

Training: Linux

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Monday 28 September 2026

Objectives

At the end of the day, you will be able to use a Linux terminal to :

- Connect to `genobioinfo` server
- Use available tools
- Transfert files between your computer and a server
- Prepare data files
- Start processes with command line

Planning of the day

Part I. 9:00 – 10:30

Presentation of GenoToul bioinformatics core facilities, asking for an account, connection procedure, tree structure of files, command line syntax

Part II. 11:00 – 12:30

File types, permissions, manipulating files, displaying files, wildcard characters, disk space control

Part III. 14:00 – 17:00

Dowloading/transferring, compressing/uncompressing, utility commands, redirections

- Presentation of GenoToul bioinformatics core facilities (mission, the team, the users, equipments, disk spaces, website)
- Introduction to Linux
 - Creating an account
 - Tree structure of file system
 - Basic Linux commands
- Connection procedure to `genobioinfo`

Genotoul-Bioinfo

Provide to public regional community

Equipment

- Storage disk space
- High Performance Computer
- Hosting facilities (virtual machine, web site)

Services

- Access to public biologic banks
- Access to bioinformatics software
- Support, Training sessions

Genotoul Bioinfo - The team



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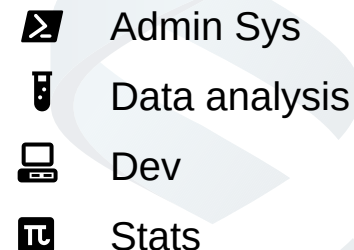
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1300+ registered users

- 50% from INRAE (national)
- 50% from other academic laboratories (regional)

Biologists or computer scientists working in bio-informatics

Genotoul Bioinfo – Equipements

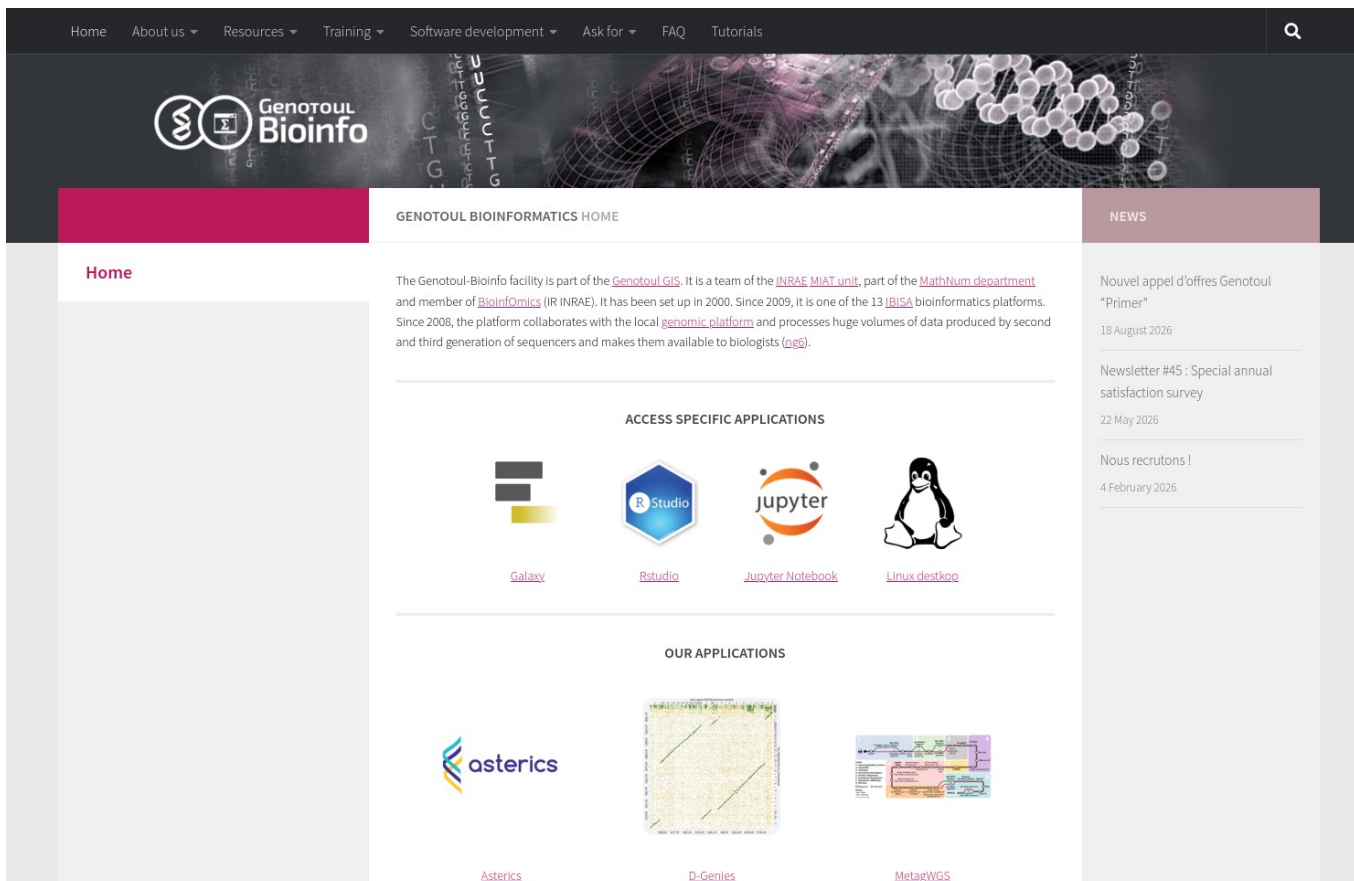
- **Computing cluster (HPC)**
 - 5000+ cores, 80+ TB RAM, 12 GPU
 - 4,5 PB disk space available for computing
- **Permanent Storage File System**
 - 2*1,6 PB disk space capacities (asynchronous replication)
- **Virtual machines (VM)**
 - capacities for servers hosting and web services



Genotoul Bioinfo – Disk spaces

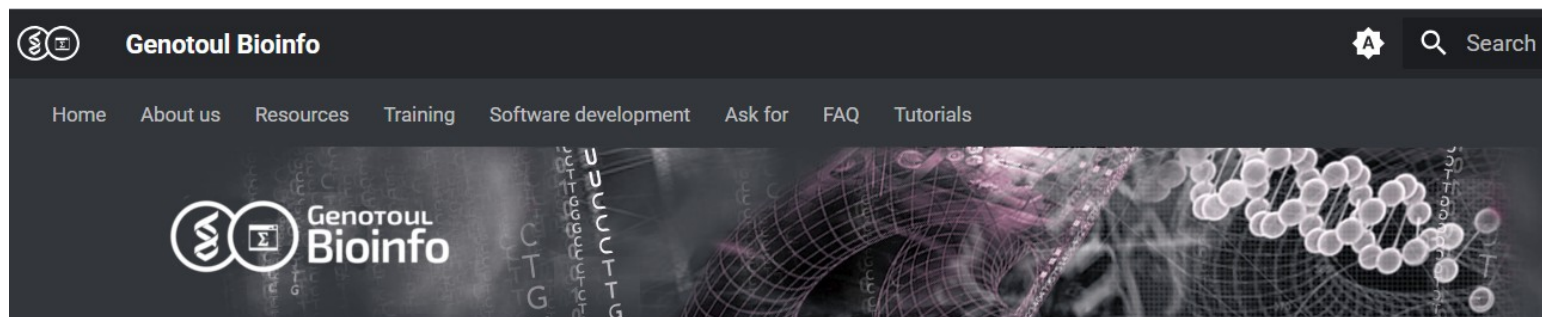
Path	Limit	Writable ^①	Description
/home/<username>	10 GB	✓	Store your configuration files Where you connect
/work/user/<username>	1 TB	✓	Working directory Where you must work (high performance storage)
/save/user/<username>	250 GB	×	Data you want to save (replication) with 30 retention days Where you must save critical data
/usr/local/bioinfo/src/	-	×	Directory gathering all bioinformatics software (FAQ)
/bank	-	×	Biological banks in different format (FAQ)
/save/project/<project>	billed	×	Save space for project (billed)
/work/project/<project>	billed	✓	Working directory for project (billed)

Genotoul Bioinfo – Entrypoint



The screenshot shows the Genotoul Bioinformatics Home page. The header includes a navigation menu with links: Home, About us, Resources, Training, Software development, Ask for, FAQ, and Tutorials. The main content area is divided into three columns. The left column has a 'Home' link. The middle column, titled 'GENOTOUL BIOINFORMATICS HOME', contains a paragraph about the facility's history and mission, followed by a section 'ACCESS SPECIFIC APPLICATIONS' with links to Galaxy, Rstudio, Jupyter Notebook, and Linux desktop. Below this is a section 'OUR APPLICATIONS' with links to Asterics, D-Genies, and MetagWGS. The right column, titled 'NEWS', lists recent updates: 'Nouvel appel d'offres Genotoul "Primer"' (18 August 2026), 'Newsletter #45 : Special annual satisfaction survey' (22 May 2026), and 'Nous recrutons !' (4 February 2026).

Genotoul Bioinfo – I need help!



