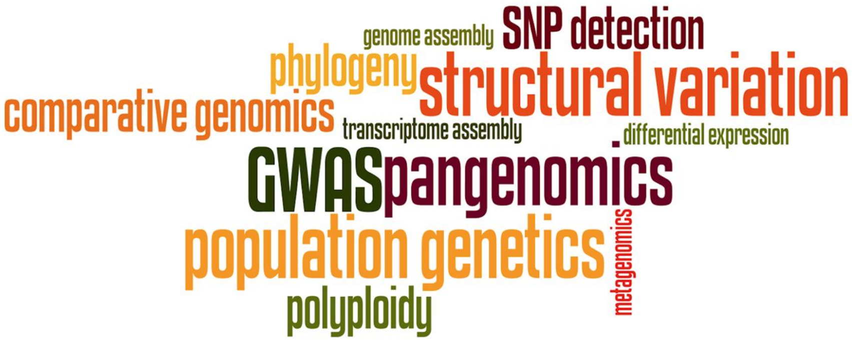
South Green
bioinformatics platform

Trainings 2022

SouthGreen

bioinformatics platform

Bioinformatics platform dedicated to the genetics and genomics of tropical and Mediterranean plants and their pathogens




Rice

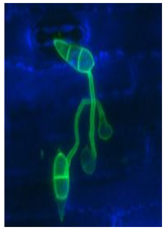

Banana


Palm


Sorghum


Coffee


Cassava


Magnaporthe

www.southgreen.fr

South Green
bioinformatics platform

Charte

diade

Larmande Pierre
Orjuela-Bouniol Julie
Sabot François
Tando Ndomassi
Tranchant-Dubreuil Christine

PHIM

Comte Aurore
Dereeper Alexis
Ravel Sébastien

agap

Bocs Stephanie
Boizet Alice
De Lamotte Fredéric
Droc Gaetan
Dufayard Jean-François
Hamelin Chantal
Martin Guillaume
Pitollat Bertrand
Ruiz Manuel
Sarah Gautier
Summo Marilyne

Bioversity International

Rouard Mathieu
Guignon Valentin
Catherine Breton

intertryp

Sempere Guilhem

Bioversity International

cirad

IRD
Institut de Recherche pour le Développement
FRANCE

INRA
SCIENCE & IMPACT

South Green
bioinformatics platform

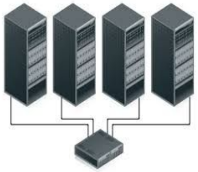
Workflow manager

TOGGLe
Toolbox for generic NGS analyses

SNAKEMAKE

Galaxy

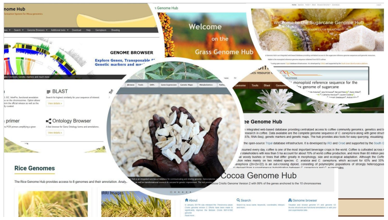
HPC and trainings….



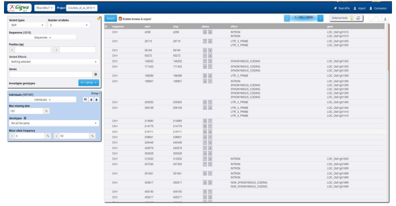
IRD
Institut de Recherche pour le Développement
FRANCE

cirad

Genome Hubs & Information System

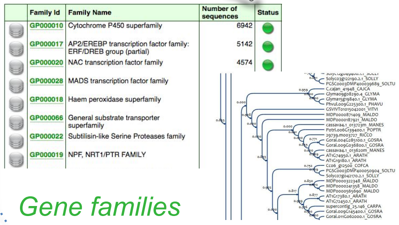


Gigwa



SNPs and Indels

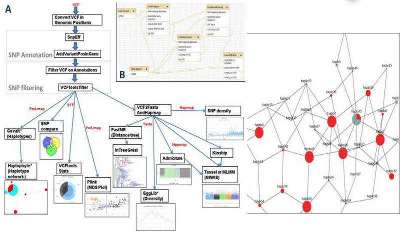
GreenPhyl



	Family Id	Family Name	Number of sequences	Status
	GP000010	Cytochrome P450 superfamily	6942	●
	GP000017	AP2/EREBP transcription factor family: ERF/DREB group (partial)	5142	●
	GP000020	NAC transcription factor family	4574	●
	GP000028	MADS transcription factor family		
	GP000018	Haem peroxidase superfamily		
	GP000066	General substrate transporter superfamily		
	GP000022	Subtilisin-like Serine Proteases family		
	GP000019	NPF, NRT1/PTR FAMILY		

Gene families

SNiPlay



https://github.com/SouthGreenPlatform

@green_bioinfo

The South Green portal: a comprehensive resource for tropical and Mediterranean crop genomics, Current Plant Biology, 2016

Tous à **20%** sauf NT

PHIM	PHIM	MiVEGEC TransVIH MI	diade	diade	diade
AURORE COMTE	ALEXIS DEREEPER	BRUNO GRANOUILLAC	JULIE ORJUELA	NDOMASSI TANDO	CHRISTINE TRANCHANT
IE bioinfo	IE bioinfo	IE systèmes d'information	IE bioinfo	IE systèmes	IR bioinfo

EURO-QUALITY SYSTEM
ISO 9001

diade
MiVEGEC
PHIM Plant Health Institute Montpellier
TransVIHMI

South Green bioinformatics platform

Formations 2022 Montpellier

4-5 Avril
Guide de survie à linux
Agropolis, salle Badiane

19-20 Avril
Linux avancé
Agropolis, salle Badiane

18-19 Mai
Utilisation avancée d'un cluster de calcul
IRD, amphi capmeditrop

30 Mai - 2 Juin
Python
Agropolis, salle Badiane

7 Juin ?
Initiation à l'analyse de données RNAseq
Agropolis, salle Badiane

14 Juin ?
Génomique bactérienne comparative
Agropolis, salle Badiane

27 et 28 Juin ?
30 Juin et 1er Juillet
Analyse de variants à partir de short and long reads
Agropolis, salle Badiane

Métagénomique

agap
Bioversity International
intertryp
diade
PHIM
MiVEGEC
TransVIH MI

South Green
bioinformatics platform

Trainings 2022

- **South Green Trainings** :

  https://southgreenplatform.github.io/trainings/

- Slides & Practices : Linux For Dummies

- Working environment : Softwares to install

ABiMS agap ASTRE Bioversity International diade PHIM intertryp MiVEGEC UMR QualiSud

South Green
bioinformatics platform

Survival Guide to Linux

www.southgreen.fr

https://southgreenplatform.github.io/trainings

Bioversity International
cirad
INRA SCIENCE & IMPACT
IRD Institut de Recherche pour le Développement FRANCE
Montpellier SupAgro

Learning objectives

The objectif!

Run your own analysis using Linux !

After this course, you will be able to :

- Know the main Linux commands
- Move into the Linux file tree : ***pwd***, ***ls***, ***cd***, ***mkdir*** etc.
- Connect to a Linux server and transfer data : ***ssh***, ***wget***
- Work with text files: ***head***, ***tail***, ***sort***, ***cut***, ***wc***, ***grep…***
- Chain and combine commands
- Run programs from the command line

Introduction

What is Linux?

- 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***

- Based on Unix (1969)

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

What is Linux?

- **Robust et multi-plateform OS**

  (computer, server, android….)

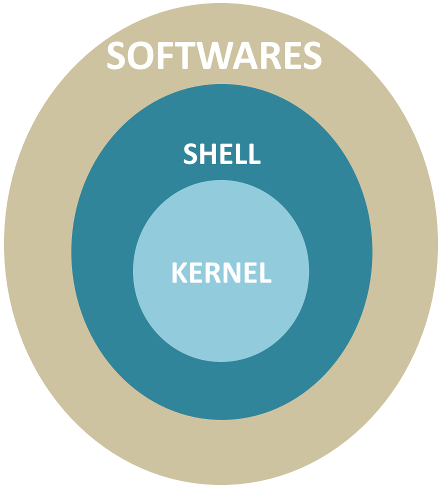
- **Multi-users system**

  Several users can work simultaneously

- **Multi-tasking system (processes/programs)**

Every user can run several programs at the same time

Linux Distribution



Distribution : Kernell + Shell + Softwares

How to use Linux?

- 2 ways:

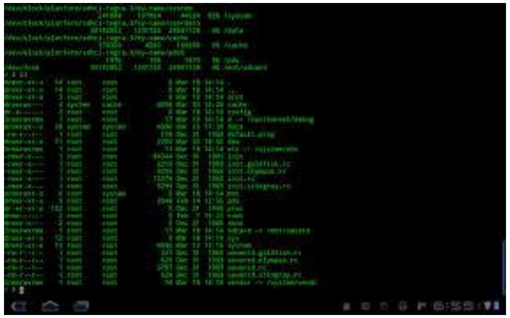
Graphical User Interface

How to use Linux?

- 2 ways :

  Graphical User Interface

  Command-Line Interface through a terminal

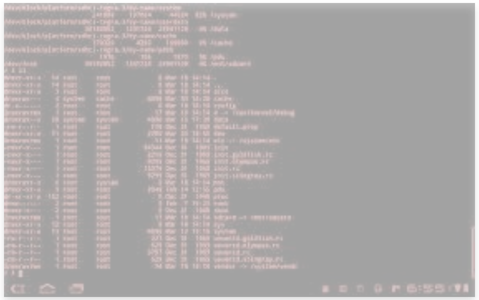


Why using Linux ?

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

Why using Linux ?

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



No graphical interface

Command line ergonomy ?

Why using Linux ?

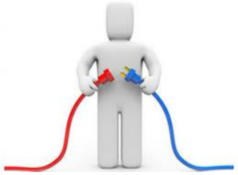
Need to practice

⬄ **Need important investissments to have good results quickly**

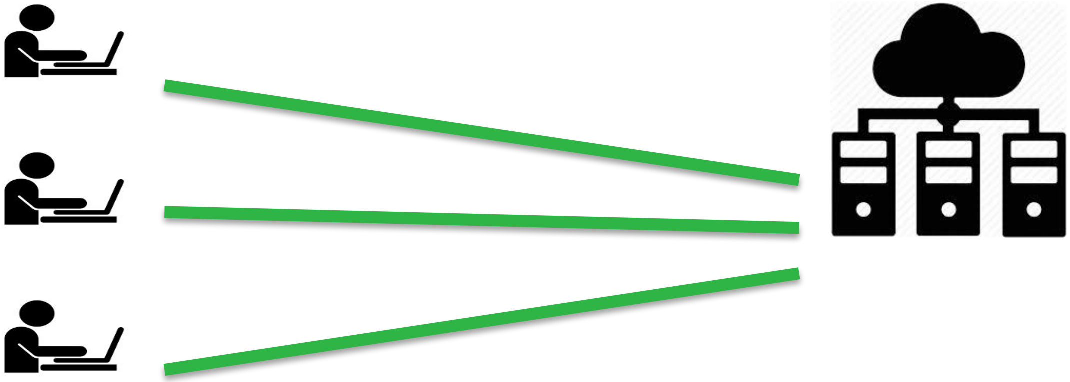
Working Environment

How to transfer files from your PC to the server ?

How to transfer files from a computer to a server?



- Get connecting on a distant linux server from your computer by ***sftp protocol***

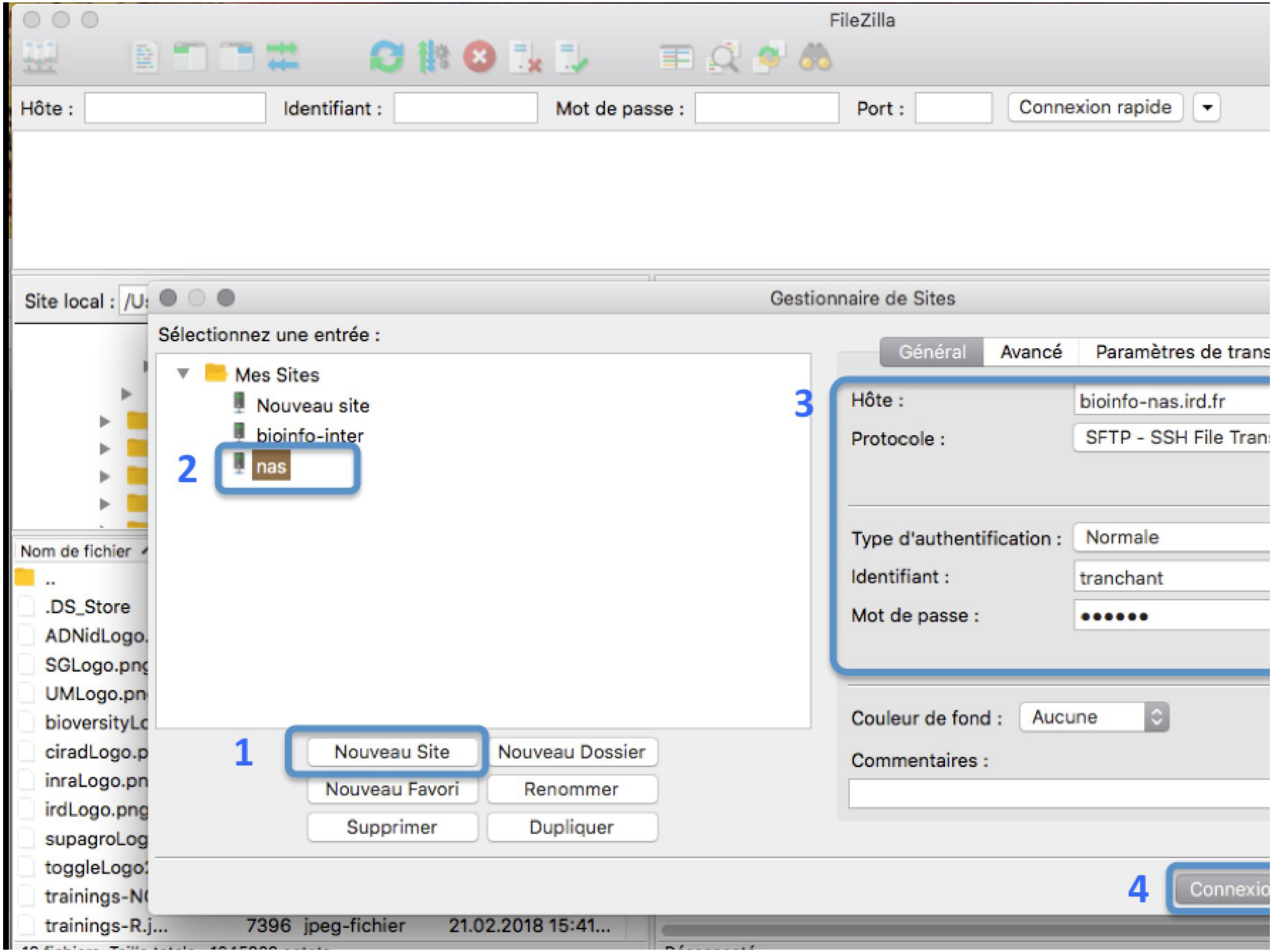


HPC South Green

- itrop (IRD)

bioinfo-nas.ird.fr

Filezilla



Sélectionnez une entrée :

