Plateforme Bioinformatique Midi-Pyrénées

geno toul bioinfo

Training Day : Linux

cc BY SA

Objectives

At the end of the day, you will be able to use Linux command line in order to :

- Connect to «genobioinfo» server
- Use available tools
- Transfer files between server and desktop
- Prepare data files
- Start processes with command line

Planning of the day

Part I : 09h00 - 10h30

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

Part II : 11h00 - 12h30

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

Part III : 14h00 - 17h00

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

Part I

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

Genotoul Bioinfo

Mission

Provide to public regional community :

Equipment

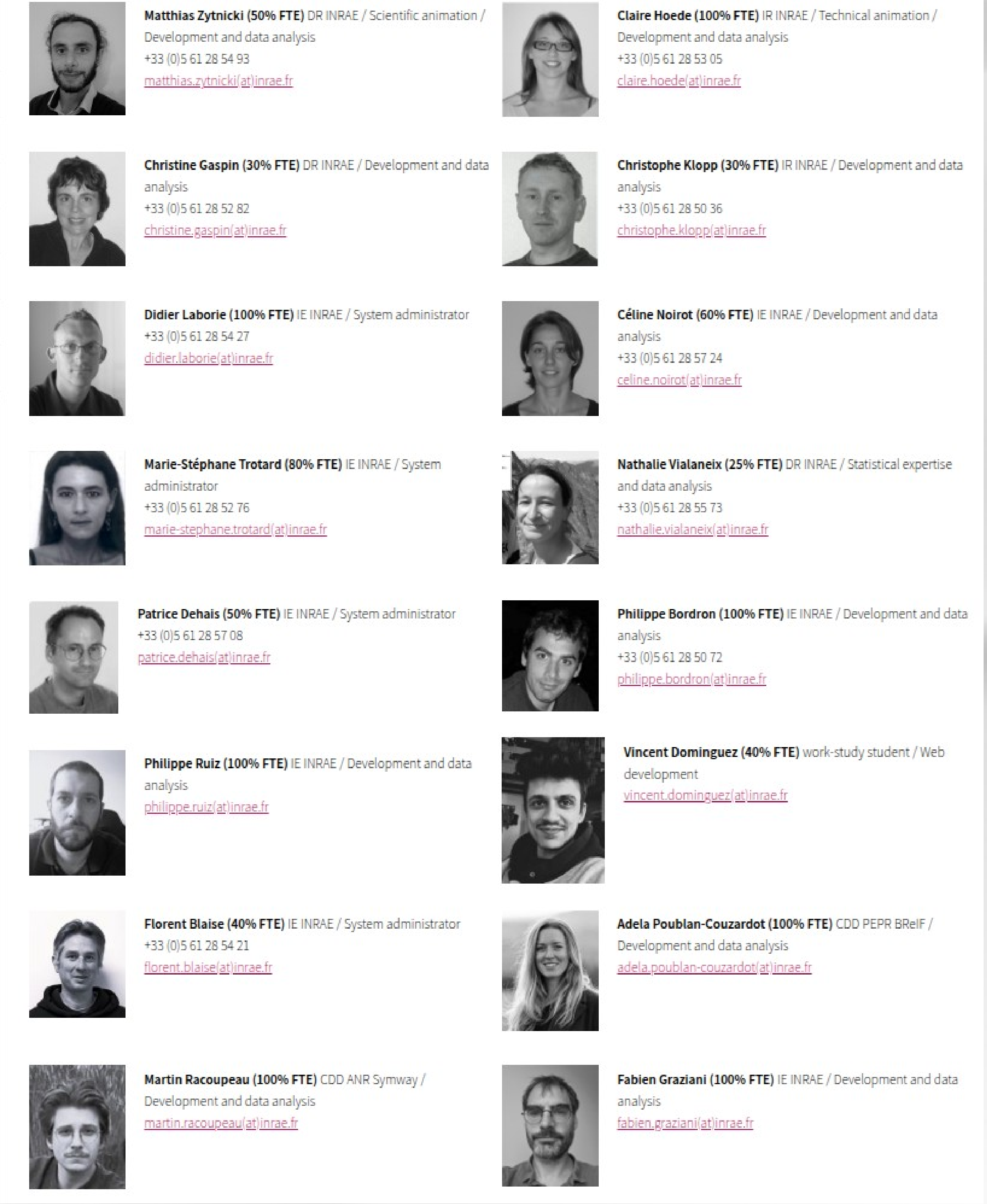
- Storage disk space
- High Performance Computer
- Hosting facilities (virtual machine, web site)

