only ROMAN letters, numbers and _ -

Rules for naming file and directory names

- linux is case sensitive
- Only ROMAN letters, numbers and _ -
- No space, accent or special symbol

```
  & ~ # ”  ' { ( [ | ` \ ^ @ ) ] } $ * % ! / ;
, ?
```

Rules for naming file and directory names

- linux is case sensitive
- Only ROMAN letters, numbers and _ -
- No space, accent or special symbol
- No need to use filename extension (.txt), just to improve readability of filenames.

A few Basic Commands

pwd	Display the full path of the current directory
ls	List all files/directories
ls -l	Display all files (Long listing)

A few Basic Commands

How to get help about one command

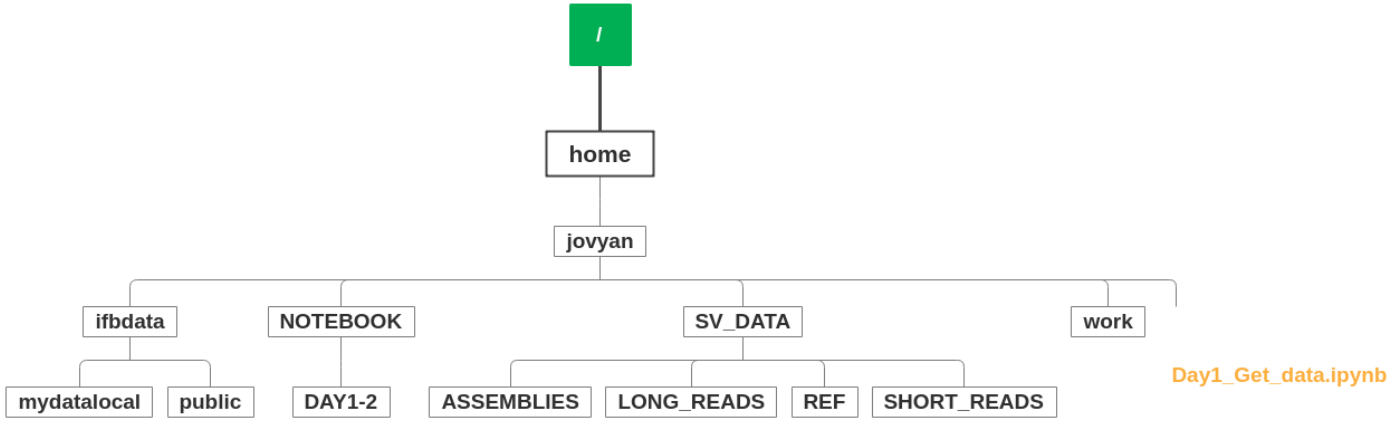
- with the ’option --help ou -h
- with the command man

Command *cd*

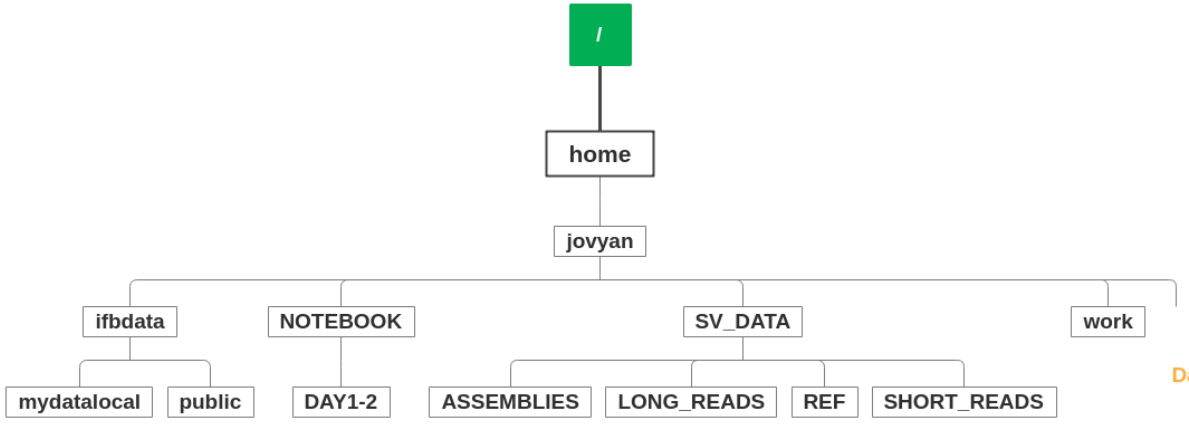
- Move from the current directory into a new directory

cd DIRECTORY NAME (absolute or relative path)