- Mes Sites
  - Nouveau site
  - bioinfo-inter
  - nas

Hôte : bioinfo-nas.ird.fr

Protocole : SFTP - SSH File Tran

Type d'authentification : Normale

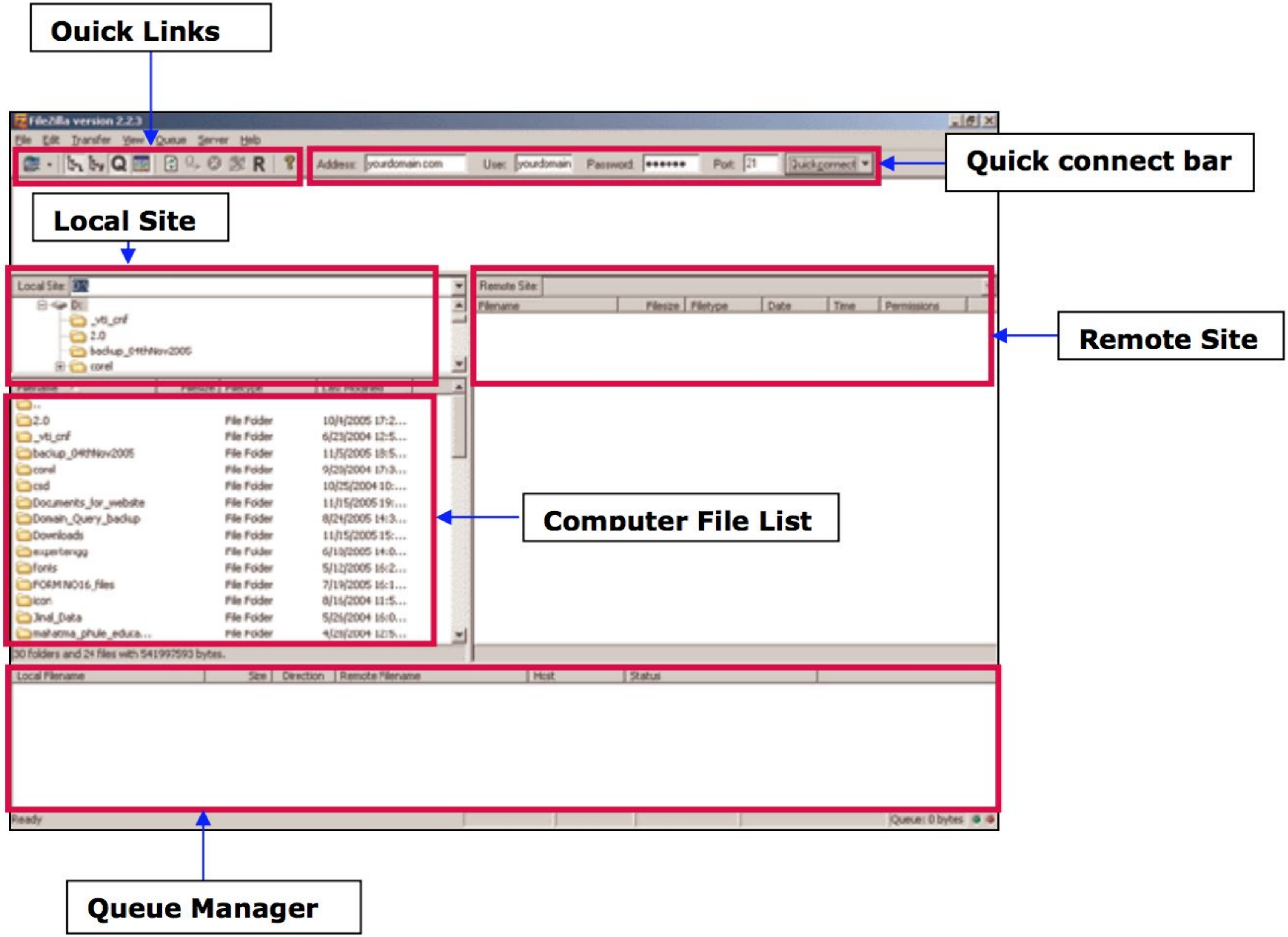
Identifiant : tranchant

Mot de passe : ••••••

Couleur de fond : Aucune

Commentaires :

Filezilla



Quick Links

Quick connect bar

Local Site

Remote Site

Computer File List

Queue Manager

Address: yourdomain.com User: yourdomain Password: •••••• Port: 21

Local Site: D:\

- D:
  - _vti_cnf
  - 2.0
  - backup_04thNov2005
  - corel

Filename	Filesize	Filetype	Last Modified
..			
2.0		File Folder	10/4/2005 17:2...
_vti_cnf		File Folder	6/23/2004 12:5...
backup_04thNov2005		File Folder	11/5/2005 18:5...
corel		File Folder	9/20/2004 17:3...
csd		File Folder	10/25/2004 10:...
Documents_for_website		File Folder	11/15/2005 19:...
Domain_Query_backup		File Folder	8/24/2005 14:3...
Downloads		File Folder	11/15/2005 15:...
expertengg		File Folder	6/10/2005 14:0...
fonts		File Folder	5/12/2005 16:2...
FORM NO16_files		File Folder	7/19/2005 16:1...
icon		File Folder	8/16/2004 11:5...
Jinal_Data		File Folder	5/26/2004 16:0...
mahatma_phule_educa...		File Folder	4/28/2004 12:5...

30 folders and 24 files with 541997593 bytes.

Practice

filezilla, sftp

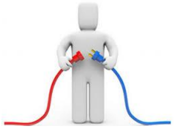
1

Go to Practice 1 *on our github*

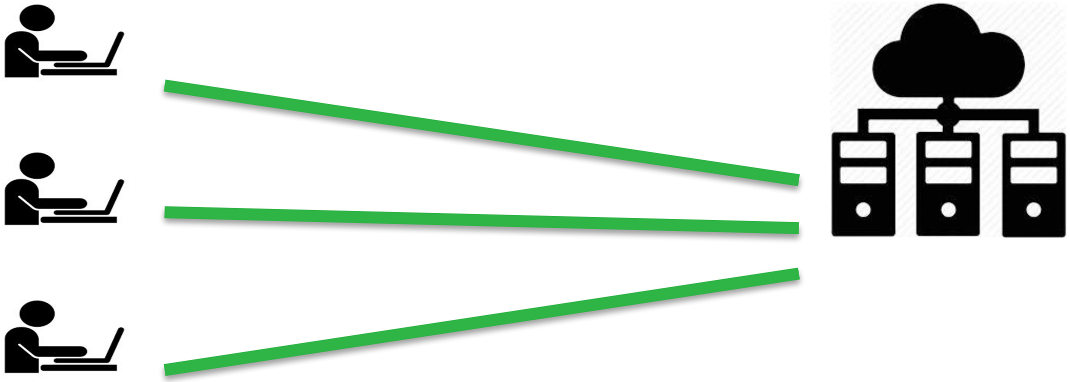
Working Environment

How to work on a distant server ?

How to work on a distant server ?



- Get connecting on a distant linux server from your computer by ***ssh protocol***
-



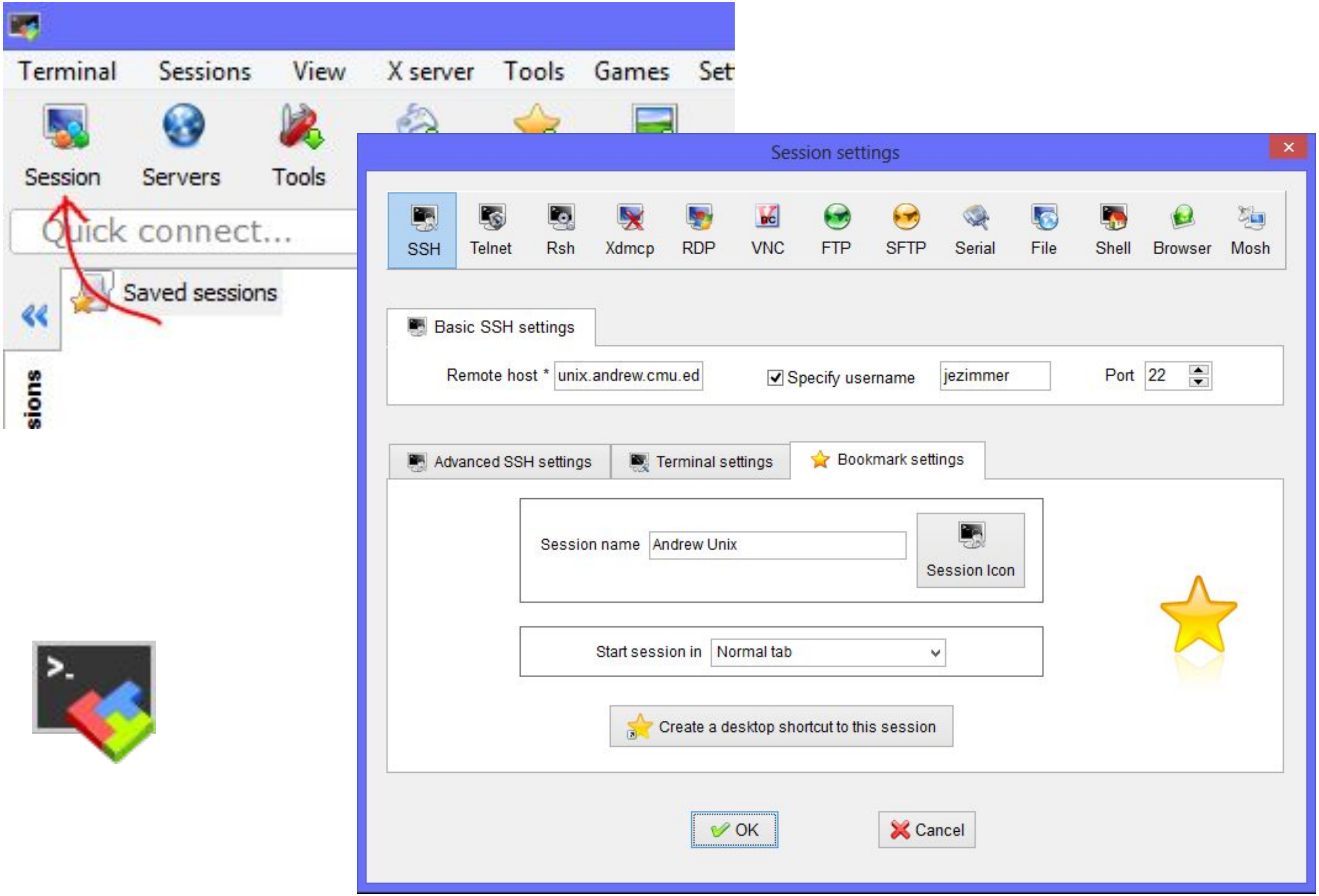
HPC South Green

- itrop (IRD)

bioinfo-inter.ird.fr

PuTTY

How to work on a distant server ?



Remote host * unix.andrew.cmu.ed

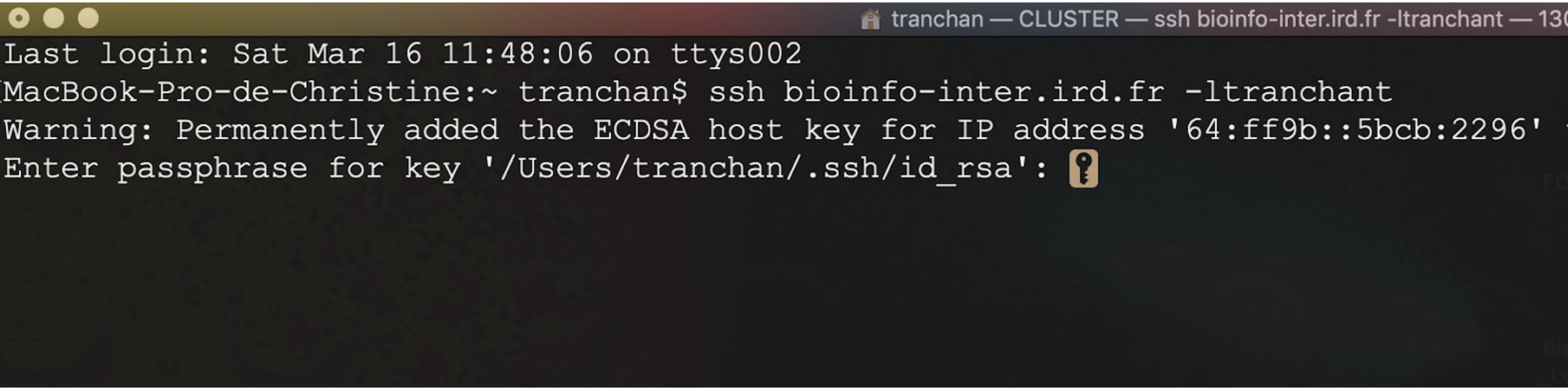
☑ Specify username jezimmer

Port 22

Session name Andrew Unix

Start session in Normal tab

Comment travailler sur le serveur ?



```
Last login: Sat Mar 16 11:48:06 on ttys002
MacBook-Pro-de-Christine:~ tranchan$ ssh bioinfo-inter.ird.fr -ltranchant
Warning: Permanently added the ECDSA host key for IP address '64:ff9b::5bcb:2296'
Enter passphrase for key '/Users/tranchan/.ssh/id_rsa':
```