Genotoul Bioinfo help resources

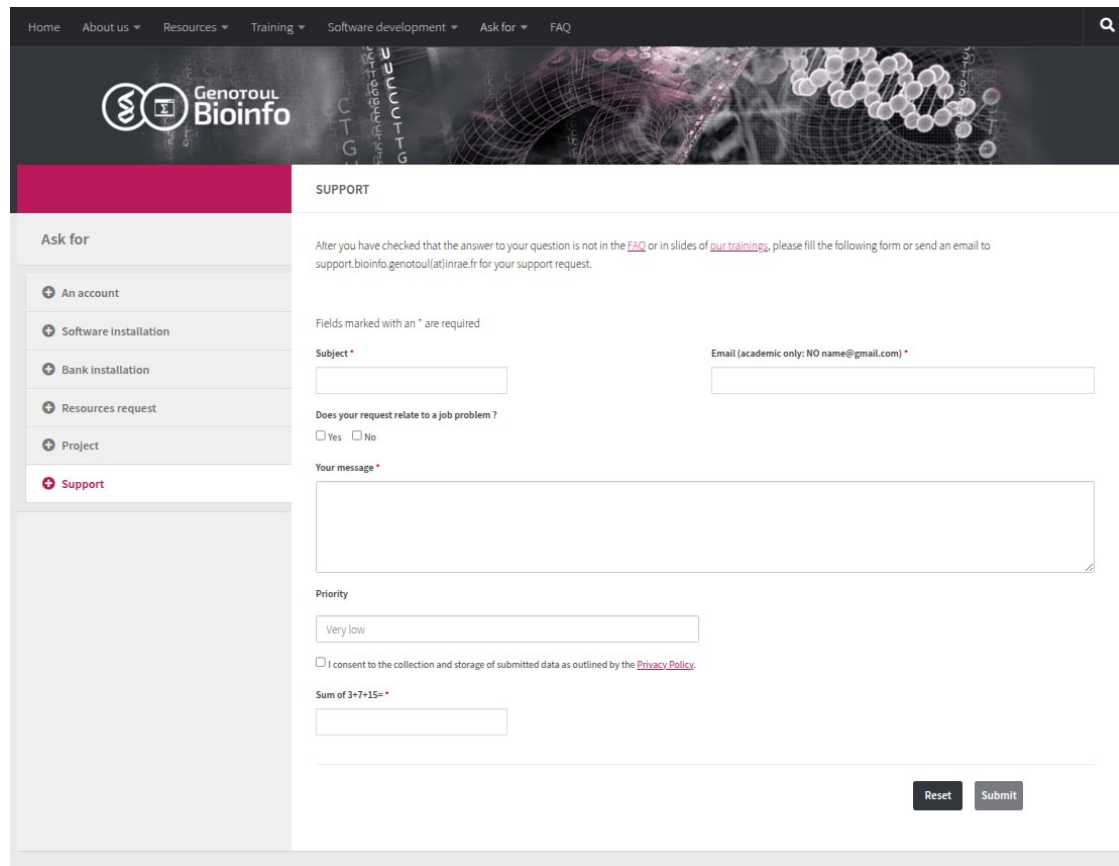


FAQ – How to ... including solving some issues ?



Tutorials – Step by step approaches to use some cluster resources?

Genotoul Bioinfo – I need more help!



The screenshot shows the 'Ask for' support page on the Genotoul Bioinfo website. The page has a dark header with navigation links: Home, About us, Resources, Training, Software development, Ask for, and FAQ. Below the header is a banner image with the Genotoul Bioinfo logo and a DNA helix. The main content area is titled 'SUPPORT' and contains a form for submitting support requests. The form includes a sidebar with a list of categories: An account, Software installation, Bank installation, Resources request, Project, and Support (selected). The form fields include: Subject (required), Email (academic only: NO name@gmail.com), a checkbox for 'Does your request relate to a job problem?', a text area for 'Your message', a dropdown for 'Priority' (set to 'Very low'), a checkbox for 'I consent to the collection and storage of submitted data as outlined by the Privacy Policy', and a CAPTCHA question 'Sum of 3+7+15='.

Home About us Resources Training Software development Ask for FAQ

Genotoul Bioinfo

SUPPORT

Ask for

- An account
- Software installation
- Bank installation
- Resources request
- Project
- Support

After you have checked that the answer to your question is not in the [FAQ](#) or in slides of [our trainings](#), please fill the following form or send an email to support.bioinfo.genotoul@inrae.fr for your support request.

Fields marked with an * are required

Subject * Email (academic only: NO name@gmail.com) *

Does your request relate to a job problem ?
☐ Yes ☐ No

Your message *

Priority
Very low

☐ I consent to the collection and storage of submitted data as outlined by the [Privacy Policy](#).

Sum of 3+7+15= *

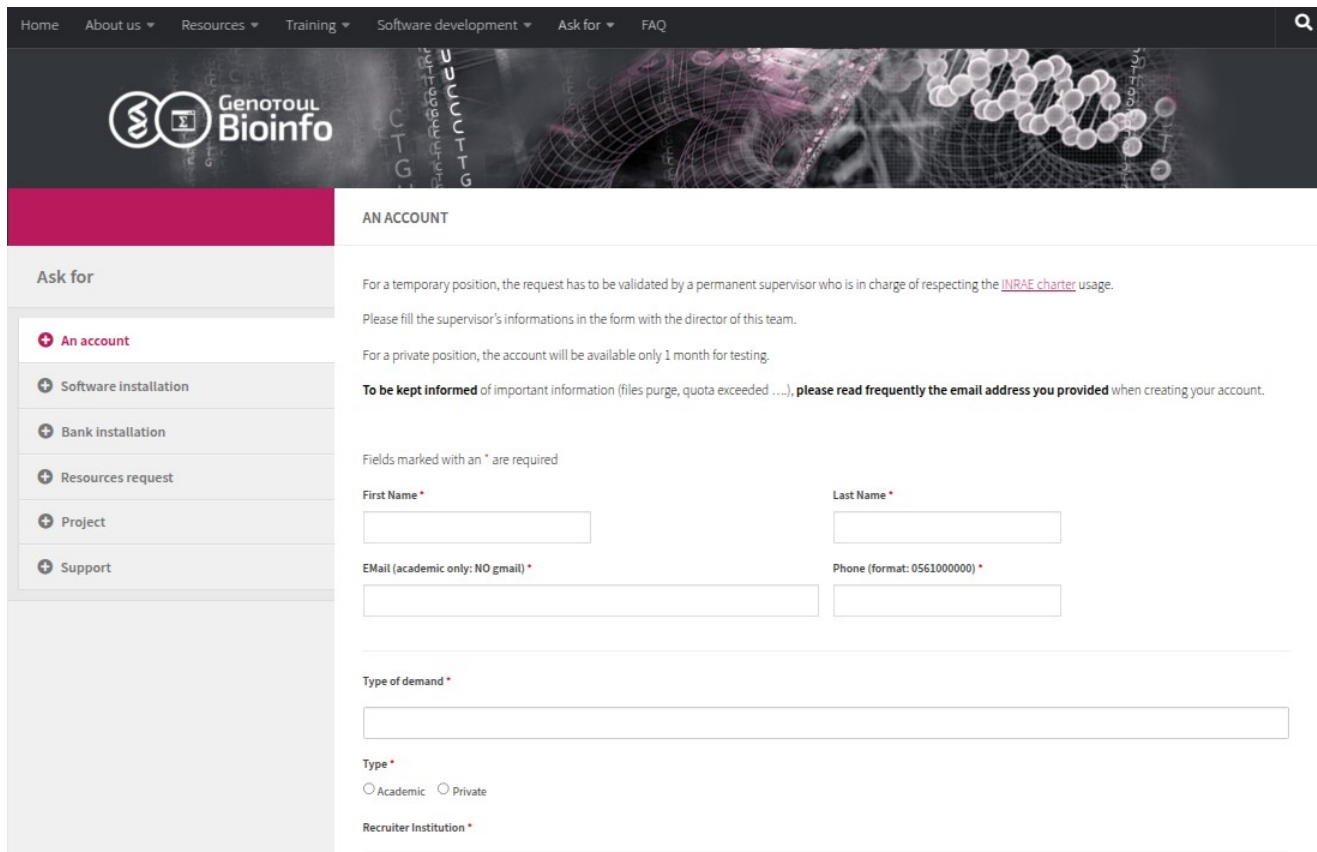
Reset Submit

Linux

GNU/Linux : Unix-like operating system

- Free and open source software
- Combination of Linux kernel and GNU project's software
- Linux kernel :
 - Initial Developer: Linus Torvalds (Helsinki), birth on 1991
- GNU project
 - Initial Developer: Richard Stallman (MIT), birth on 1983
- Large community of developers
- Hundreds of active distributions : Ubuntu, Fedora, Debian...
 - Some are commercial : RedHat, SUSE...

Linux – Ask for an account



Home About us Resources Training Software development Ask for FAQ

AN ACCOUNT

For a temporary position, the request has to be validated by a permanent supervisor who is in charge of respecting the [INRAE charter](#) usage.

Please fill the supervisor's informations in the form with the director of this team.

For a private position, the account will be available only 1 month for testing.

To be kept informed of important information (files purge, quota exceeded ...), **please read frequently the email address you provided** when creating your account.

Fields marked with an * are required

First Name * Last Name *

EMail (academic only: NO gmail) * Phone (format: 0561000000) *

Type of demand *

Type *

☐ Academic ☐ Private

Recruiter Institution *

Access to a 'work' environment on cluster

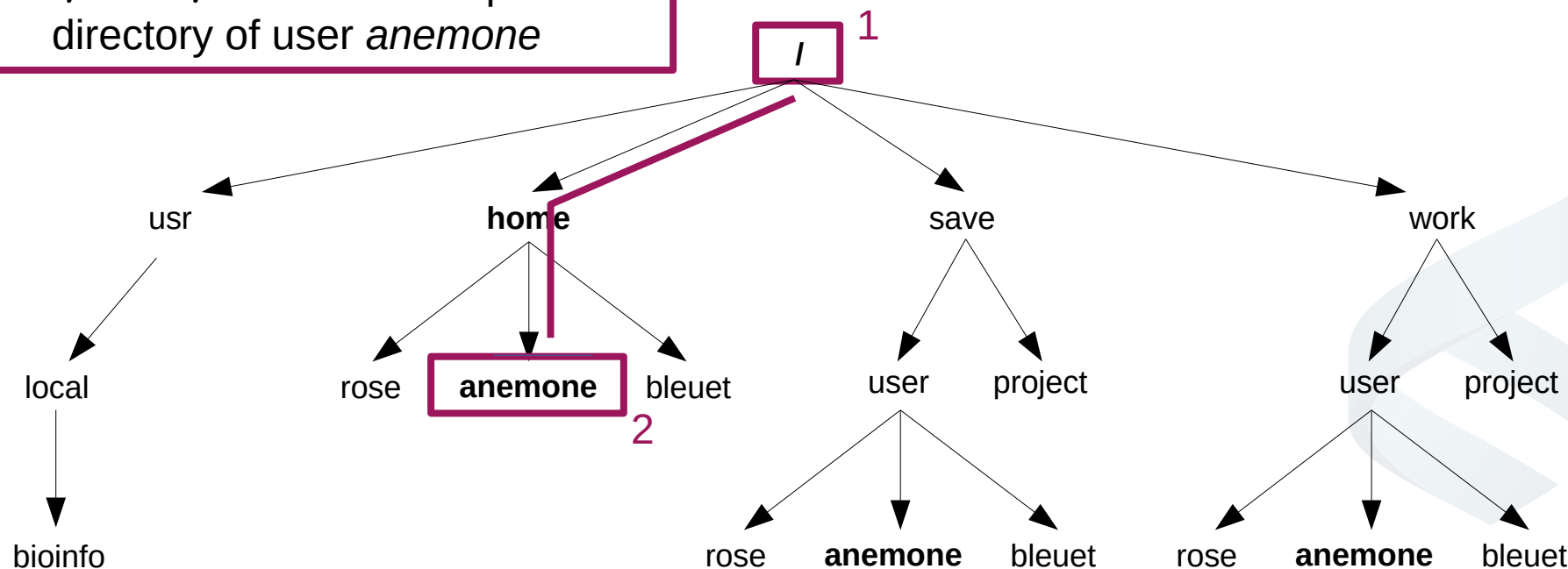
- Login + password (login nodes)
- Shared resources (cpu, memory, disk)
- Usage of software installed
- Free access to computational cluster
- Own space disk (`/save` & `/work` directory)