Services

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

Plateforme Bioinformatique Midi-Pyrénées

The team



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Genotoul Bioinfo

The users

1100+ registered users :

- 85% from INRAe (national) or other academic laboratories (regional)
- Biologists or computer scientists working in bio-informatics

Genotoul Bioinfo

Equipments

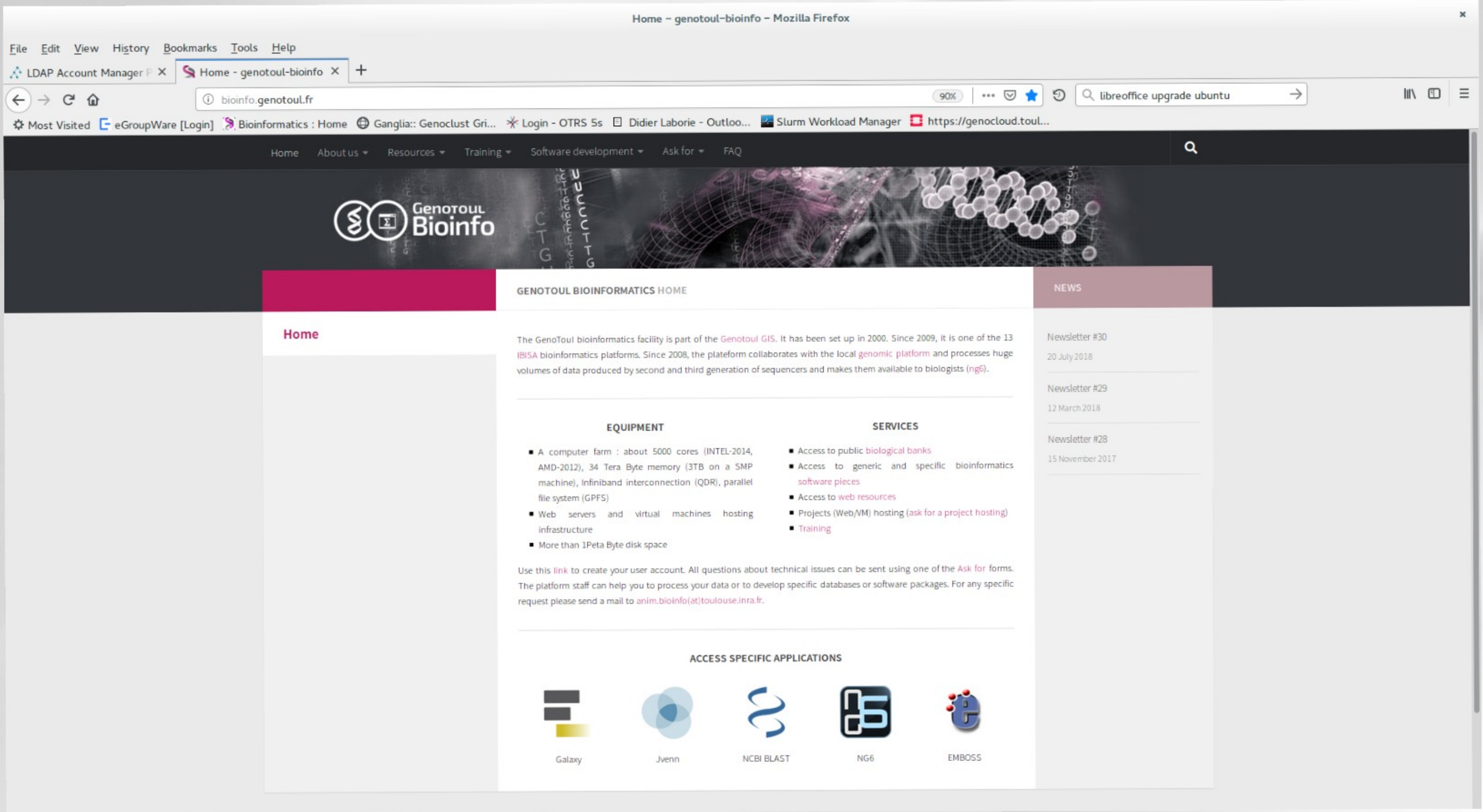
- **Computing cluster (HPC)**
  about 5000 cores, 80TB RAM
  4,5 PB disk space available for computing
- **Permanent Storage File System**
  2*1,6 PB disk space capacities (asynchronous replication)
- **Virtual machines (VM)**
  capacities for servers hosting and web services