Practice

putty,
terminal, ssh

2

Go to Practice 2 *on our github*

First steps on Linux

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

The Prompt

Always on the terminal, just before where user type commands

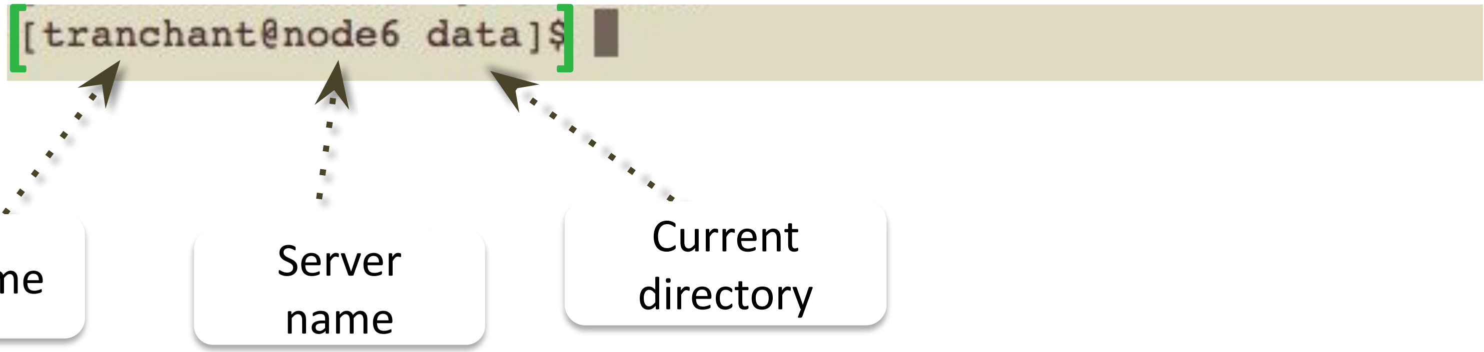
Prompt

```
[tranchant@node6 data]$
```

The Prompt

Always on the terminal, just before where user type commands

Prompt



```
[tranchant@node6 data]$
```

User name

Server name

Current directory

Command syntax

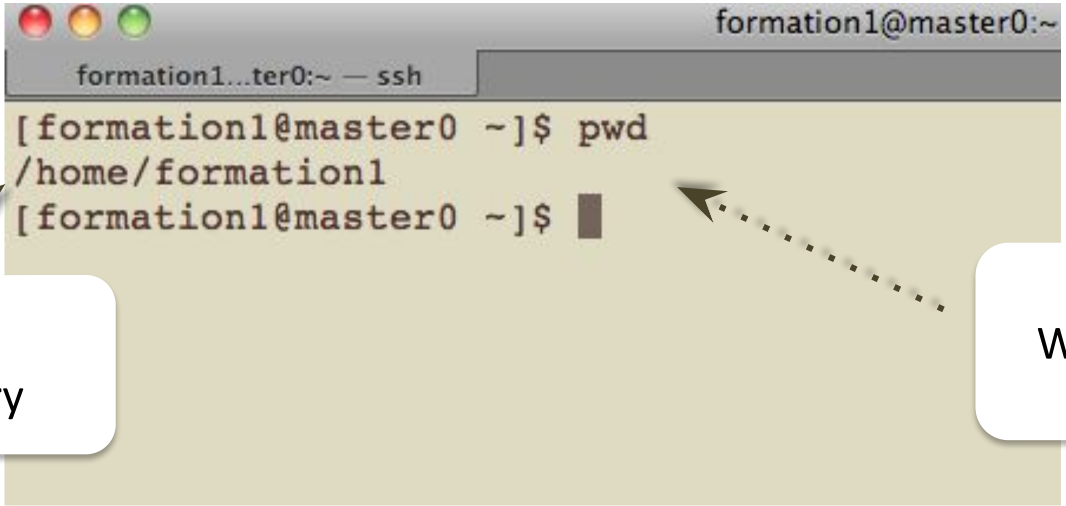
```
command [ -options ] [ arguments ]
```

Your First command pwd

pwd

Present Work Directory

Print the name of the current directory (the full path)



```
[formation1@master0 ~]$ pwd
/home/formation1
[formation1@master0 ~]$ 
```

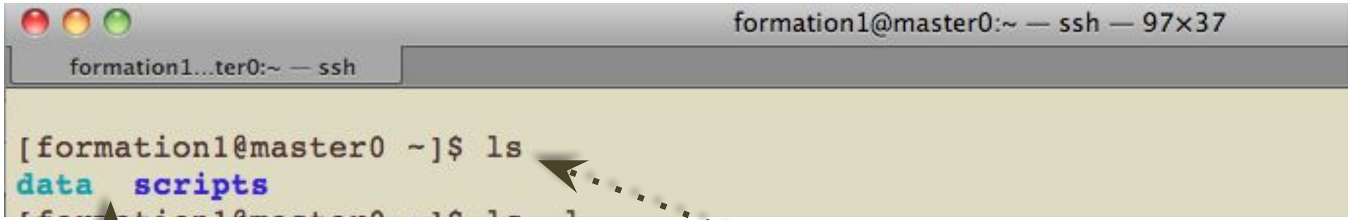
Name of the current directory

Command
Without option and argument

2nd commande *ls*

ls
list

List the content of the current directory



```
[formation1@master0 ~]$ ls
data   scripts
```

List all the files in the current directory (by default)

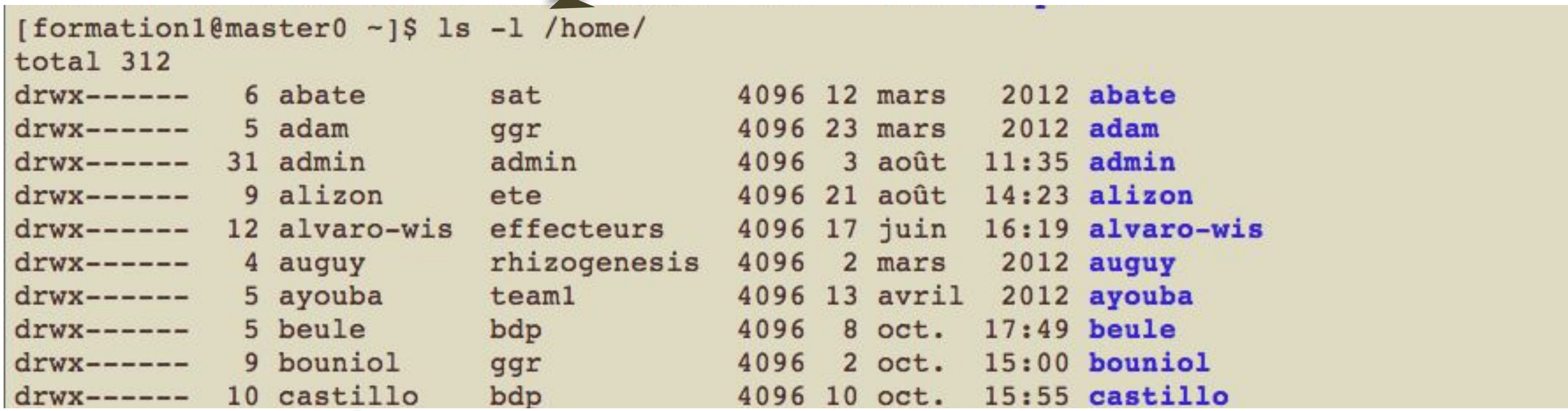
Command without option and argument

2nd command + option *ls -l*

ls -l *ist files with more information about each file*

list long

Command with the option **–l** and a directory name gived as argument



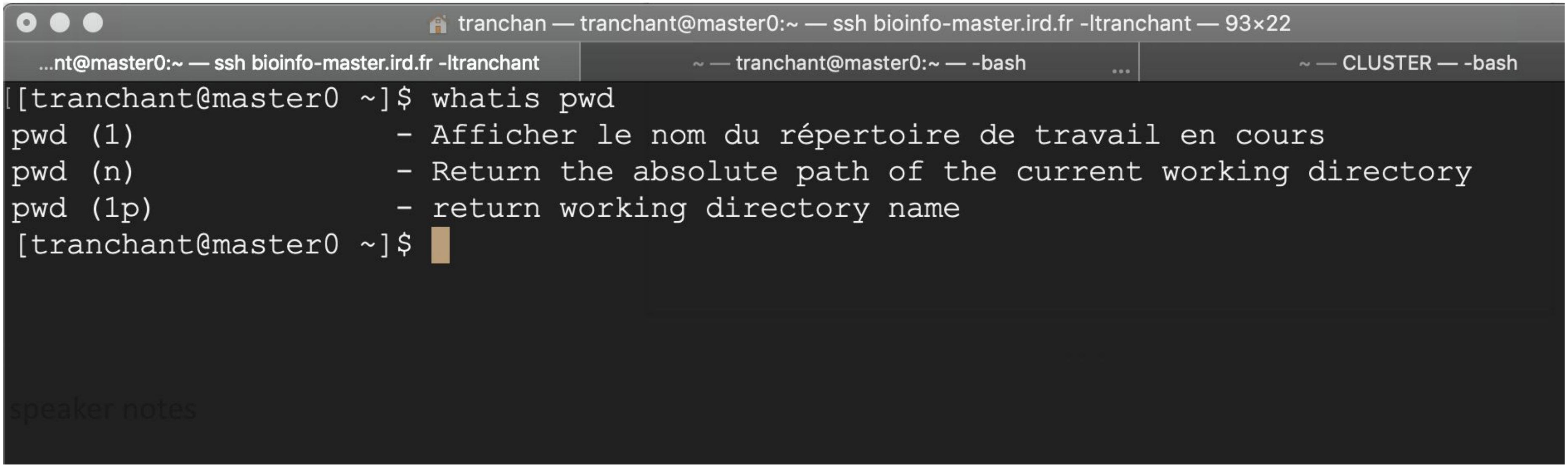
```
[formation1@master0 ~]$ ls -l /home/
total 312
drwx------   6 abate      sat         4096 12 mars   2012 abate
drwx------   5 adam       ggr         4096 23 mars   2012 adam
drwx------  31 admin      admin       4096  3 août  11:35 admin
drwx------   9 alizon     ete         4096 21 août  14:23 alizon
drwx------  12 alvaro-wis effecteurs  4096 17 juin  16:19 alvaro-wis
drwx------   4 auguy      rhizogenesis 4096  2 mars   2012 auguy
drwx------   5 ayouba     team1       4096 13 avril  2012 ayouba
drwx------   5 beule      bdp         4096  8 oct.  17:49 beule
drwx------   9 bouniol    ggr         4096  2 oct.  15:00 bouniol
drwx------  10 castillo   bdp         4096 10 oct.  15:55 castillo
```

Display the long format listing of all files in the directory

A Few Basic Commands

How to get help about one command

- with the ’option --*help* ou -*h* *ls* ***--help*** *blastn* ***-h***
- with the command *man* ***man*** *ls*
- whith the command *whatis* ***whatis*** *ls*



```
[[tranchant@master0 ~]$ whatis pwd
pwd (1)              - Afficher le nom du répertoire de travail en cours
pwd (n)              - Return the absolute path of the current working directory
pwd (1p)             - return working directory name
[tranchant@master0 ~]$ 
```

speaker notes

A Few Basic Commands

Basics

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

Practice

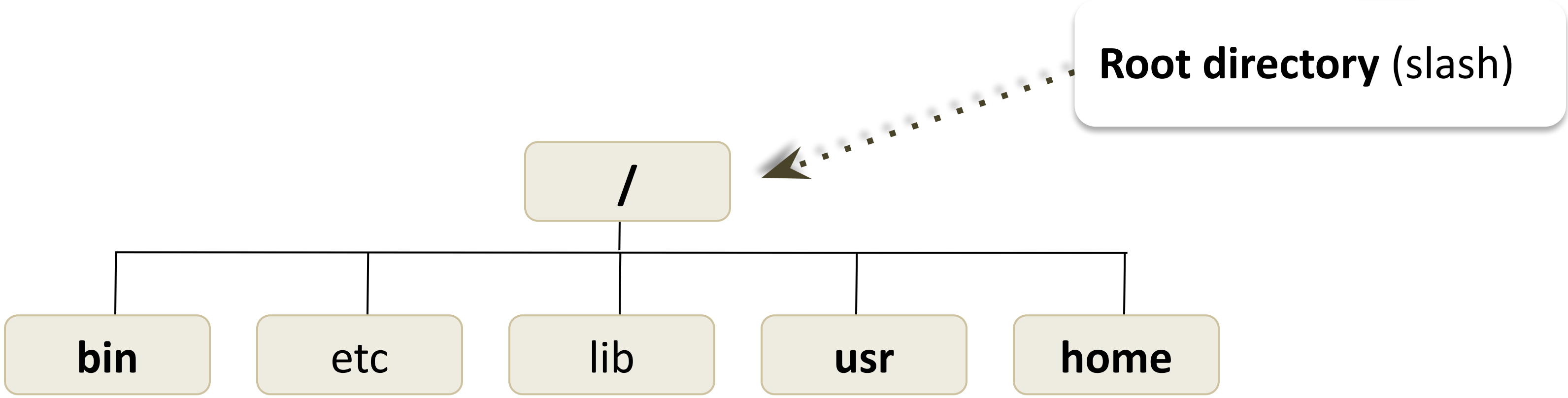
prompt, pwd

3

Go to Practice 3 *on our github*

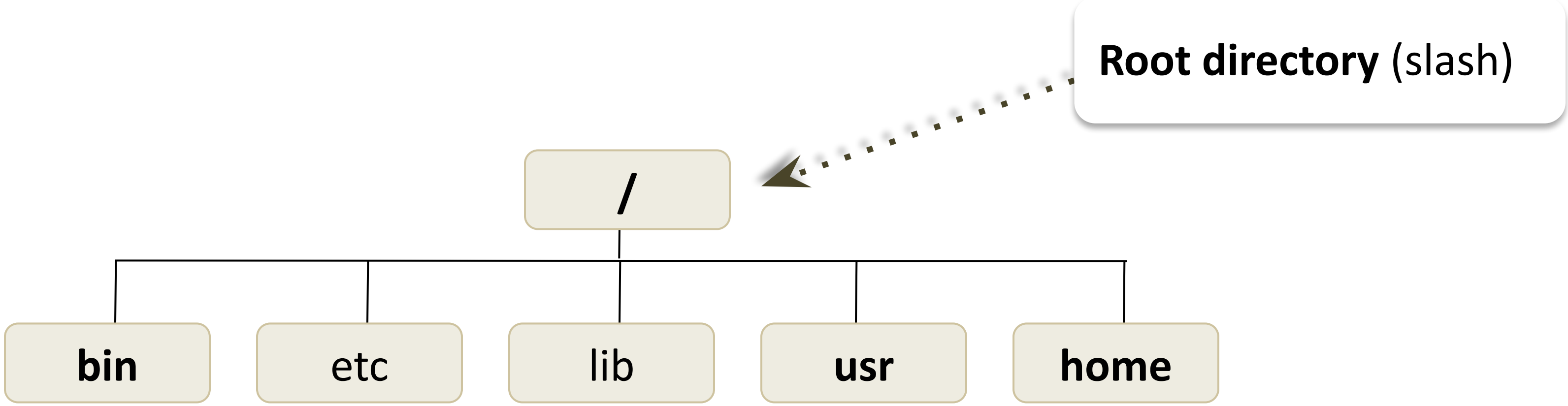
The file tree - Filesystem

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



The file tree - Filesystem

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

Path of a file

Path : location to a file/directory in the file system

absolute

- Complete path of a file starting from the root directory /

Path of a file

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 the user is working**

Path of a file

Path : location to a file/directory in the file system

absolu

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

relative

- Path related to the present working directory (where the user is working)