Correct social behaviour is expected

Linux – The tree structure

Some important places

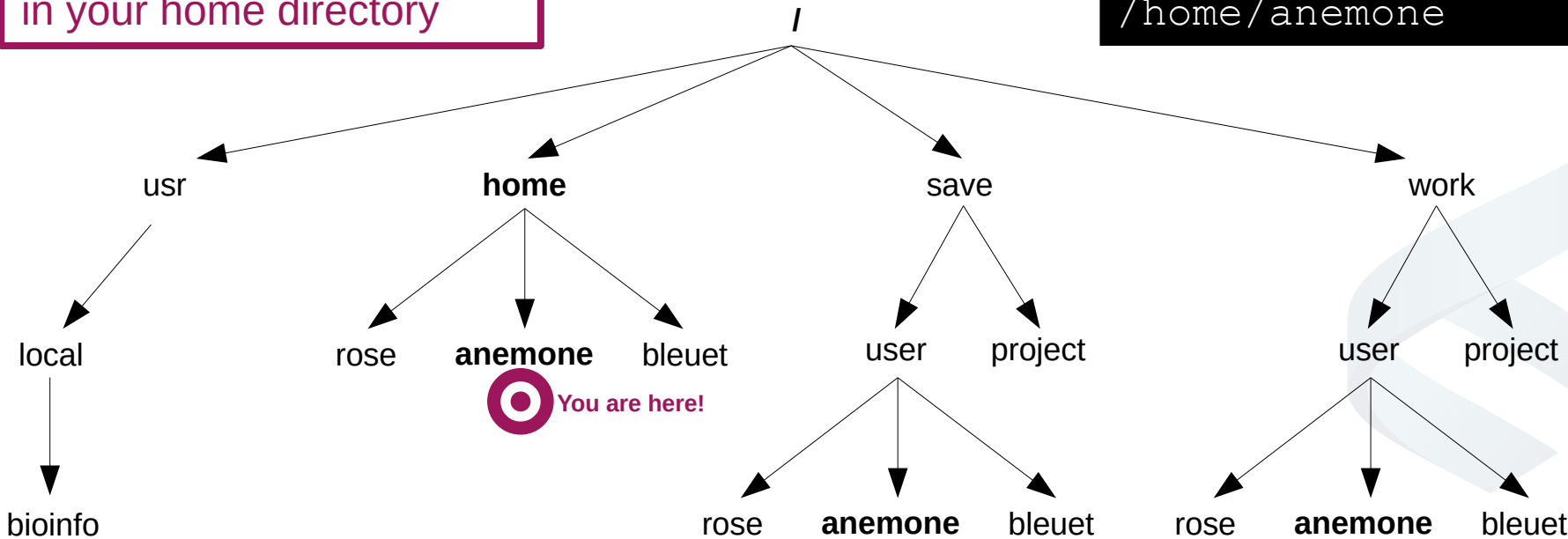
1. / : the root
2. /**home**/**anemone**: the personal directory of user *anemone*



In a terminal, you are always ‘somewhere’

When connecting, you are in your home directory

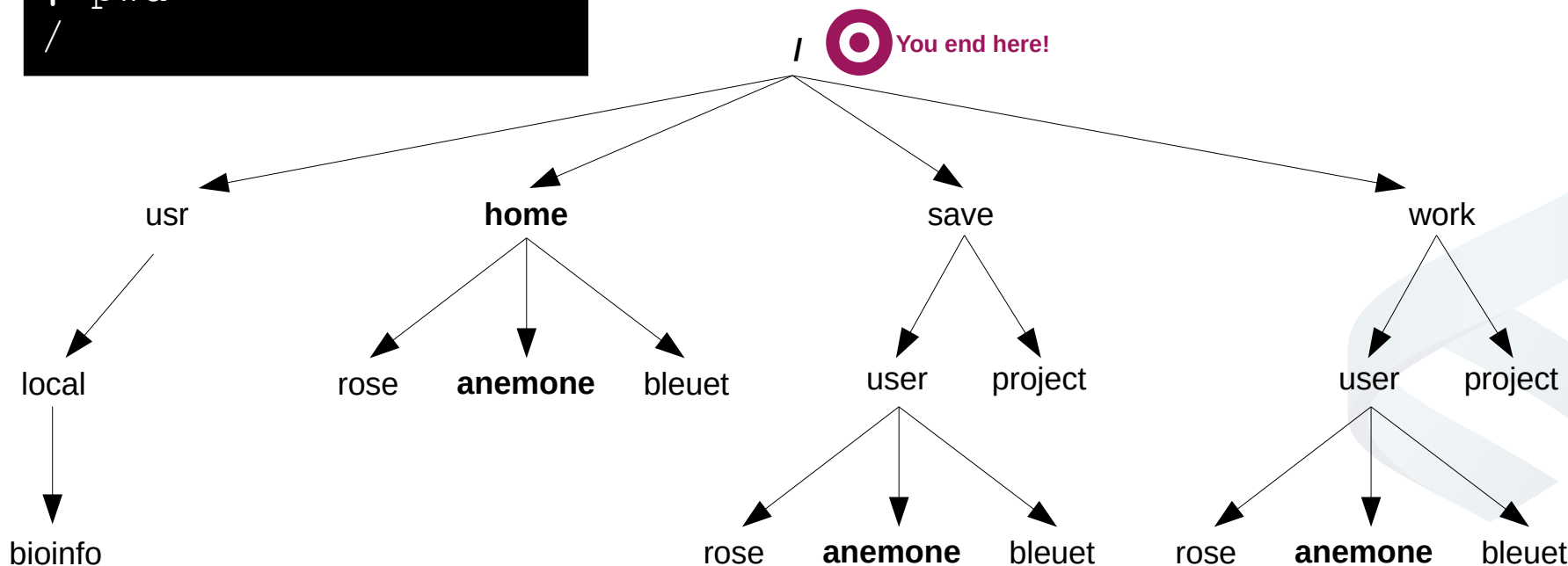
```
$ pwd
/home/anemone
```



Linux – Moving in the tree

```
# Move to root
$ cd /
# Check where we are
$ pwd
/
```

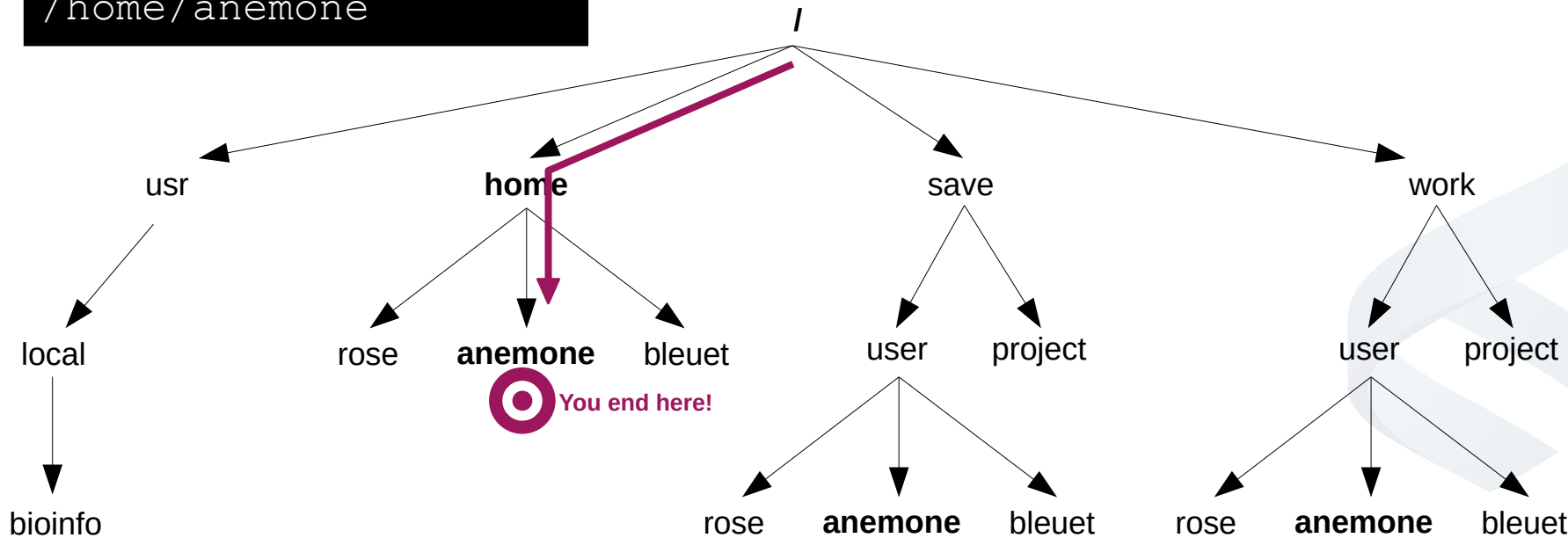
Notation	Meaning
/	the root directory



Linux – Absolute path

```
# Move to my home
$ cd /home/anemone
# Check where we are
$ pwd
/home/anemone
```