- Move into the REF directory (absolute path)

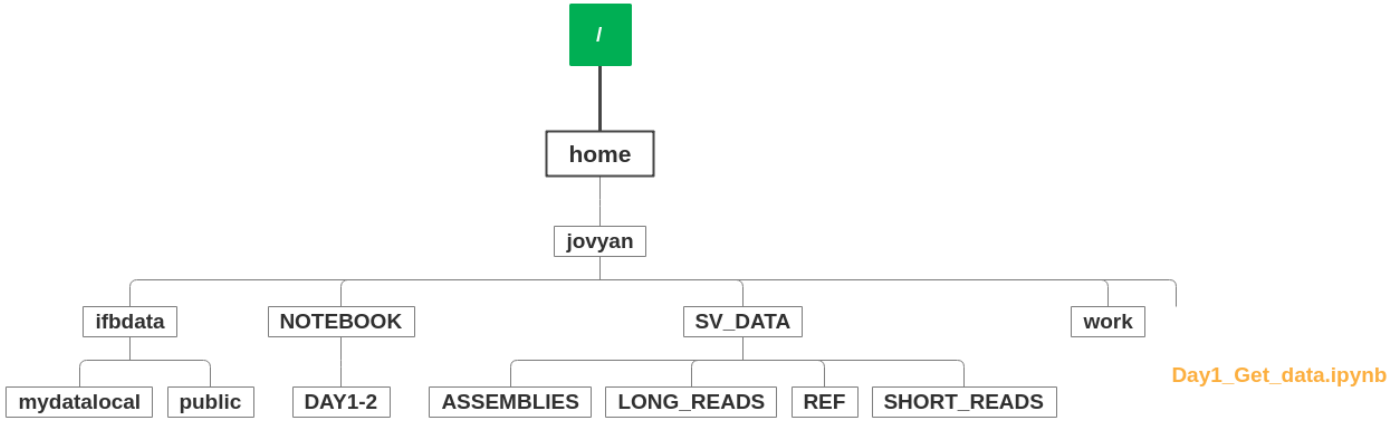


- Move into the SV_DATA directory (absolute path)



Day1_Get_data.ipynb

- Move into the SHORT_READS directory (relative path)



Some Commands

pwd	Display the full path of the current directory
ls	List all files/directories
cd DIR_NAME	Change the working directory
rm nom_fichier	Remove a directory
cp file1 file2	Make a copy of file1 and calls it file2
cp FILE_NAME DIR_NAME	Copy the file FILE_NAME in the directory DIR_NAME
cp FILE DIR/NEW_FILE	Mix of 2

Commands for displaying text files and searching word

command cat

- `cat nom_fichier` : Displays the content of a file on the screen

(Don’t use it with big files!!)

command cat

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(Don’t use it with big files!!)

In [ ]:
```
cat _PUT_THE_CORRECT_PATH_TO_ASSEMBLIES/assembly-stats.txt_
```

command wc

- `wc -l` : Displays the nomber of lines in a file

command wc

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In [ ]:
```
wc -l PUT_THE_CORRECT_PATH_TO_REF/GCA_002220235.1_ASM222023v1_genomic.gf
```

command head

- `head nom_fichier` : writes the first ten lines of a file to the screen

command head

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In [ ]:
```
head PUT_THE_CORRECT_PATH_TO_REF/GCA_002220235.1_ASM222023v1_genomic.gff
```

command head

- `head nom_fichier` : writes the first ten lines of a file to the screen

In [ ]:
```
head PUT_THE_CORRECT_PATH_TO_REF/GCA_002220235.1_ASM222023v1_genomic.gf
```

In [ ]:
```
head -n 20 PUT_THE_CORRECT_PATH_TO_REF/GCA_002220235.1_ASM222023v1_genom
```

command tail

- `tail nom_fichier` : writes the last ten lines of a file to the screen

command tail

- `tail nom_fichier` : writes the last ten lines of a file to the screen

In [ ]:
```
tail PUT_THE_CORRECT_PATH_TO_REF/GCA_002220235.1_ASM222023v1_genomic.gf
```