Path of a file

Path : location to a file/directory in the file system

absolu

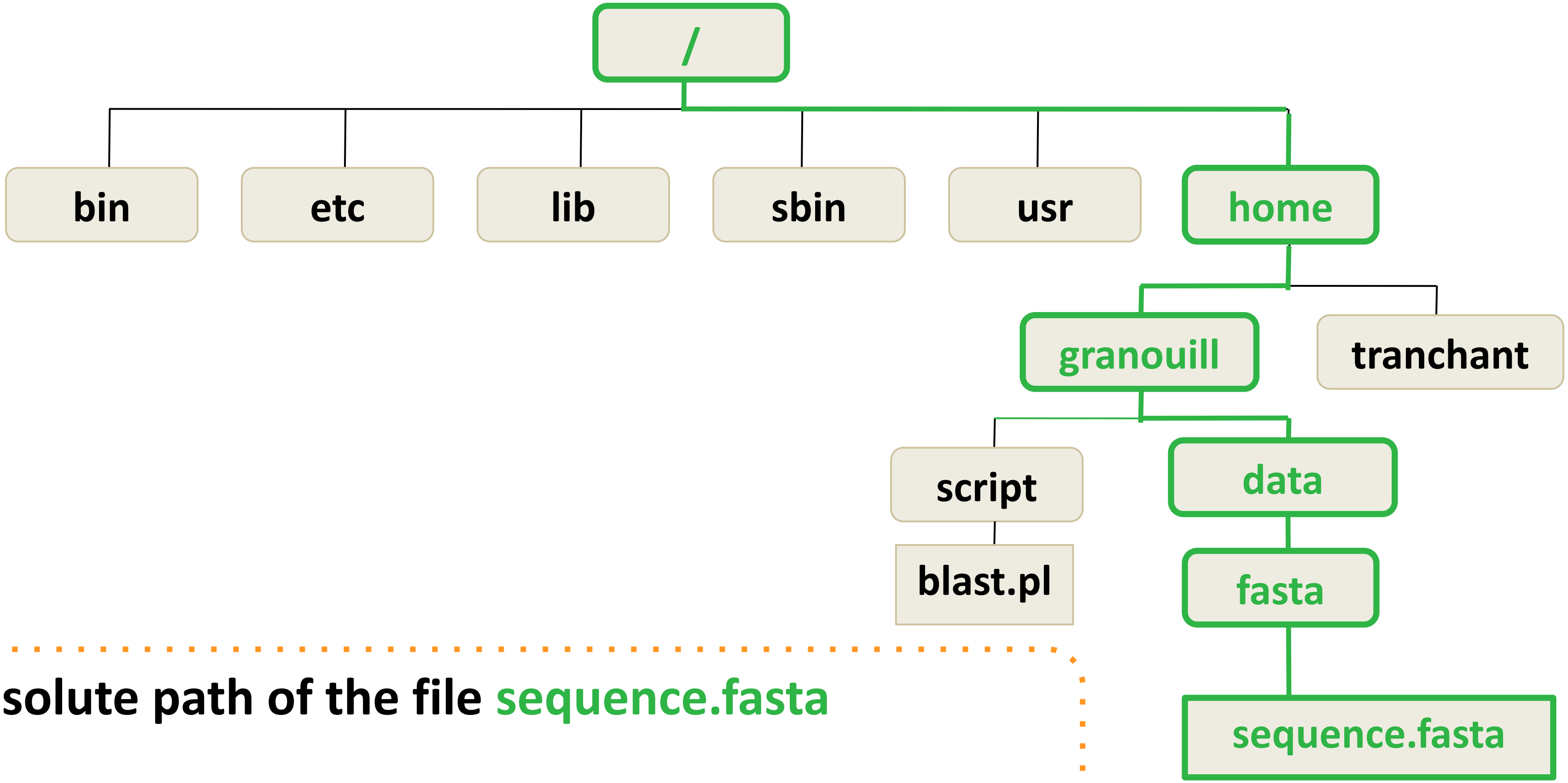
- Complete path of a file starting from the root directory /
- ***starts always with /***
- **always good wherever user is working**

relative

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

Absolute Path

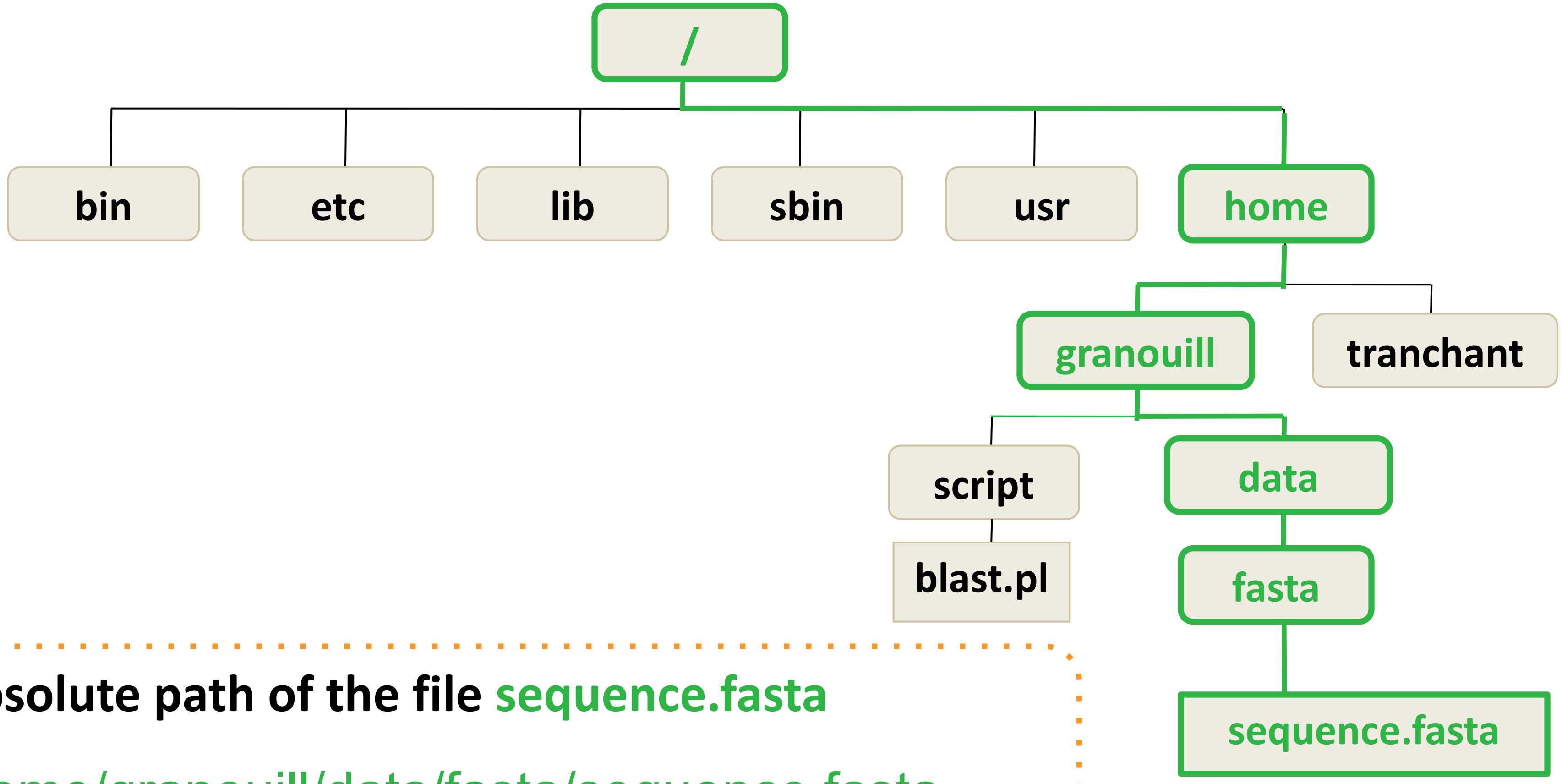
- Always starts with / (root directory)
- **Always works wherever user is working**



Absolute path of the file sequence.fasta

Absolute Path

- Always starts with / (root directory)
- **Always works wherever user is working**

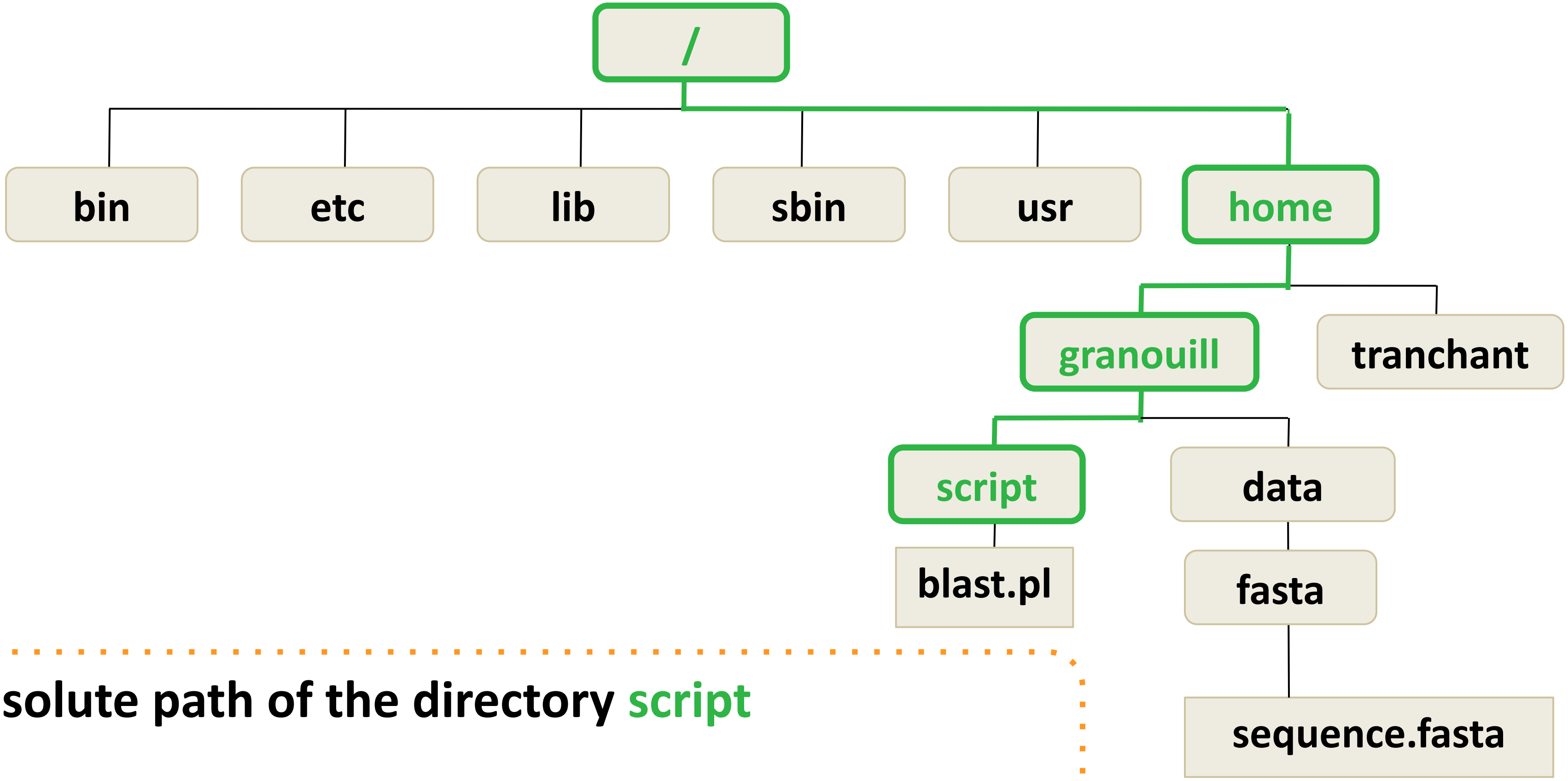


Absolute path of the file sequence.fasta

/home/granouill/data/fasta/sequence.fasta

Absolute Path

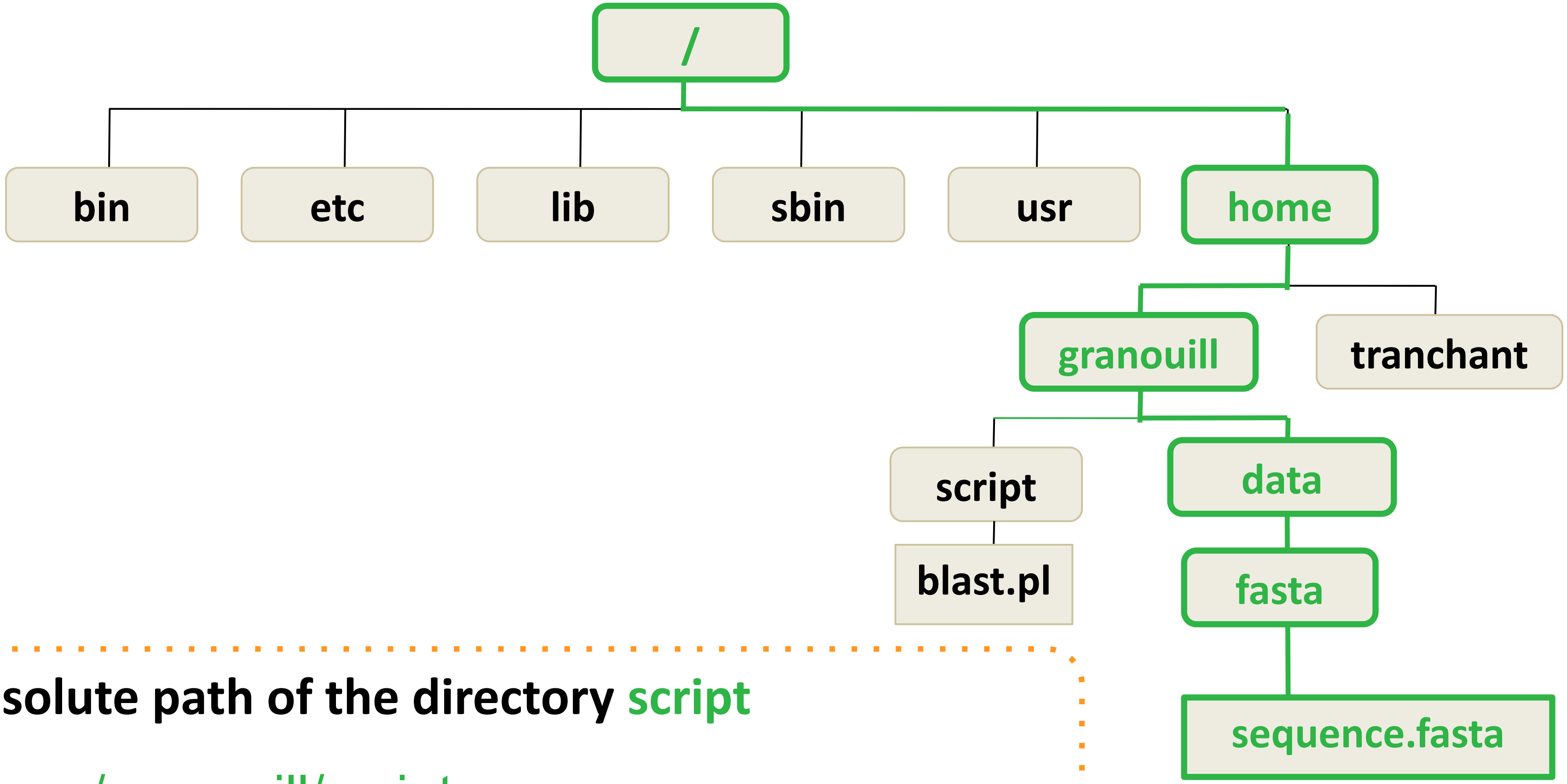
- Always starts with / (root directory)
- Always works wherever user is working