Disk spaces

/usr/local/bioinfo/src	Bioinformatics software
/bank	Genomic reference databanks
***/home/*username**	User **configuration files** ONLY (10 GB user quota)
***/work/*user/username**	**Temporary** computational disk space (1 TB user quota)
***/save/*user/username**	**Permanent** disk space (**with BACKUP**) (250 GB user quota + replication)
/save/project/XXX ***/work/project/XXX***	**Billed** project disk space (**work** and / or **save**)

Genotoul Bioinfo

https://bioinfo.genotoul.fr



GENOTOUL BIOINFORMATICS HOME

The GenoToul bioinformatics facility is part of the Genotoul GIS. It has been set up in 2000. Since 2009, it is one of the 13 IBISA bioinformatics platforms. Since 2008, the plateform collaborates with the local genomic platform and processes huge volumes of data produced by second and third generation of sequencers and makes them available to biologists (ng6).

EQUIPMENT

- A computer farm : about 5000 cores (INTEL-2014, AMD-2012), 34 Tera Byte memory (3TB on a SMP machine), Infiniband interconnection (QDR), parallel file system (GPFS)
- Web servers and virtual machines hosting infrastructure
- More than 1Peta Byte disk space

SERVICES

- Access to public biological banks
- Access to generic and specific bioinformatics software pieces
- Access to web resources
- Projects (Web/VM) hosting (ask for a project hosting)
- Training

Use this link to create your user account. All questions about technical issues can be sent using one of the Ask for forms. The platform staff can help you to process your data or to develop specific databases or software packages. For any specific request please send a mail to anim.bioinfo(at)toulouse.inra.fr.