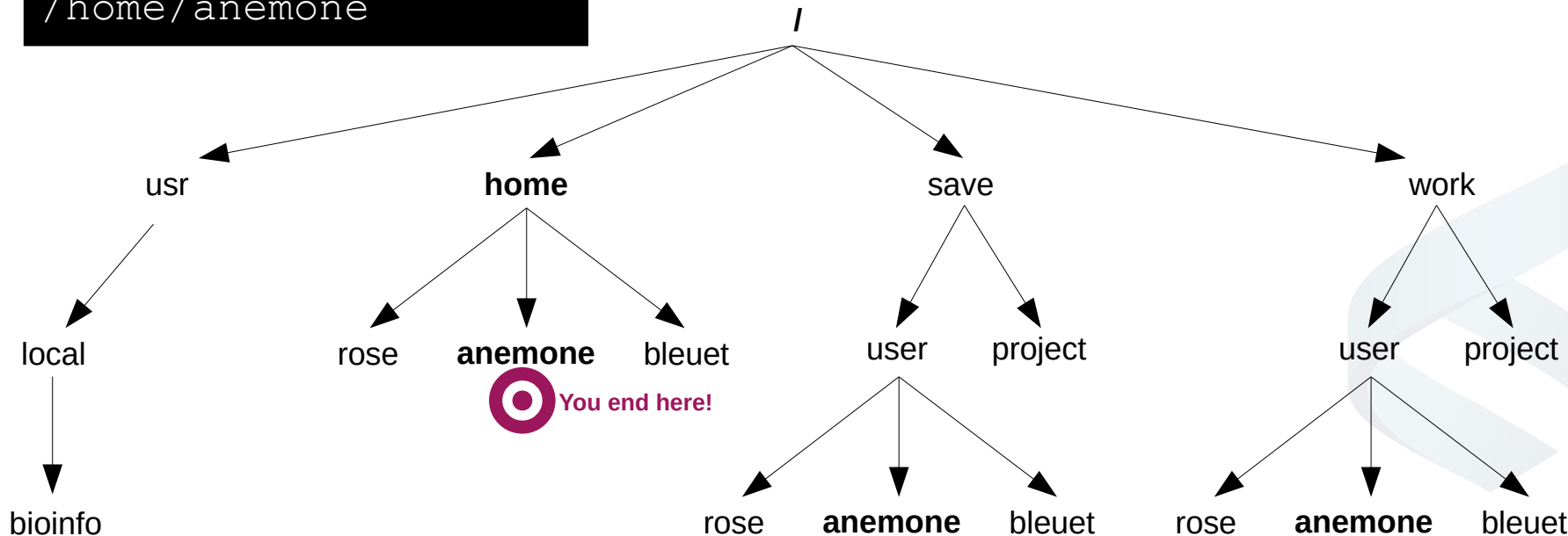
Notation	Meaning
/	the root directory, separator in path



Linux – Go home (lazy edition)

```
# Move to my home
$ cd ~
# Check where we are
$ pwd
/home/anemone
```

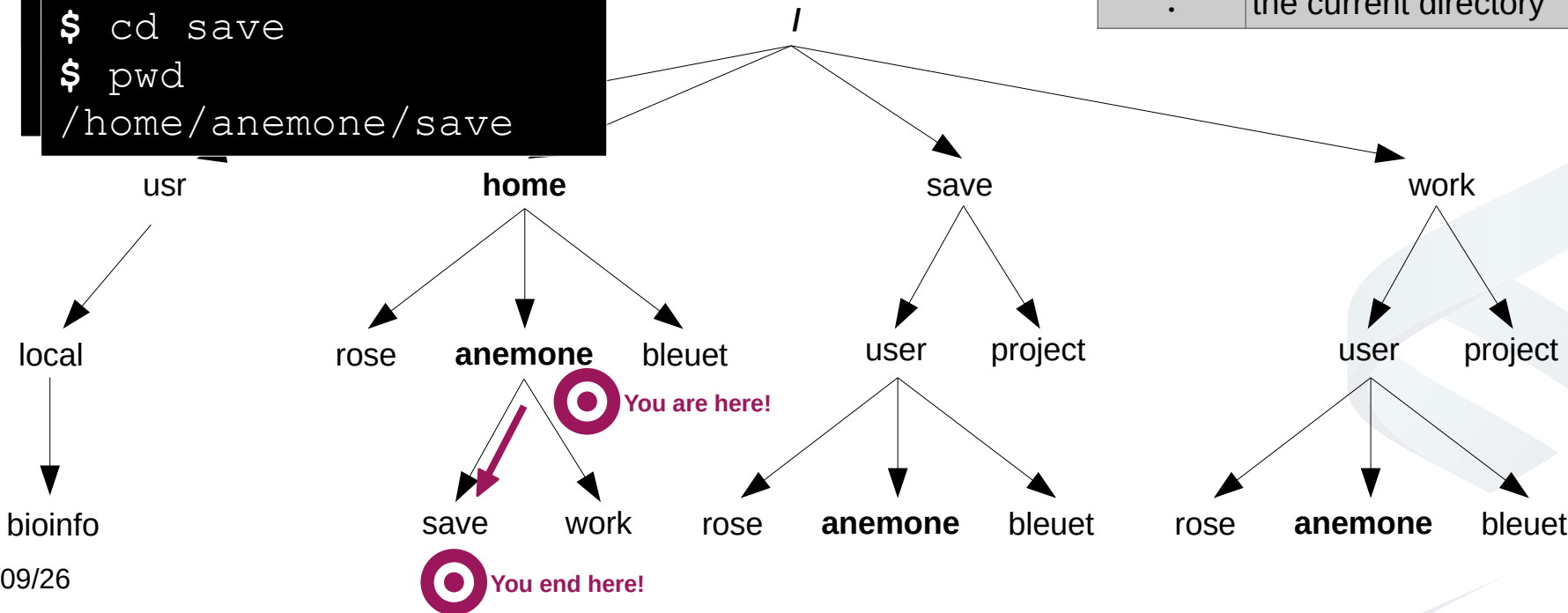
Notation	Meaning
/	the root directory, separator in path
~	your home directory



Linux – Relative path

```
# List my files/dir
$ ls
save  work
# Go to 'save' dir
$ cd save
$ pwd
/home/anemone/save
```

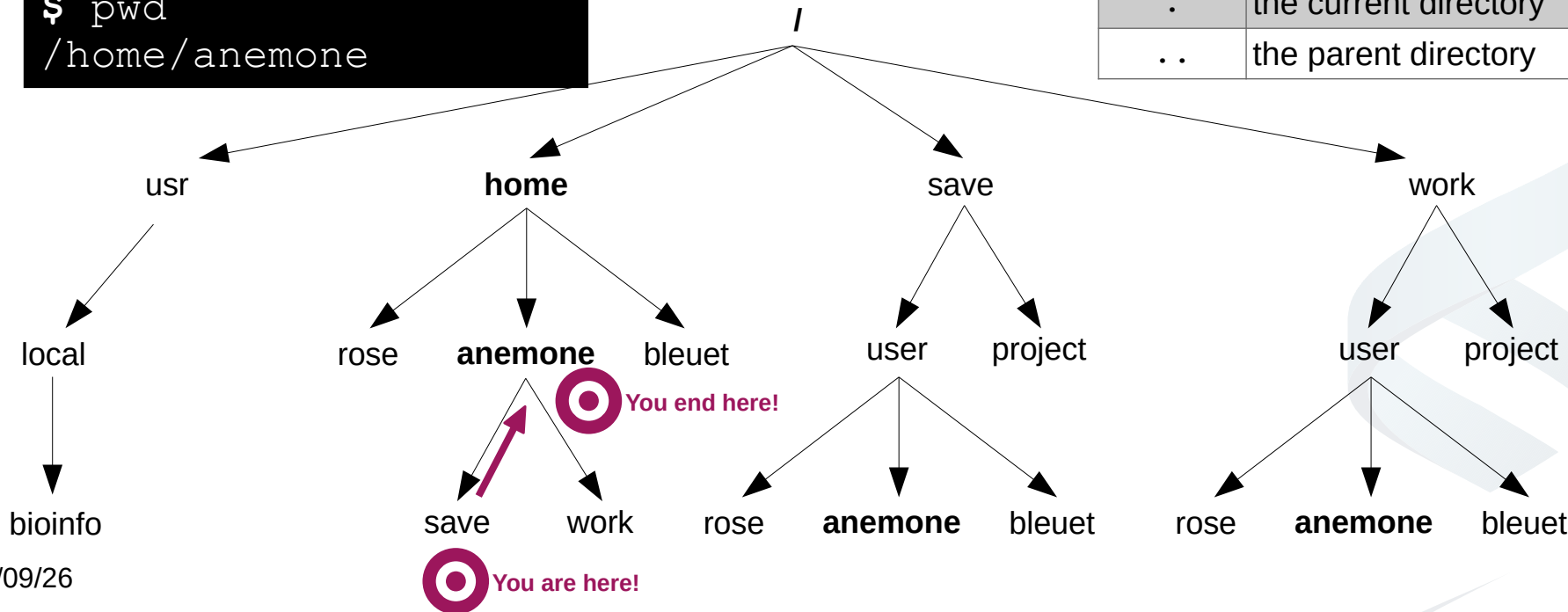
Notation	Meaning
/	the root directory, separator in path
~	your home directory
.	the current directory



Linux – Relative path

```
$ pwd
/home/anemone/save
# Go back home
$ cd ..
$ pwd
/home/anemone
```