Absolute path of the directory script

Absolute Path

- Always starts with / (root directory)
- Always works wherever user is working

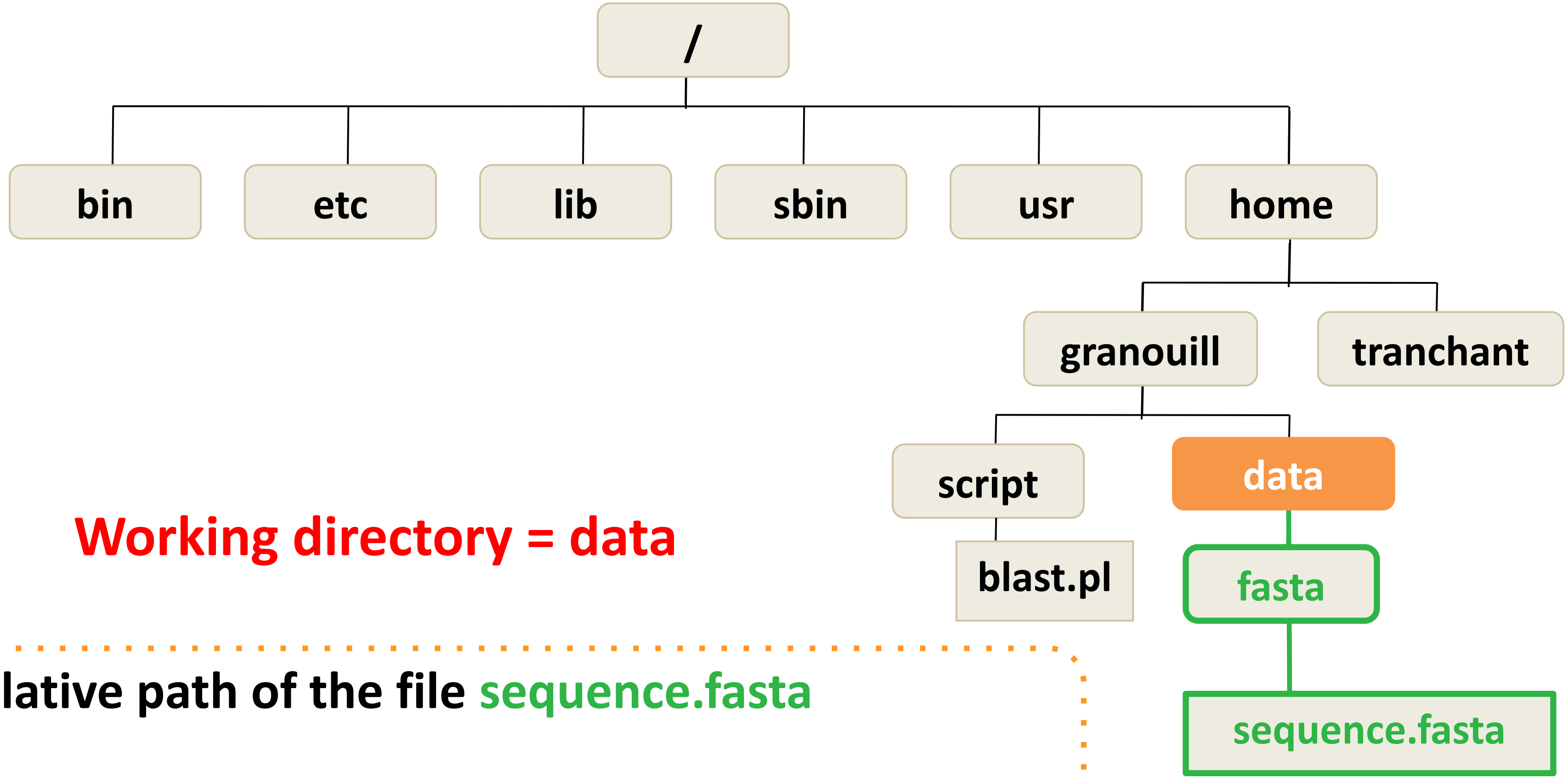


Absolute path of the directory script

/home/granouill/script

Relative Path

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

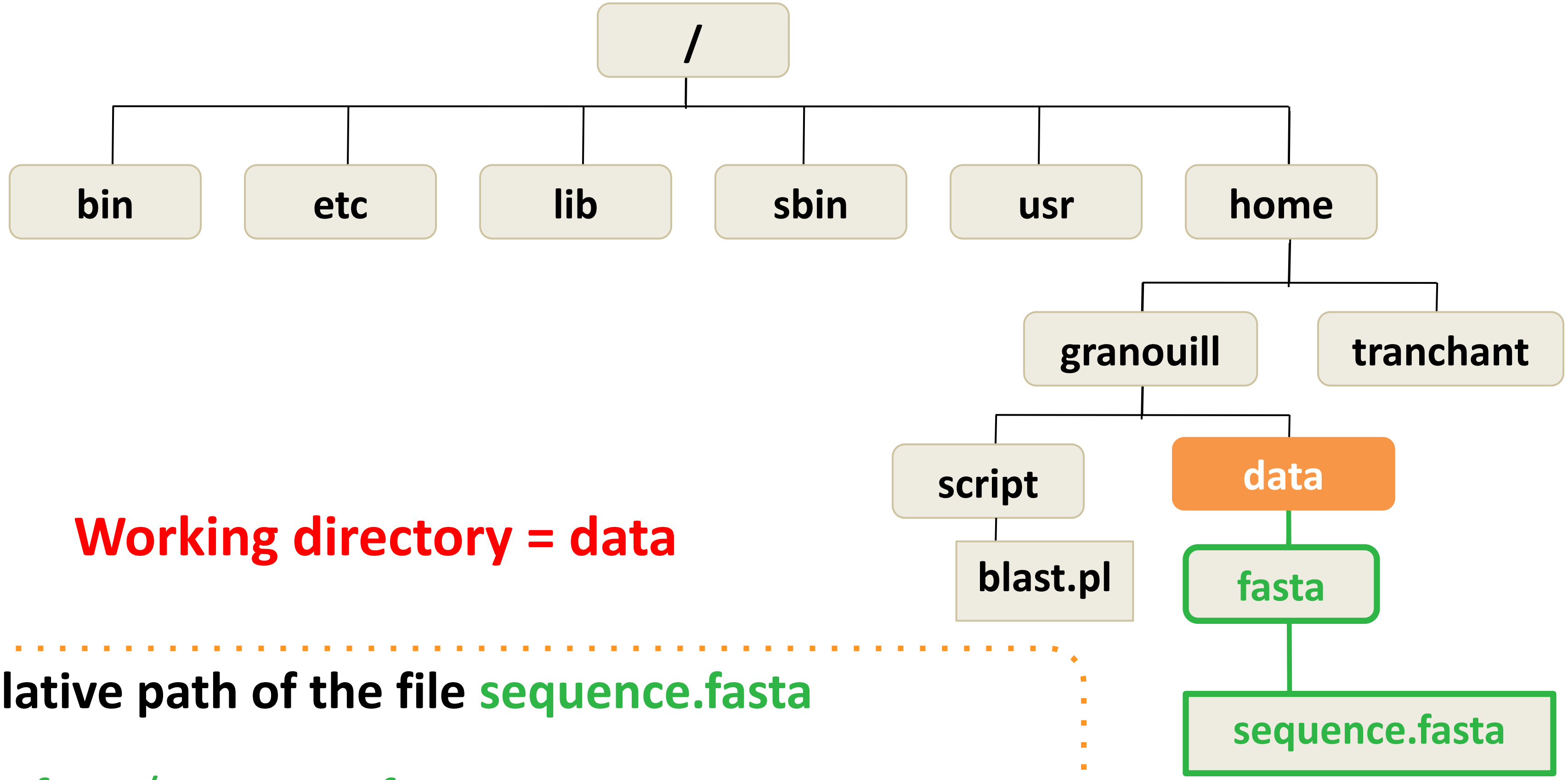


Working directory = data

Relative path of the file sequence.fasta

Relative Path

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



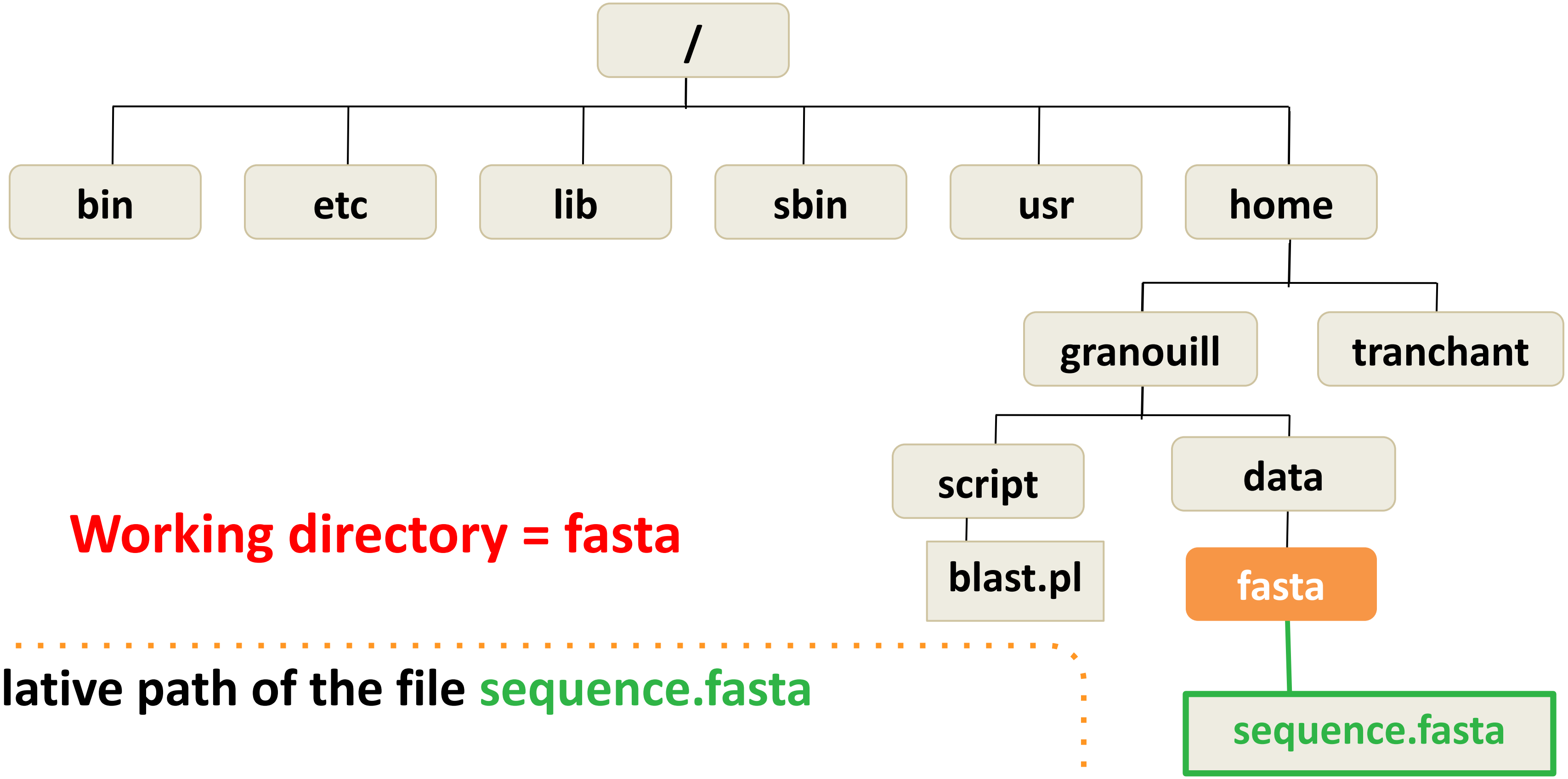
Working directory = data

Relative path of the file sequence.fasta

fasta/sequence.fasta

Relative Path

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

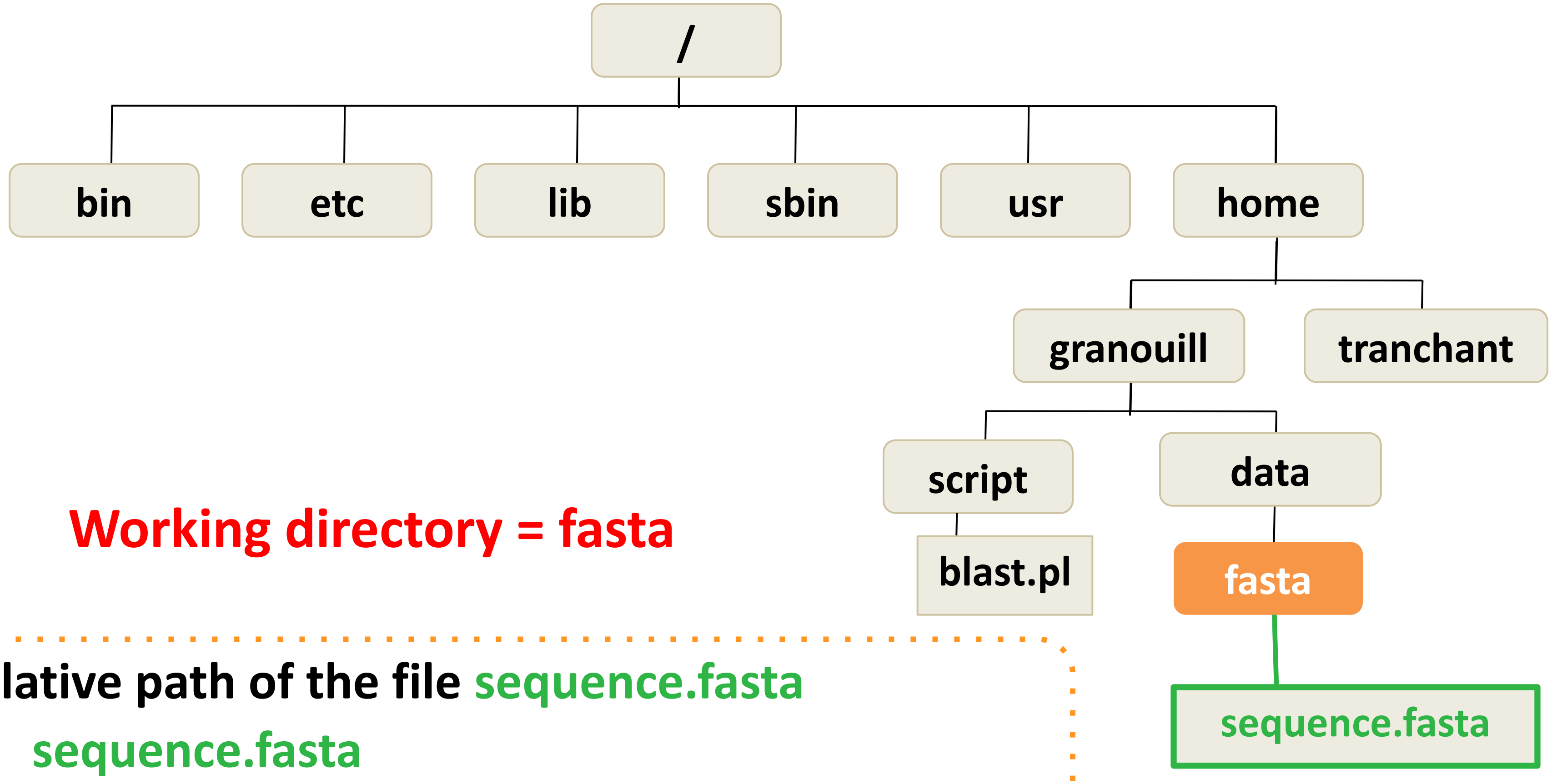


Working directory = fasta

Relative path of the file sequence.fasta

Relative Path

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



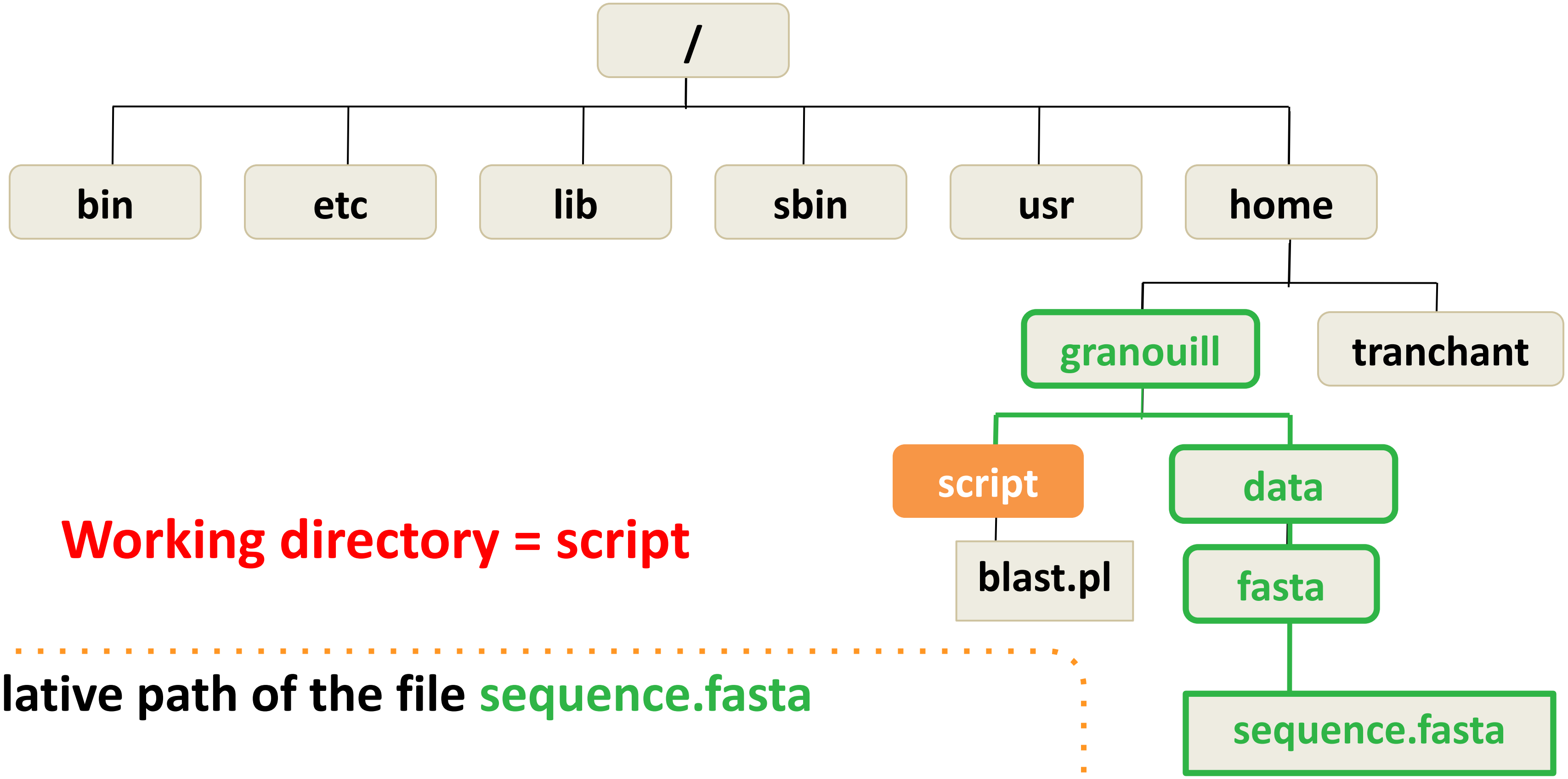
Working directory = fasta

Relative path of the file sequence.fasta

sequence.fasta

Relative Path

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

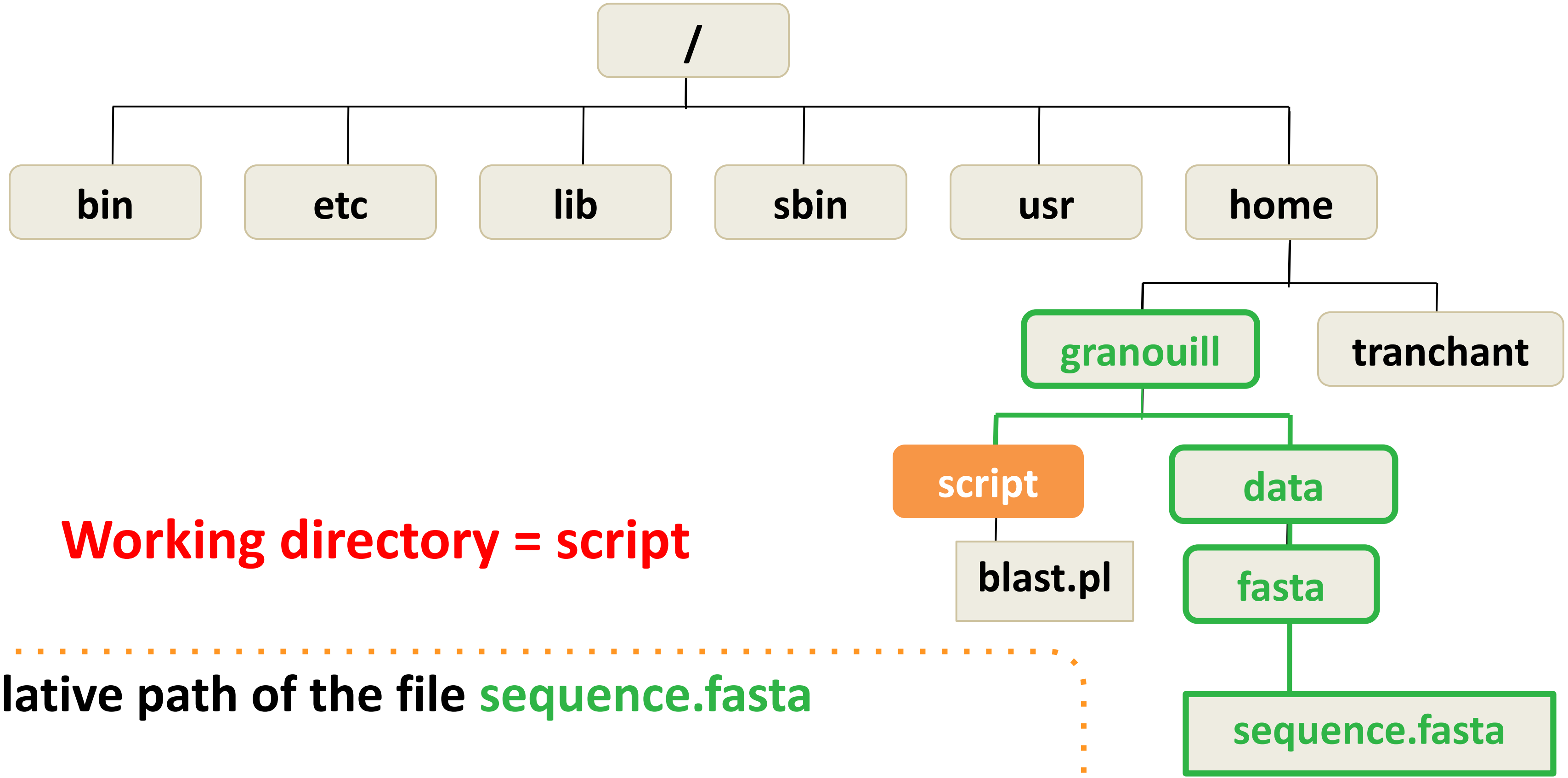


Working directory = script

Relative path of the file sequence.fasta

Relative Path

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



Working directory = script

Relative path of the file sequence.fasta

../data/fasta/sequence.fasta

Practice

ls

Go to Practice 4 on our github

Useful Keyboard Shortcuts

Working with processes

<Ctrl> + C Interrupt (kill) the current process running in
<Ctrl> + Z the terminal

Tab completion

<Tab> Automatically complete the file, directory or command you’re typing

<Tab><Tab> if multiple files or directories, print the list of possibilities

Useful Keyboard Shortcuts

Working with the command history

Up/Down arrow Go to the previous / next command in the command history. Press it multiple times to walk back through the history

<Ctrl> + R Recall the last command matching the characters typed. Press this shortcut and start typing to search your bash history for a command.

Rules for naming file and directory names

- Linux is case sensitive