ACCESS SPECIFIC APPLICATIONS

NEWS

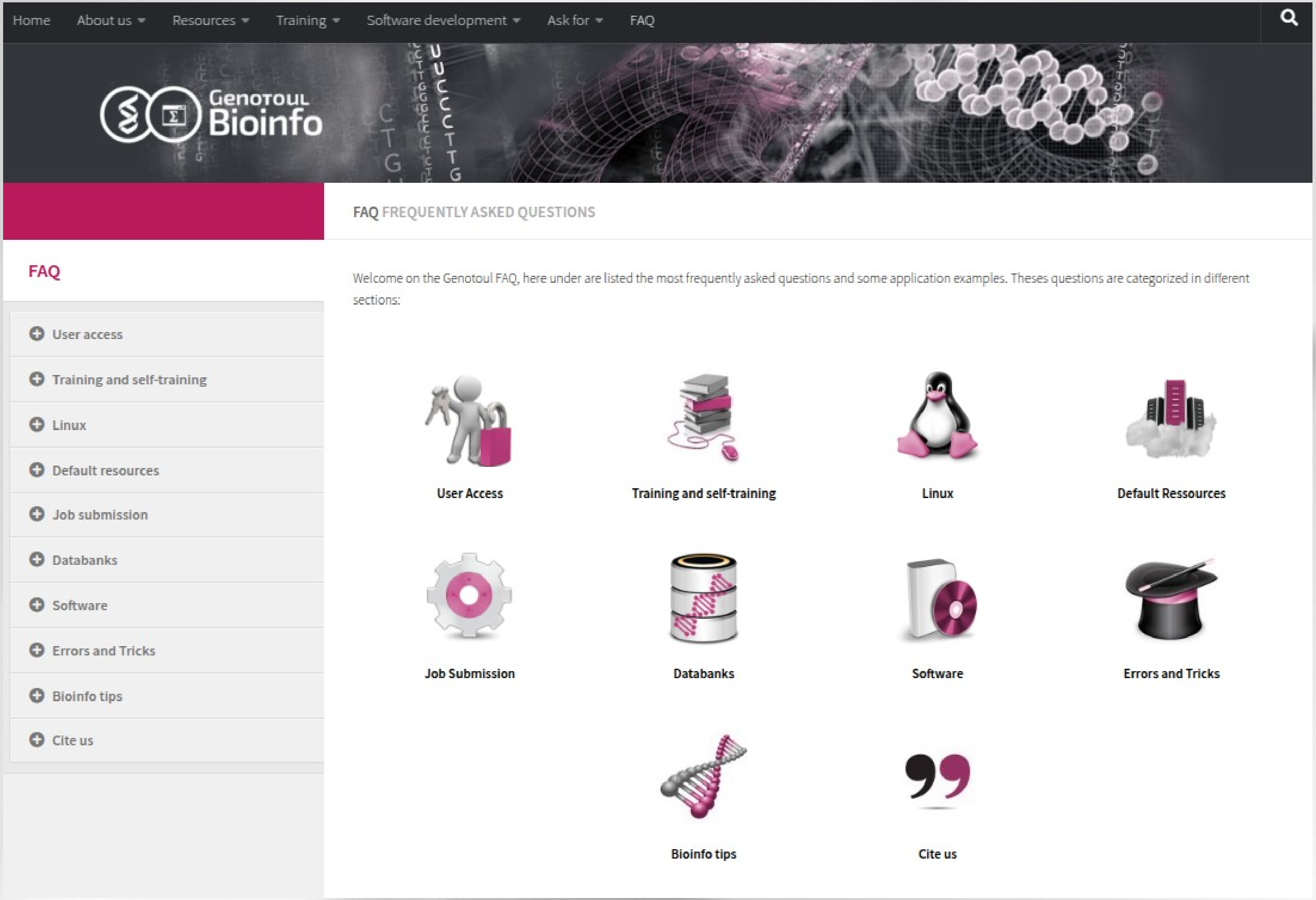
Newsletter #30
20 July 2018

Newsletter #29
12 March 2018

Newsletter #28
15 November 2017

FAQ

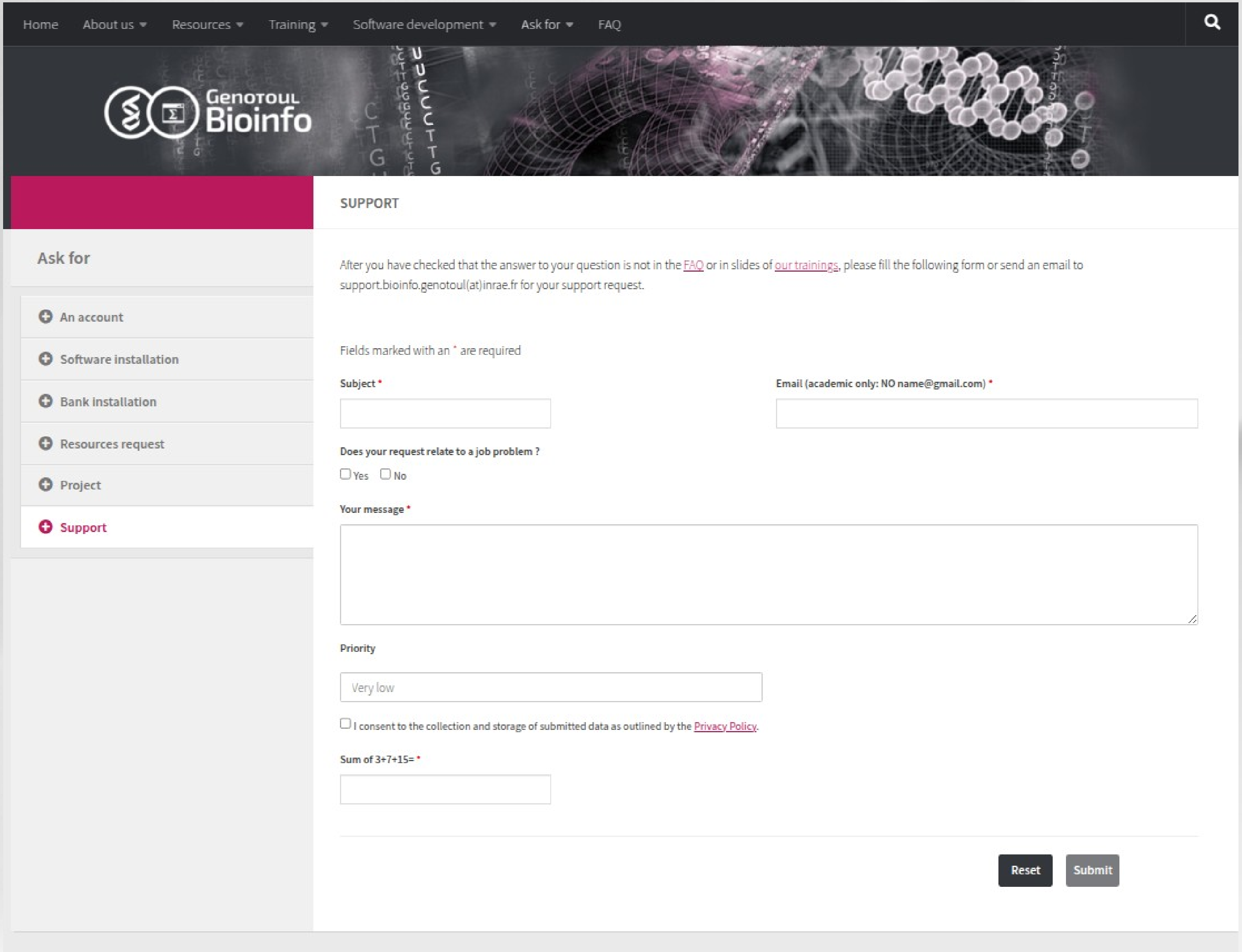
https://bioinfo.genotoul.fr/index.php/faq/
https://vm-genoword.toulouse.inrae.fr/FAQ/



Welcome on the Genotoul FAQ, here under are listed the most frequently asked questions and some application examples. Theses questions are categorized in different sections:

Support

mailto: support.bioinfo.genotoul@inrae.fr



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(at)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= *

Linux

Introduction to Linux

GNU-Linux : Unix-like operating system

- Initial Developer = Linus Torvalds (Helsinki)
- Birth of kernel Linux on 1991
- GNU project = free and open source software
- Hundreds of active distributions : Ubuntu, Fedora, Debian...
- Large community of developers
- Some are commercial : RedHat, SUSE...