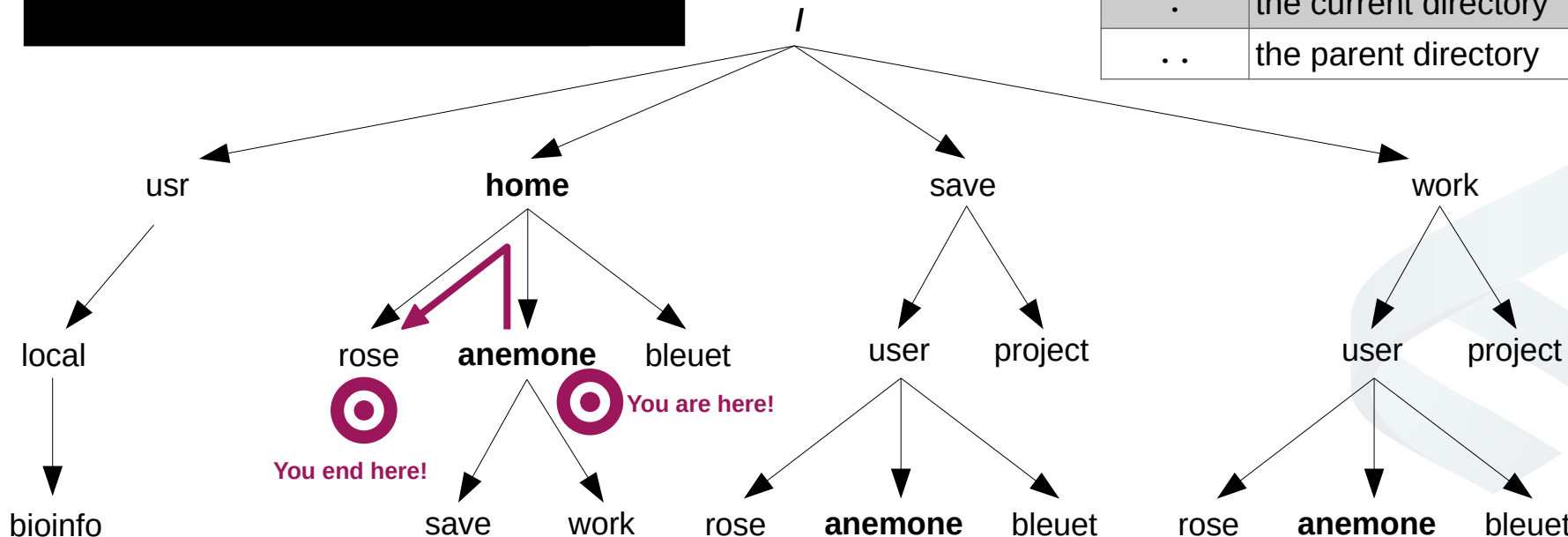
Notation	Meaning
/	the root directory, separator in path
~	your home directory
.	the current directory
..	the parent directory



Linux – Composing a path

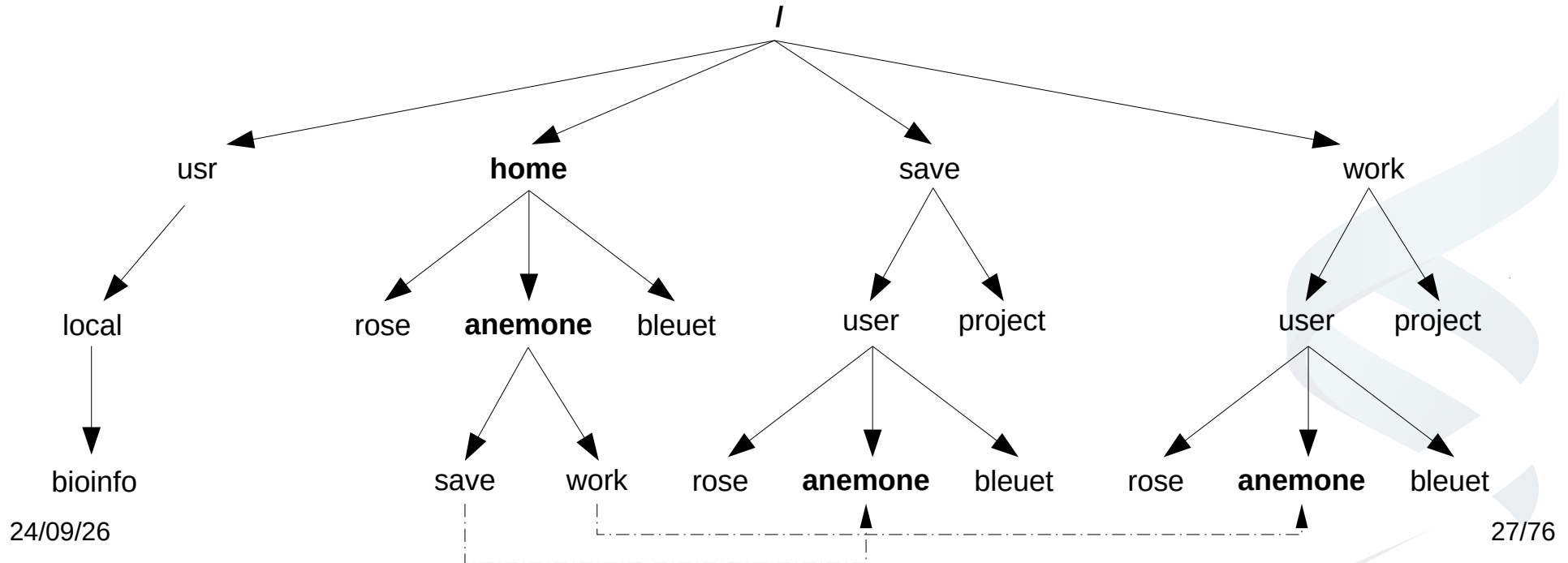
```
# What is in rose's home
$ ls ../rose
```

Notation	Meaning
/	the root directory, separator in path
~	your home directory
.	the current directory
..	the parent directory



A file/directory can point to another, like a shortcut.

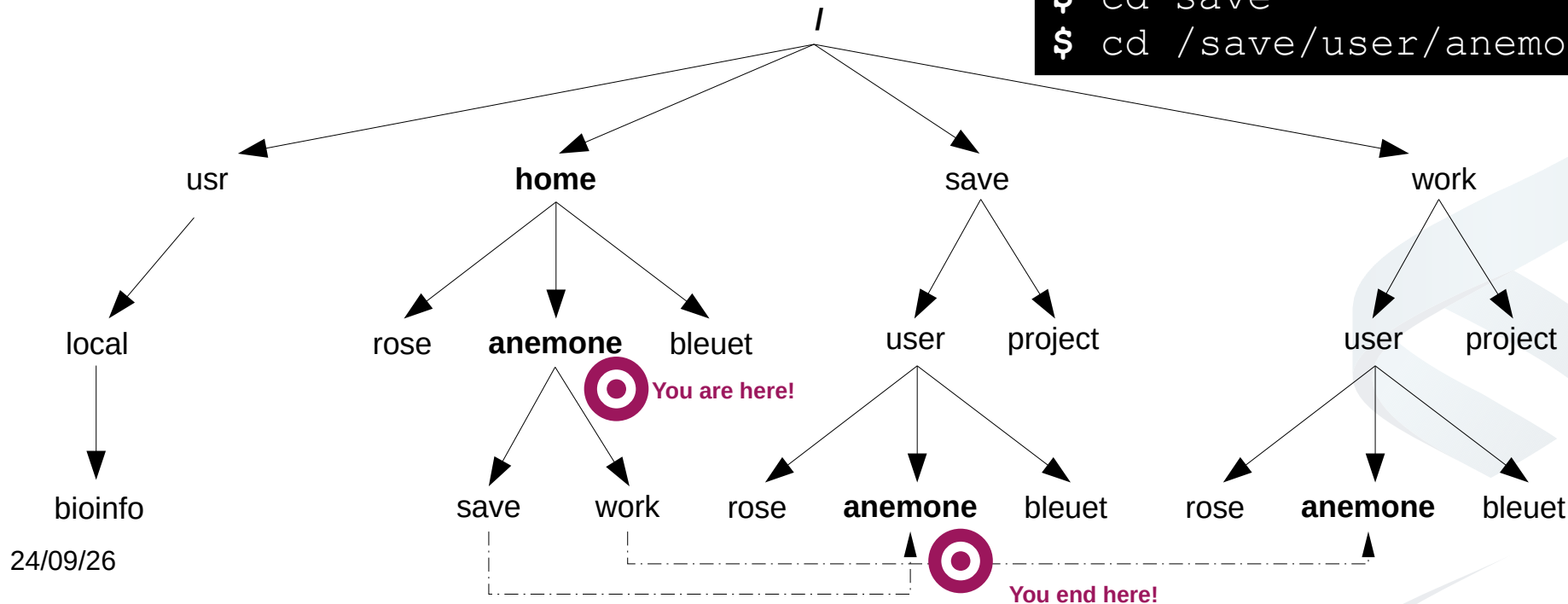
```
$ ls -l
lrwxrwxrwx 1 root root 19 18 janv. 2023 save -> /save/user/anemone
lrwxrwxrwx 1 root root 19 18 janv. 2023 work -> /work/user/anemone
```



Linux – Many ways

From your **home**, how to go in your **save**?

```
$ cd /home/anemone/save
$ cd ~/save
$ cd ./save
$ cd save
$ cd /save/user/anemone
```



To sum up

- Elements in a path are separated by /
 - **Absolute path** starts with /
 - **Relative path** doesn't
- Symbolic links are shortcuts
- When opening a terminal, you are in your home
- ~ is an alias to your home directory
- There are many ways to achieve the same result

Linux – base command anatomy

```
command_name [-option] [parameter]
```

Square brackets means element is optional

- `command_name` : What you want to do
- `option` : How to do it
- `parameter` : on which?

It concerns most of system commands

Examples

```
$ ls
$ ls -l /home
$ ls -a
$ ls -a -l
$ ls -l -a
$ ls -la
$ ls -al
```