  Sequence.fasta ≠ SEQUENCE.fasta ≠ sequence.fasta

- Only ROMAN letters, numbers and _ -

- No space, accent or special symbol

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

- No need to use filename extension (.txt), just to improve readability of filenames.

Working with wildcard

Metacharacters : *, [ ]

What is a wildcard ?

It is a character that can be used as a substitute for any of a class of characters in a search

Can be used with numerous linux commands

How to use wildcards ?

Star wildcard *	can represent zero characters, all single characters or any string

KYVF-01.R1.fastq KYVF-02.R1.fastq KYVF.sam ZO16.fastq
KYVF-01.R2.fastq KYVF-02.R2.fastq KYVF.bam ZO16.bam

```
ls *fastq
```

How to use wildcards ?

Star wildcard can represent zero characters, all single characters or any string

*****

KYVF-01.R1.fastq KYVF-02.R1.fastq KYVF.sam ZO16.fastq
KYVF-01.R2.fastq KYVF-02.R2.fastq KYVF.bam ZO16.bam

```
ls *fastq
```

```
KYVF-01.R1.fastq     KYVF-02.R1.fastq    ZO16.fastq
KYVF-01.R2.fastq     KYVF-02.R2.fastq
```

How to use wildcards ?

Star wildcard
*****

can represent zero characters, all single characters or any string

KYVF-01.R1.fastq
KYVF-01.R2.fastq
KYVF-02.R1.fastq
KYVF-02.R2.fastq
KYVF.sam
KYVF.bam
ZO16.fastq
ZO16.bam

```
ls KYVF*fastq
```

How to use wildcards ?

Star wildcard
*****

can represent zero characters, all single characters or any string

KYVF-01.R1.fastq
KYVF-01.R2.fastq
KYVF-02.R1.fastq
KYVF-02.R2.fastq
KYVF.sam
KYVF.bam
ZO16.fastq
ZO16.bam

```
ls KYVF*fastq

KYVF-01.R1.fastq        KYVF-02.R1.fastq
KYVF-01.R2.fastq        KYVF-02.R2.fastq
```

How to use wildcards ?

Star wildcard can represent zero characters, all single
***** characters or any string

Square Brackets wildcards [ ]
can represent any of the characters enclosed in the brackets.

KYVF-01.R1.fastq
KYVF-01.R2.fastq
KYVF-02.R1.fastq
KYVF-02.R2.fastq
KYVF.sam
KYVF.bam
ZO16.fastq
ZO16.bam

```
ls *.[sb]am
```

How to use wildcards ?

Star wildcard can represent zero characters, all single
***** characters or any string

Square Brackets wildcards []
can represent any of the characters enclosed in the brackets.