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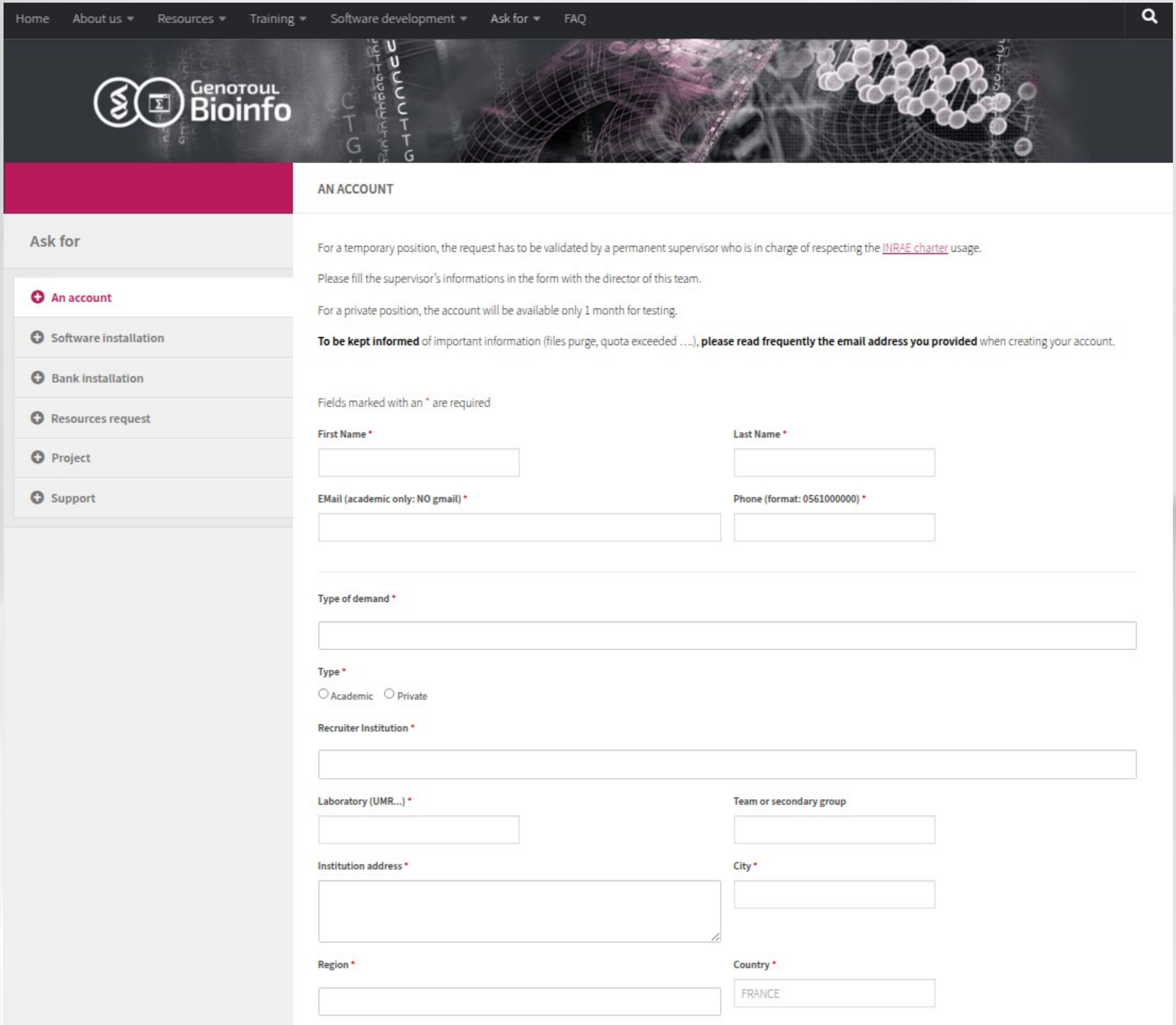
Linux

Asking for an account

https://bioinfo.genotoul.fr/index.php/ask-for/create-an-account



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 *

Laboratory (UMR...) *

Team or secondary group

Institution address *

City *

Region *

Country *

FRANCE

Linux

Linux account

Access to a “work” environment

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

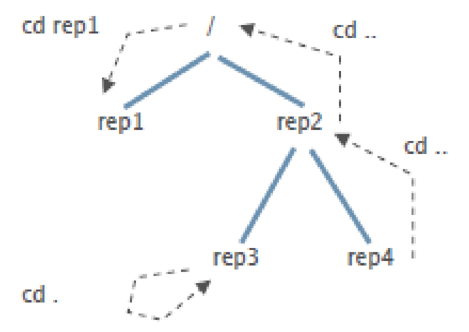
- Correct social behaviour is expected

The tree structure

Navigation

Tree structure

« **/** »	root directory
« **~** »	home directory (user)
« **.** »	current directory
« **..** »	parent directory