} Same thing

Linux – Help on command

In a terminal

```
$ command_name [--help/-help/-h]  
$ man command_name
```

Examples

```
$ man ls  
$ man cd
```

On the web

- Linux man pages online
- tldr: <https://tldr.inbrowser.app/>

Linux – Some basic commands

cd : change directory

pwd : print working directory

ls : list directory contents

tree : list contents in a tree like format

who : show who is logged on the server

passwd : update user's authentication token

history : display the commands history

How to connect to genobioinfo

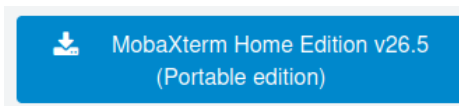
From *Linux / macOS*

- In a terminal

```
ssh -X username@genobioinfo.toulouse.inrae.fr
```

From *Windows*

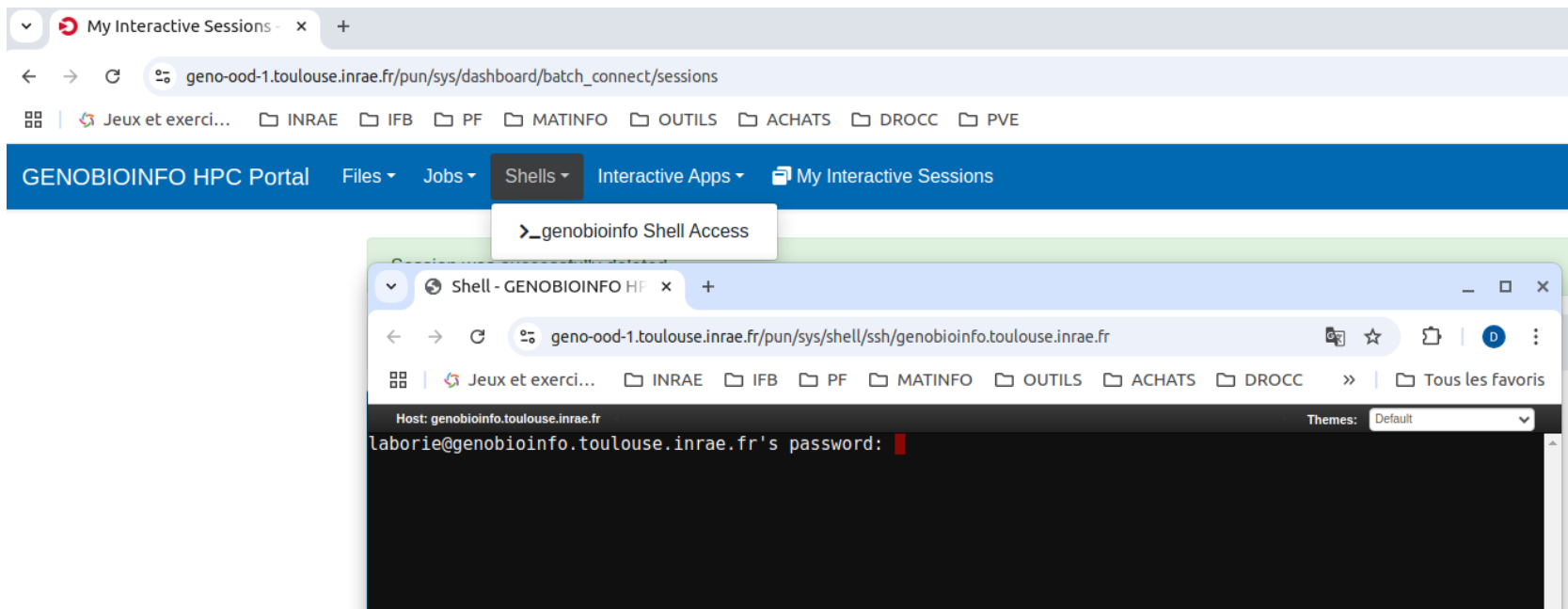
- MobaXterm
- WSL / openssh



How to connect to genobioinfo

By using Open On demand (OOD)

- Go to <https://geno-ood.toulouse.inrae.fr/>



Linux – Tricks and tips

Stop a process: Use `CTRL + C` key combination

Copy / Paste with mouse:

- Select a text (it is automatically copied)
- Click on the mouse wheel (the text is pasted where the cursor is located)

Quality of life

- Navigate in command history: `Up` key / `Down` key
- Bash completion: `Tab` / `Tab Tab`
<https://vm-genoword.toulouse.inrae.fr/FAQ/faq/linux/#efficient-shell>

When lost

- `pwd` : Print where you are
- `cd` : Go to home



- Connect yourself to `genobioinfo` server with your (training) login/password
- Do the exercices (TP1)

<https://genotoul-bioinfo.pages-forge.inrae.fr/linux-cluster/linux-initiation/tp1/>

Linux - Manipulating files

Linux - Manipulating files

Everything is file

Under Linux, **everything is file**

- File types
- Manipulating files
- Wildcard characters

} TP 2.1

- File permissions
- Search for files

} TP 2.2

Linux - Manipulating files

List files

List the content of a directory

```
ls [-option] [directory_path]
```

Options:

- a : display hidden files/dir
- l : use the long format
- t : sort the content
- r : reverse the sort order

```
$ ls -lh
-rw-r--r-- 1 laborie BIOINFO    69 22 oct.   2015 SAMPLE.nhr
-rw-r--r-- 1 laborie BIOINFO   144 22 oct.   2015 SAMPLE.nin
-rw-r--r-- 1 laborie BIOINFO 106K 22 oct.   2015 SAMPLE.nsq
```

Linux - Manipulating files

File types

The `ls -l` command (long listing format)

```
$ ls -l
-rwxr-xr-x 1 cnoirot BIOINFO 123 Jun 14 17:16 blastforeach.sh
-rw-r--r-- 1 cnoirot BIOINFO 3683591 Jun 9 11:56 Diapo_F10a.odp
drwxr-xr-x 3 cnoirot BIOINFO 4096 Jul 8 14:56 igv
-rwxr-xr-x 1 cnoirot BIOINFO 20 Apr 16 11:21 monscript.sh
-rw-r--r-- 1 cnoirot BIOINFO 954415 Oct 3 2009 Presentation_pyrocleaner.odp
lrwxrwxrwx 1 cnoirot BIOINFO 13 Mar 15 2009 save -> /save/user/cnoirot
lrwxrwxrwx 1 cnoirot BIOINFO 13 Mar 18 2009 work -> /work/user/cnoirot
```

Type +
Permissions

Nb elements

Owner

Group

Size

Date

Name

File

- Create

```
touch file_name
```

- Delete

```
rm file_name
```

Linux - Manipulating files

Create and delete files

Directory

- Create

```
mkdir dir_name
```

- Delete

```
rmdir dir_name
```

- Delete with content

```
rm -r dir_name
```

Linux - Manipulating files

Copy and moving files

Copy

- File

```
cp source_file target_file
```

- Directory

```
cp -r source_dir target_dir
```

Move

- Just move

```
mv file_name existing_dir_name/
```

- Rename

```
mv old_file_name new_file_name
```

- Move and rename

```
mv old_file_name existing_dir_name/new_file_name
```

Linux - Manipulating files

Wildcards characters

? replace one character by any character

```
ls bov?.seq
```

***** replace zero, one or many characters

```
ls *.seq
rm bacterie*
```

[] replace any character between a selection

```
ls [123]*
ls f[a-c]*
```

Linux - Manipulating files

Symbolic link

A kind of shortcut

```
ln -s source_filename target_file_name
```

```
$ ls -l work
lrwxrwxrwx 1 cnoirot BIOINFO      13 Mar 18  2009 work -> /work/user/cnoirot
```

file type: `l` = symbolic link

link resolution

Linux - Manipulating files Practice

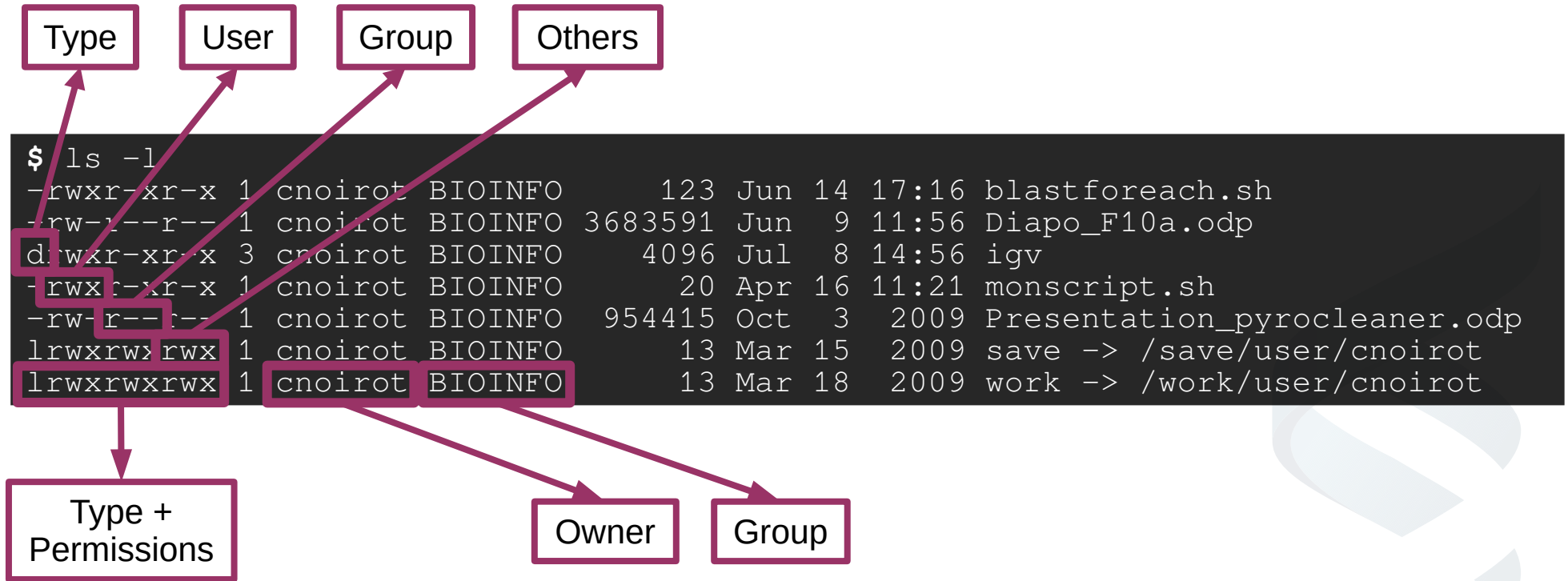
TP 2.1

<https://genotoul-bioinfo.pages-forge.inrae.fr/linux-cluster/linux-initiation/tp2.1/>

Linux - Manipulating files

File permissions

POSIX permissions: read, write, execute



Linux - Manipulating files

Set file permissions

You can manage permissions of our own files

```
chmod [option] file_name
```

With [option] a composition of

- **u** : user, **g** : group, **o** : other, **a** : all (one or many)
- **+** : allow, **-** : forbid (only one)
- **r** : read, **w** : write, **x** : execute (one or many)

```
# Allow the group to write on a file  
$ chmod g+w file_name
```

Linux - Manipulating files

Search for file

Find some files of directory

```
find dir_name [-option] [parameters]
```

```
# Find all files and directories ending with .seq (case sensitive)
$ find /home/formation -name "*.seq"

# Find all directories in this directory and its subdirectories
$ find . -type d

# Find all files in this directory and its subdirectories
$ find . -type f

# Find on the computer all files and dirs with size >1000 kB
$ find / -size +1000k
```