KYVF-01.R1.fastq
KYVF-01.R2.fastq
KYVF-02.R1.fastq
KYVF-02.R2.fastq
KYVF.sam
KYVF.bam
ZO16.fastq
ZO16.bam

```
ls *.[sb]am                    = ls *.[!f]*
KYVF.sam    ZO16.bam
KYVF.bam
```

Practice

ls, *

5

Go to Practice 5 *on our github*

Commands for moving around the file system

Command cd

Command *cd*

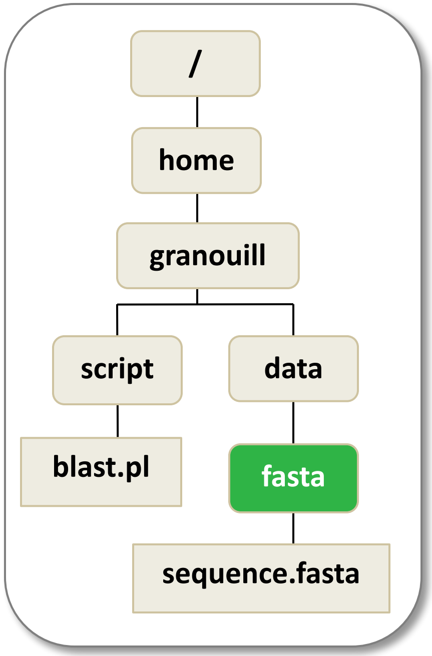
cd *Change **D**irectory*	*Move from the current directory into a new directory*

```
cd DIRECTORY_NAME(absolute or relative path)
```

Command *cd*

```
cd DIRECTORY_NAME(absolute or relative path)
```

Absolute path :

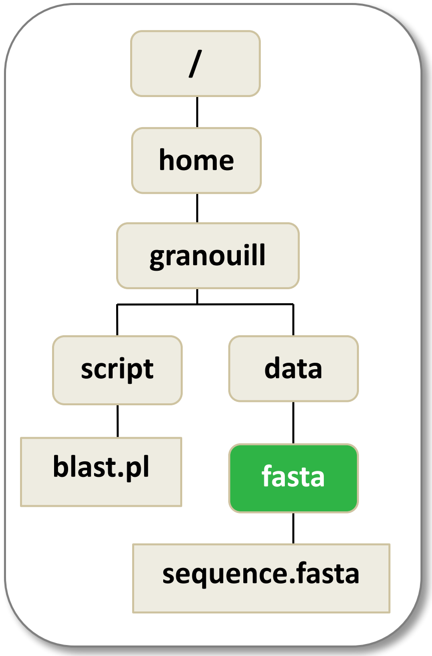


Command *cd*

```
cd DIRECTORY_NAME(absolute or relative path)
```

Absolute path :

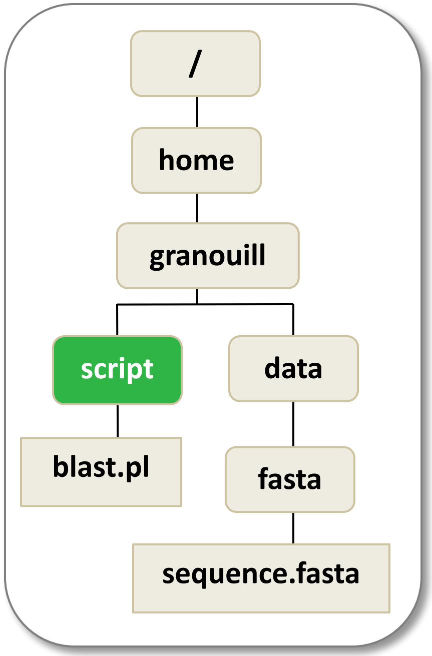
```
cd /home/granouill/data/fasta
```



Command *cd*

`cd DIRECTORY_NAME` *(absolute or relative path)*

Absolute path :

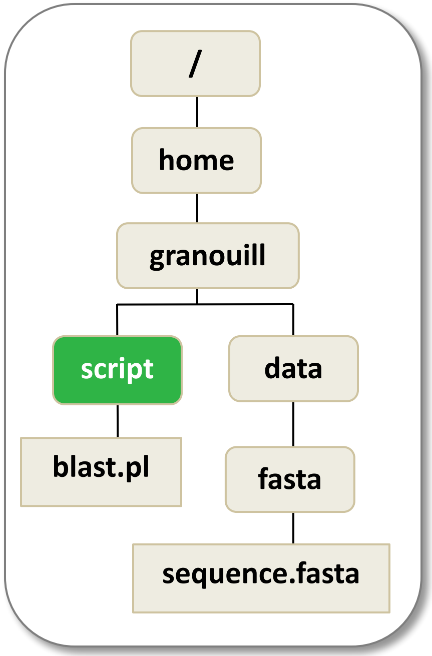


Command *cd*

`cd DIRECTORY_NAME(absolute or relative path)`

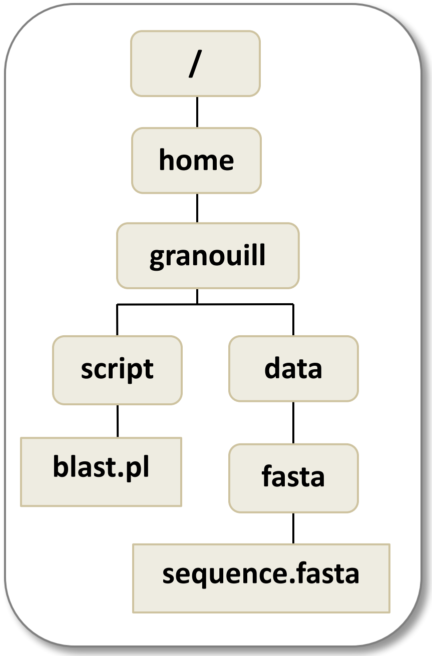
Absolute path :

```
cd /home/granouill/script/
```



Command *cd*

```
cd DIRECTORY_NAME (absolute or relative path)
```



Relative path :

Command	Go to
cd directory_name	directory_name
cd	*home directory*
cd ..	Parent directory
cd ../..	?

Go to home directory

One folder up

2 folders up

Some Commands

Linux file tree

pwd	Print the full path of the current directory
ls	Display the list of files in a directory
cd DIR_NAME	Change the working directory

mkdir rep_name	Create a new 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, keeping the same name
cp FILE DIR/NEW_FILE	Mix of 2

Practice

pwd, cd, ls

Go to [Practice 6](#) *on our github*

Practice

mkdir, mv, ls, cp, rm

7

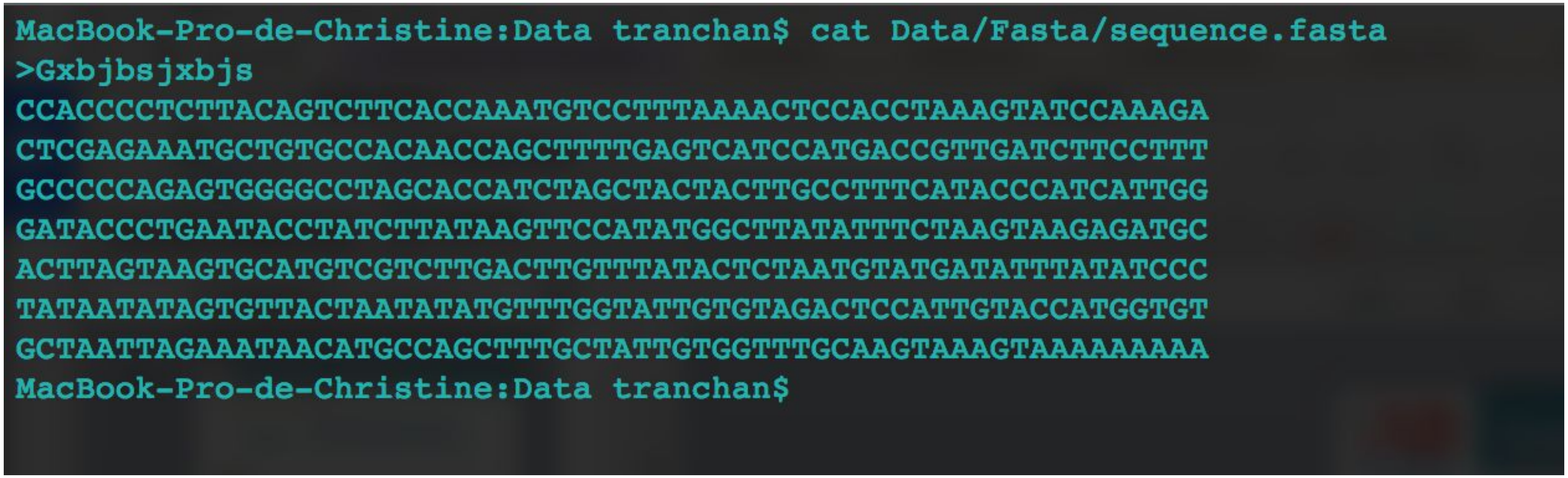
Go to Practice 7 *on our github*

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!!)



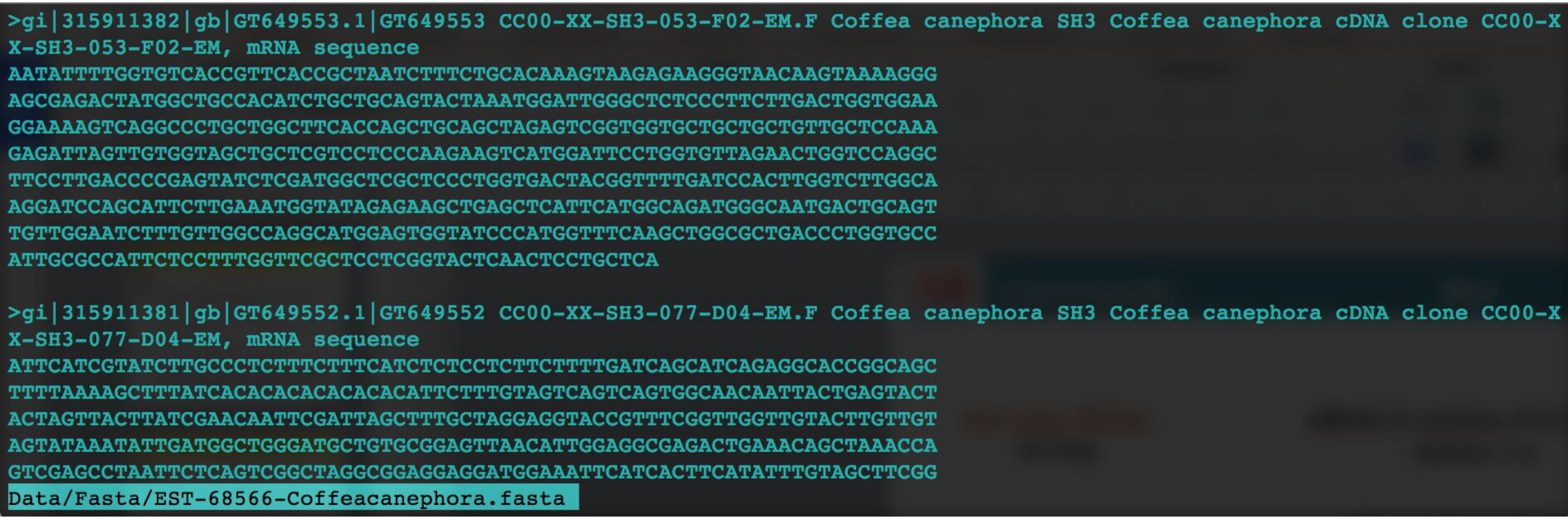
```
MacBook-Pro-de-Christine:Data tranchan$ cat Data/Fasta/sequence.fasta
>Gxbjbsjxbjs
CCACCCCTCTTACAGTCTTCACCAAATGTCCTTTAAAACTCCACCTAAAGTATCCAAAGA
CTCGAGAAATGCTGTGCCACAACCAGCTTTTGAGTCATCCATGACCGTTGATCTTCCTTT
GCCCCCAGAGTGGGGCCTAGCACCATCTAGCTACTACTTGCCTTTCATACCCATCATTGG
GATACCCTGAATACCTATCTTATAAGTTCCATATGGCTTATATTTCTAAGTAAGAGATGC
ACTTAGTAAGTGCATGTCGTCTTGACTTGTTTATACTCTAATGTATGATATTTATATCCC
TATAATATAGTGTTACTAATATATGTTTGGTATTGTGTAGACTCCATTGTACCATGGTGT
GCTAATTAGAAATAACATGCCAGCTTTGCTATTGTGGTTTGCAAGTAAAGTAAAAAAAAA
MacBook-Pro-de-Christine:Data tranchan$
```

Command less

less nom_fichier *writes the contents of a file a page at a time.*

[space-bar] to see another page
[q] to quit reading
[/] followed by the word to search

less Data/Fasta/EST-68566-Coffeacanephora.fasta



```
>gi|315911382|gb|GT649553.1|GT649553 CC00-XX-SH3-053-F02-EM.F Coffea canephora SH3 Coffea canephora cDNA clone CC00-X
X-SH3-053-F02-EM, mRNA sequence
AATATTTTGGTGTCACCGTTCACCGCTAATCTTTCTGCACAAAGTAAGAGAAGGGTAACAAGTAAAAGGG
AGCGAGACTATGGCTGCCACATCTGCTGCAGTACTAAATGGATTGGGCTCTCCCTTCTTGACTGGTGGAA
GGAAAAGTCAGGCCCTGCTGGCTTCACCAGCTGCAGCTAGAGTCGGTGGTGCTGCTGCTGTTGCTCCAAA
GAGATTAGTTGTGGTAGCTGCTCGTCCTCCCAAGAAGTCATGGATTCCTGGTGTTAGAACTGGTCCAGGC
TTCCTTGACCCCGAGTATCTCGATGGCTCGCTCCCTGGTGACTACGGTTTTGATCCACTTGGTCTTGGCA
AGGATCCAGCATTCTTGAAATGGTATAGAGAAGCTGAGCTCATTCATGGCAGATGGGCAATGACTGCAGT
TGTTGGAATCTTTGTTGGCCAGGCATGGAGTGGTATCCCATGGTTTCAAGCTGGCGCTGACCCTGGTGCC
ATTGCGCCATTCTCCTTTGGTTCGCTCCTCGGTACTCAACTCCTGCTCA

>gi|315911381|gb|GT649552.1|GT649552 CC00-XX-SH3-077-D04-EM.F Coffea canephora SH3 Coffea canephora cDNA clone CC00-X
X-SH3-077-D04-EM, mRNA sequence
ATTCATCGTATCTTGCCCTCTTTCTTTCATCTCTCCTCTTCTTTTGATCAGCATCAGAGGCACCGGCAGC
TTTTAAAAGCTTTATCACACACACACACACATTCTTTGTAGTCAGTCAGTGGCAACAATTACTGAGTACT
ACTAGTTACTTATCGAACAATTCGATTAGCTTTGCTAGGAGGTACCGTTTCGGTTGGTTGTACTTGTTGT
AGTATAAATATTGATGGCTGGGATGCTGTGCGGAGTTAACATTGGAGGCGAGACTGAAACAGCTAAACCA
GTCGAGCCTAATTCTCAGTCGGCTAGGCGGAGGAGGATGGAAATTCATCACTTCATATTTGTAGCTTCGG
Data/Fasta/EST-68566-Coffeacanephora.fasta
```

Other Useful Commands

head	writes the first ten lines of a file to the screen	`head -n 20 script.pl`
tail	writes the last ten lines of a file to the screen	`tail -n 5 script.pl`
wc	Count for word, lines, characters in a file	`wc script.pl` `wc -l  script.pl`

Command grep

grep *searching a word, a pattern in a file*

```
grep [options] motif [file1, … ]
```

To search for a phrase or pattern,

you must enclose it in single quotes

Command grep

grep *searching a word, a pattern in a file*

```
grep [options] motif [file1, … ]
```

Option	Description
-c	Count the number of lignes where *MOTIF* was found at least once
-l	Print only the name of files where *MOTIF* was found
-i	Case insensitive
-v	Print lines **WITHOUT** the *MOTIF*

Practice

ls, head, tail, wc

8

Go to Practice 8 *on our github*

Command *cut*

cut Extracts columns/fields from a file

```
cut -d SEPARATOR -f fieldNumber fileName
```

```
cut –d “:” -f1,5 /etc/passwd
```

Picked un the FIRST and FIFTH columns of FILE, separated by :

Command sort

sort sort the content of a text file, line by line

`sort -k2 fileName`	Alphabetical sorting based on the second column
`sort -k2r  fileName`	Reverse Alphabetical sorting based on the 2nd col
`sort -k2g -k1r fileName`	Numeral sorting on the 2nd column then the 1st col
`sort -t: -k3g fileName`	-t option defines the field separator (by default :)

Practice

9

Go to [Practice 9](#) *on our github*

INPUT/OUTPUT REDIRECTION

For saving the output of a command to a file

Saving the output of a command to a file

The output of commands can be written in a file

using the 2 operators :

>

>>

```
cut -d: -f1 /etc/passwd > userName.txt
```

Saving the output of a command to a file

```
cut -d: -f1 /etc/passwd > userName.txt
```

Redirection	Action
`Command > file1`	- redirect the output in a newly created file *file1* - **If *file1* exists, will overwrite it**
`Command >> file1`	- redirect the output at the end of *file1 (add)* - **If *file1* does not exist, will create it**

Practice

10

Go to Practice 10 *on our github*

Connecting commands together

- The standard output of one command can be send as the standard input of another with the operator |
- To connect multiple commands together with what are called pipelines (without tempory files)
- Pipelines= *workflow*

```
cmd1 | cmd2 | cmd3
```

Connecting commands together

```
cut -d: -f1 /etc/passwd
Root
troot
iroot
ctroot
//
```

Connecting commands together

```
cut -d: -f1 /etc/passwd
Root
troot
iroot
ctroot
//
cut -d: -f1 /etc/passwd | sort
abate
adm
adroot
ais
#albar
alvaro-wis
anthony
apache
```

Connecting commands together

```
cut -d: -f1 /etc/passwd
Root
troot
iroot
ctroot
//
cut -d: -f1 /etc/passwd | sort
abate
adm
adroot
ais
#albar
alvaro-wis
anthony
apache
cut -d: -f1 /etc/passwd | sort | head
```

Connecting commands together

```
cut -d: -f1 /etc/passwd
Root
troot
iroot
ctroot
//

cut -d: -f1 /etc/passwd | sort
abate
adm
adroot
ais
#albar
alvaro-wis
anthony
apache

cut -d: -f1 /etc/passwd | sort > /etc/passwd.sort
```

Practice

2

Go to [Practice 11](#) *on our github*

Other useful commands

Disk space and file size

Disk (free) size: **df** disk free

`df`	occupied space in bytes
`df -h`	human-readable

Directory size: **du** disk usage

```
du
du -h
du -h *
```

Searching for a file by its name **find**

```
find -name "transcritsAssembly.fasta"
```

symbolic links

Allow to attribute another path to a file by pointing to a file name.