Linux - Manipulating files

Kinds of file

Extension is a convention, not an obligation

```
file file_name
```

```
$ file find_result.txt  
ASCII text
```

```
$ file work  
work: symbolic link to /work/user/anemone
```

```
$ file extract_users_stats.py  
Python script, ASCII text executable
```

Linux - Manipulating files

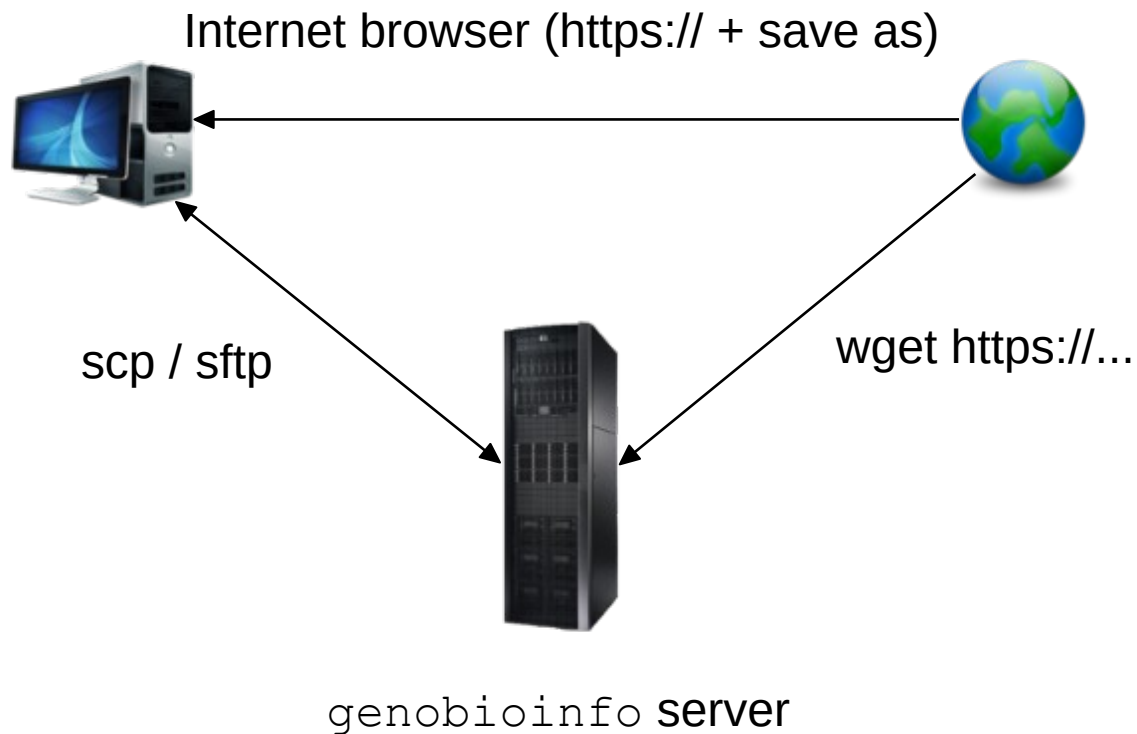
Practice again

TP 2.2

<https://genotoul-bioinfo.pages-forge.inrae.fr/linux-cluster/linux-initiation/tp2.2/>

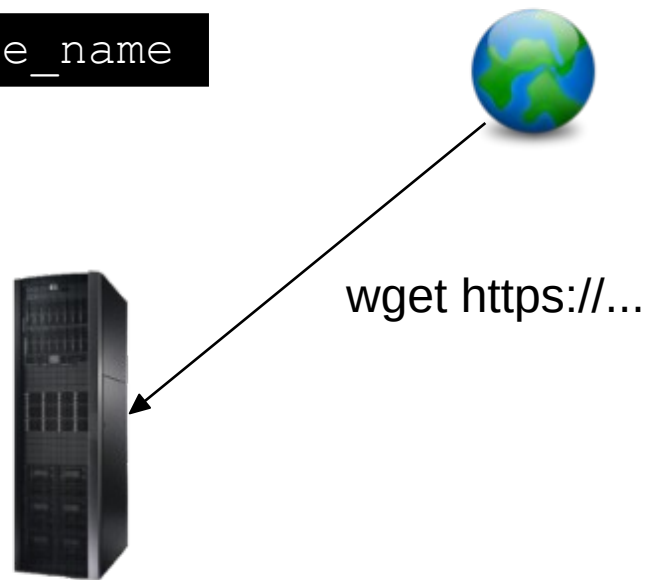
- Downloading / transferring
- Disk space control
- Compressing / uncompressing
- TP 3.1
- Displaying files
- Utility commands
- Data extraction
- Redirections
- TP 3.2
- My first script

Downloading / transferring



Directly from internet to genobioinfo

```
wget https://download.url/file_name
```



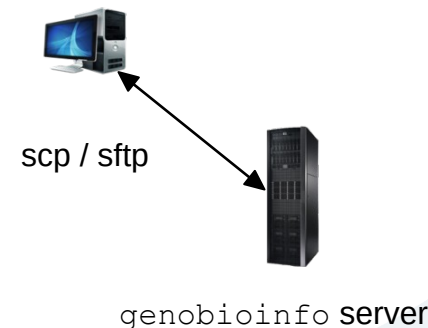
Transferring

Transfer between genobioinfo and a personal computer

- *Reminder* : copy a file

```
cp [-r] source_name target_name
```

- Copy a file across network
(Commands are run from your desktop)



```
# Send file(s) to cluster
scp [-r] source_name anemone@genobioinfo.toulouse.inrae.fr:target_name

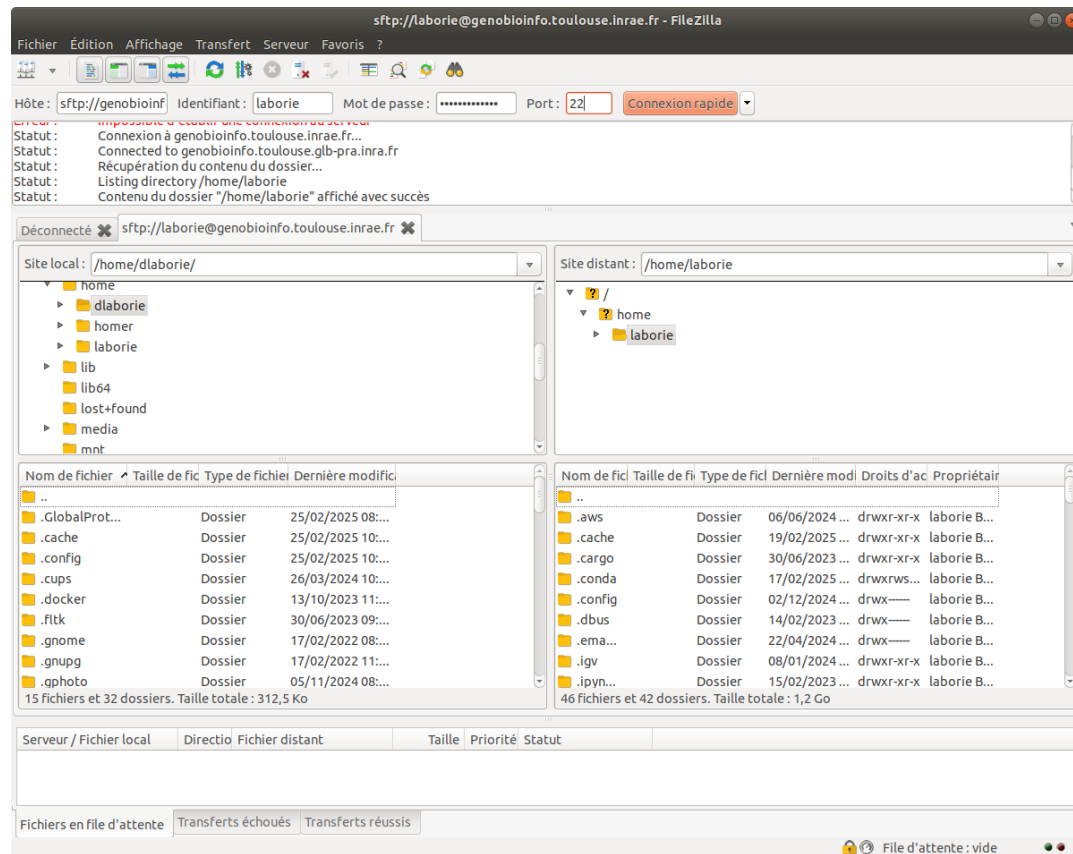
# Get file(s) from cluster
scp [-r] anemone@genobioinfo.toulouse.inrae.fr:source_name target_name
```

The same thing you use to connect with ssh

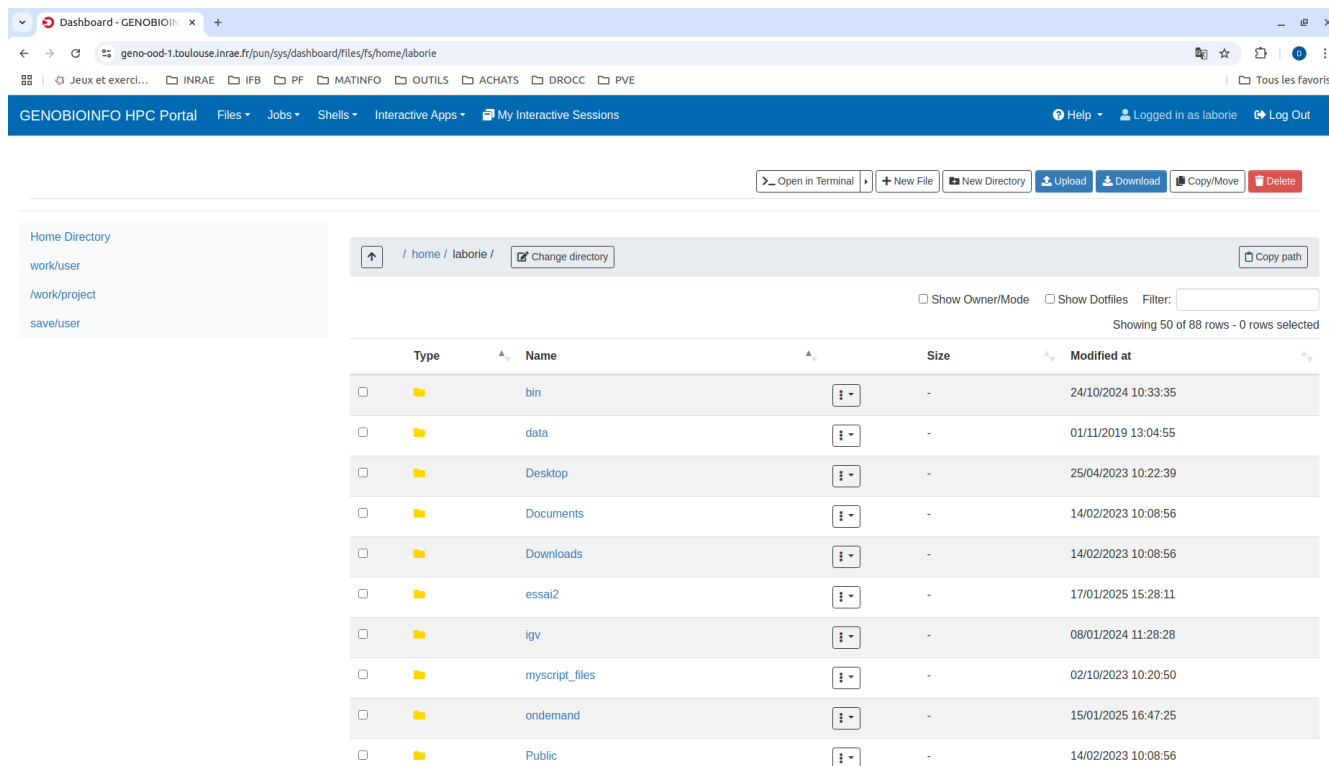
Transferring with graphical interface

Sftp clients:

- Filezilla on Linux/macOS/Windows
- Cyberduck for macOS/Windows



Open On Demand : Upload / Download



The screenshot shows the GENOBIOINFO HPC Portal web interface. The browser address bar displays the URL: `geno-ood-1.toulouse.inrae.fr/pun/sys/dashboard/files/ty/home/laborie`. The page header includes navigation links: GENOBIOINFO HPC Portal, Files, Jobs, Shells, Interactive Apps, and My Interactive Sessions. A top navigation bar contains buttons for Open in Terminal, New File, New Directory, Upload, Download, Copy/Move, and Delete. The main content area shows the file management interface for the user 'laborie' in the 'home' directory. A sidebar on the left lists the Home Directory, work/user, /work/project, and save/user. The main area displays a table of files and directories.

Type	Name	Size	Modified at
bin		-	24/10/2024 10:33:35
data		-	01/11/2019 13:04:55
Desktop		-	25/04/2023 10:22:39
Documents		-	14/02/2023 10:08:56
Downloads		-	14/02/2023 10:08:56
essai2		-	17/01/2025 15:28:11
igv		-	08/01/2024 11:28:28
myscript_files		-	02/10/2023 10:20:50
ondemand		-	15/01/2025 16:47:25
Public		-	14/02/2023 10:08:56

Disk spaces available

Show the different disk spaces

```
df [-option] [partition_name]
```

```
$ df -h
```

Filesystem	Size	Used	Avail	Use%	Mounted on
/dev/sda5	204G	8.7G	185G	5%	/
tmpfs	63G	16K	63G	1%	/dev/shm
/dev/sda1	124M	35M	84M	30%	/boot
/dev/sda3	9.9G	559M	8.8G	6%	/var
isi-ceri:/ifs/save	60T	47T	14T	78%	/save
isi-ceri:/ifs/home	100G	47G	54G	47%	/home

Disk space usage

- Get the size of a file/directory

```
du -csh --apparent-size dir_name
```

- Check your quota (specific to the cluster)

<https://vm-genoword.toulouse.inrae.fr/FAQ/faq/default-resources/#how-to-get-my-disk-quota-and-usage>

Compressing / uncompressing

Several formats: **gzip** (gz), bzip2 (bz2), zstandard (zstd), xz, zip, 7zip (7z), rar, Z, ...

- **gzip** : compress a file to .gz

```
gzip file_to_compress
```

- **gunzip** : uncompress a file from .gz

```
gunzip file_to_uncompress.gz
```

The tar command (tape archive)

- Create an archive

```
tar -cvf formation.tar /home/formation
```

- Extract an archive

```
tar -xvf formation.tar /tmp
```

- Create and compress on the fly an archive

```
tar -cvzf formation.tar.gz /home/formation
```

- Uncompress and extract on the fly an archive

```
tar -xvzf formation.tar.gz /tmp
```

Transfert and archives Practice

TP 3.1

<https://genotoul-bioinfo.pages-forge.inrae.fr/linux-cluster/linux-initiation/tp3.1/>

Looking into files

- Display a file content

```
cat file_name
```

```
$ cat /bank/ncbi/genbank/genbankRelease/current/fasta/gbphg1.fasta  
>AB000833.1 Bacteriophage Mu DNA for ORF1, sheath protein gpL, ORF2,  
ORF3, complete cds.  
ACGGTCAGACGTTTGGCCCGACCACCGGGATGAGGCTGACGCAGGTCAGAAATCTTTGTGACGACAACC  
GTATCAATGCCGGTGTGG...
```

- Display many files content

```
cat file_name1 file_name2 ...
```

Display a file content with pagination

```
more file_name
```

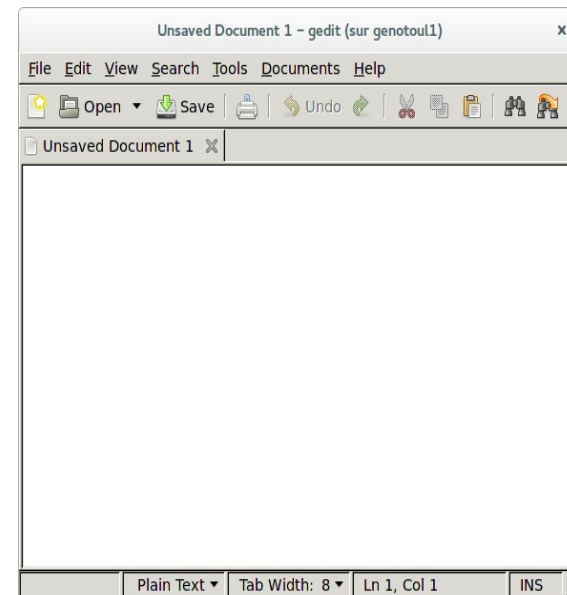
```
less file_name
```

`less` has more fonctionnalities than `more`

```
$ less my_file.txt
```

Modify a text file content

- **vi** : installed anywhere, powerful, but not easy to use
- **nano** : simple to use
- **gedit** : graphical editor *
- **emacs** : advanced features but difficult



* You need to be connected with option
`ssh -X ...`

Some text manipulation commands

Count words(words count)

```
wc [-option] file_name
```

```
# Number of characters
```

```
$ wc -c file_name
```

```
# Number of words
```

```
$ wc -w file_name
```

```
# Number of lines
```

```
$ wc -l file_name
```

Sort a file

```
sort [-option] file_name
```

```
# Numeric sort by column 1
```

```
$ sort -n -k 1
```

Part of a file

Display the beginning of a file

```
head [-number] file_name
```

```
# Display 100 first lines
```

```
$ head -100 file_name
```

Display the end of a file

```
tail [+/-number] file_name
```

```
# Display 100 last lines
```

```
$ tail -100 file_name
```

```
# Display from 6th line to end of file
```

```
$ tail -n +6 file_name
```

Select some columns

```
cut [-number] file_name
```

```
# Get the first character
```

```
$ cut -c 1 file_name
```

```
# Get columns 2 and 3
```

```
$ cut -f 2,3 file_name
```

Find text content in files

```
grep [-options] 'pattern' file_name [...]
```

pattern can use wildcard

```
# Simple search
$ grep SEQRES pdb_file
# Case insensitive search
$ grep -i SEQRES pdb_file
# Count the number of lines matching the pattern
$ grep -c SEQRES pdb_file
# Search lines that don't match the pattern
$ grep -v SEQRES pdb_file
```

Standard input & output

Most commands use the standard input / output

- Standard input (*sdtin*) : the keyboard
- Standard output (*sdtout*) : the console

Input / Output (I/O) may be **redirected** by using the following operators : `<`, `>`, `|`, and `>>`

Redirections

Redirect the *stdout* to a new file

```
command > output_file_name
```

```
$ grep -i Human uniprot.fasta > fic_result
```

Redirect the *stdout* to another software *stdin*

```
command1 | command2
```

Redirect the *stdout* to an existing file by appending it to the end of file

```
command >> output_file_name
```

```
$ grep -i Human uniprot.fasta | wc -l
```

```
$ grep -i bovin uniprot.fasta >> fic_result
```

Merge split files

Merge files

```
cat [-options] file_name ...
```

```
$ cat file1.txt file2.txt > merged_file
```

Split a file in many files

```
split [-options] file_name
```

```
# Split file_name.txt into  
# many files of 500 lines each  
$ split -l 500 file_name.txt
```

Look a difference between files (line per line)

- with command line

```
diff file_1 file_2
```

- with graphical interface*

```
meld file_1 file_2
```

* You need to be connected with option
ssh -X ...

Transfert and archives Practice

TP 3.2

<https://genotoul-bioinfo.pages-forge.inrae.fr/linux-cluster/linux-initiation/tp3.2/>

My first script

- A script = a succession of commands
- Put commands into a text file

```
$ gedit prog &
```

- Give the execution right

```
$ chmod +x prog
```

- Execute the script

```
$ ./prog
```

My first script

- Automation and plan
- Win of time (re-utilization)
- Templates : easy to find on the web
- Portable (running on all Unix-like systems)

Be careful to the syntax between different shell languages (csh, bash, ...)

Run a `blast` for all the fasta files of the directory :

```
#!/bin/bash

## COMMENT : THIS IS THE INPUT VARIABLE
REPERTOIRE=$1

## COMMENT : LIST ALL OF FILES
LISTE=$(ls $REPERTOIRE)
echo $LISTE

## COMMENT : REPETITION
for FILE in $LISTE
do
    blastall -p blastn -i $REPERTOIRE/$FILE -d swissprot -o
$FILE.out
    echo "Blastall sur le fichier : $FILE: ok"
done
exit
```

Continuous improvement

<https://enquetes.inrae.fr/index.php/84236?lang=fr>