It is a shortcut **ln**

```
ln -s theright thewrong
```

```
Example: ln -s /opt/jdk-7.01 /opt/jdk
```

Save disk space on a system: only the "real" file weighs

Practice

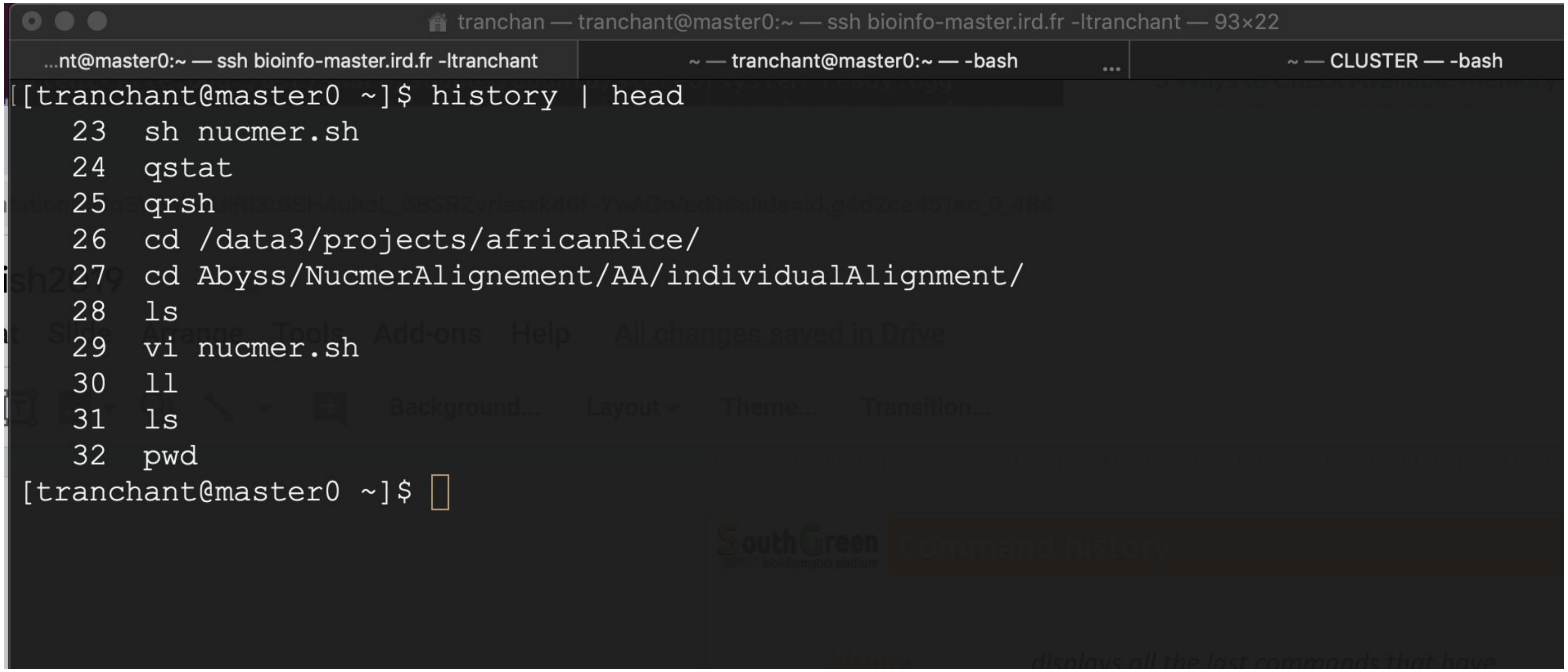
12-13-14

Go to Practice 12,13 and 14*on our github*

Command history

history *displays all the last commands that have been executed in all the previous sessions*

The entire history is saved into the file .bash_history



```
[tranchant@master0 ~]$ history | head
   23  sh nucmer.sh
   24  qstat
   25  qrsh
   26  cd /data3/projects/africanRice/
   27  cd Abyss/NucmerAlignement/AA/individualAlignment/
   28  ls
   29  vi nucmer.sh
   30  ll
   31  ls
   32  pwd
[tranchant@master0 ~]$ 
```

Command history

history *displays all the last commands that have been executed in all the previous sessions*

The entire history is saved into the file .bash_history

Filtering the History Output

```
history | grep “blastn”
```

displays only the commands including the search keyword “blastn”

```
history | tail
```

displays the commands recently used

```
history | grep “blastn” | tail -n 5
```

```
history | head -n 5
```

displays the oldest commands

Manipulating compressed files

Compressing files: **tar,gzip**

```
tar -zcvf tarfile.tar.gz dirToCompress
gzip fileToCompress
```

Decompressing archives: **gunzip, tar**

```
gunzip file.gzip
tar -xvf file.tar
tar -zxvf file.tar.gz
gzip -d file.gz
```

Displaying the contents of an archive: **zcat**

```
zcat data.txt.gz
```

Searching for an expression/pattern in a compressed file: **zgrep**

```
zgrep ‘NM_000020’ data.gz
```

Renaming files

rename

Example	Description
`rename ‘s/.txt/.fasta/’ *`	rename the extension of all files
`rename ‘y/a-z/A-Z/’ *`	rename files in uppercase

Trainers - iTrop / South Green

- **Guilhem Sempere**
- **Ndomassi Tando**

- Alice Boizet
- Bruno Granouillac
- Christine Tranchant-Dubreuil





Support created by C. Tranchant and B. Granouillac and updated …….

Citations

If you use i-Trop Bioinformatics resources.

Thank you for citing with:

“The authors acknowledge the ISO 9001 certified IRD i-Trop HPC (South Green Platform) at IRD montpellier for providing HPC resources that have contributed to the research results reported within this paper.
URL: https://bioinfo.ird.fr/- http://www.southgreen.fr”

Projects

- Include a budget for bioinformatics resources in your answer to projects funding

- A need in hard drives, renew machines etc…

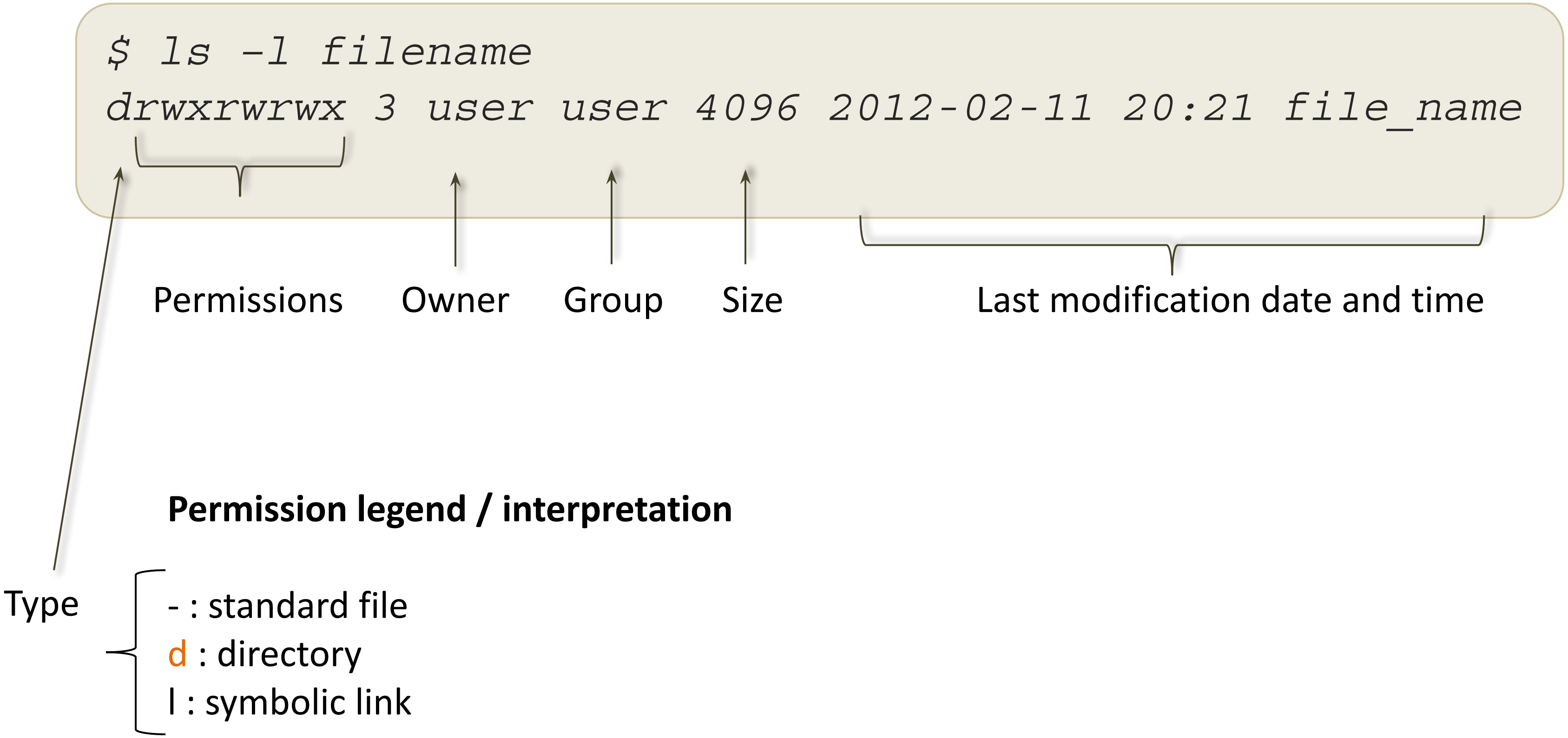
- Available quotations

- Contact bioinfo@ird.fr : help, needs definition, quotations...

Thank you for your attention !

File attributes / permission

Command: ls –l



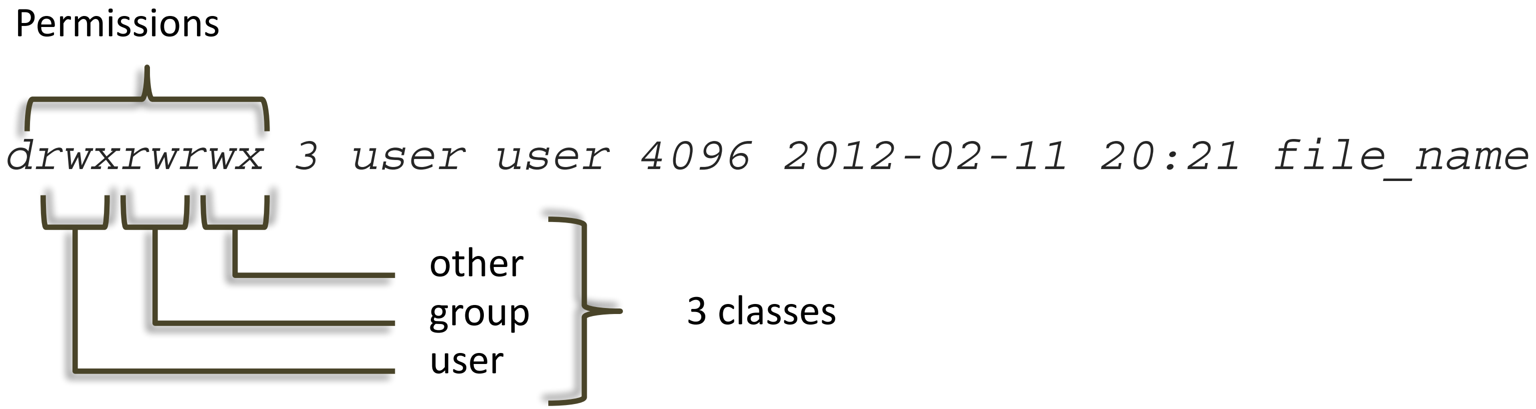
```
$ ls -l filename
drwxrwrwx 3 user user 4096 2012-02-11 20:21 file_name
```

Permission legend / interpretation

Type
- : standard file
d : directory
l : symbolic link

File attributes / permission

ls –l command



Permissions

`drwxrwrwx 3 user user 4096 2012-02-11 20:21 file_name`

other
group
user

3 classes

3 types of permissions :

Permission	File	Directory
Read r	Open and read	List and et copy files
Write w	Modify and remove	Manipulate contents: copy, create, modify, overwrite
Execution x	Execute file	Access to contained files for execution

File attributes / permission

permission managment command: chmod

```
chmod <perm> file_name
```

Each permission = 1 value

R	**4**
W	2
X	1
none	0

Example

```
chmod 740 script.sh                # Owner=rwx Group=r-- Other=---
chmod 755 script.sh                # Owner=rwx Group=r-x Other=r-x
```

Visualize and modify permissions

chmod, ls

Provide owner name, group name and permissions for files contained in directoty “~/Data/454-projet1/raw”

Modify permissions on file Scripts/blast.pl to set them as follows:
read and write for the group
read, write, execute for the owner
read for others (public)