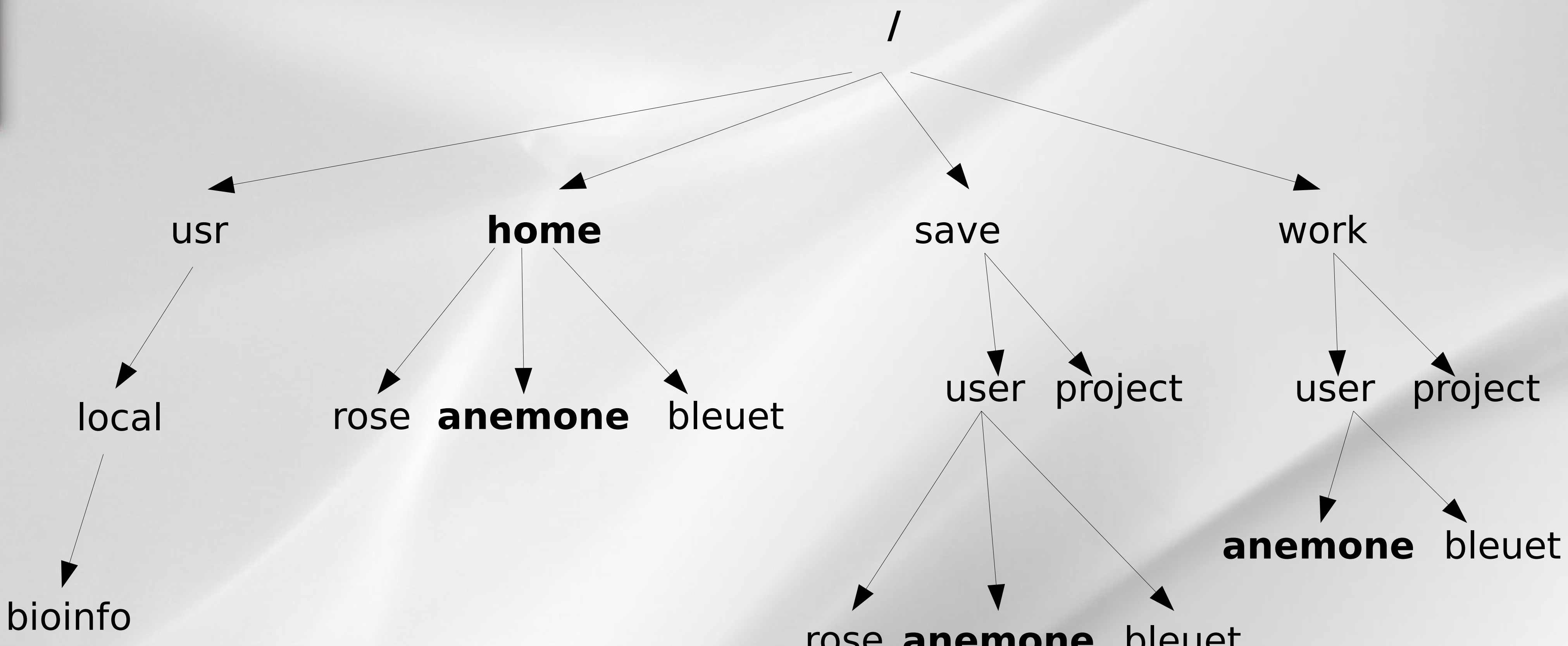
cd [nom_répertoire] : Change directory

Absolute path : `/home/bleuet`

Relative path : `../../usr`

The tree structure

Notion of « Root »



/

usr

local

bioinfo

home

rose

anemone

bleuet

save

user

rose

anemone

bleuet

project

work

user

anemone

bleuet

project

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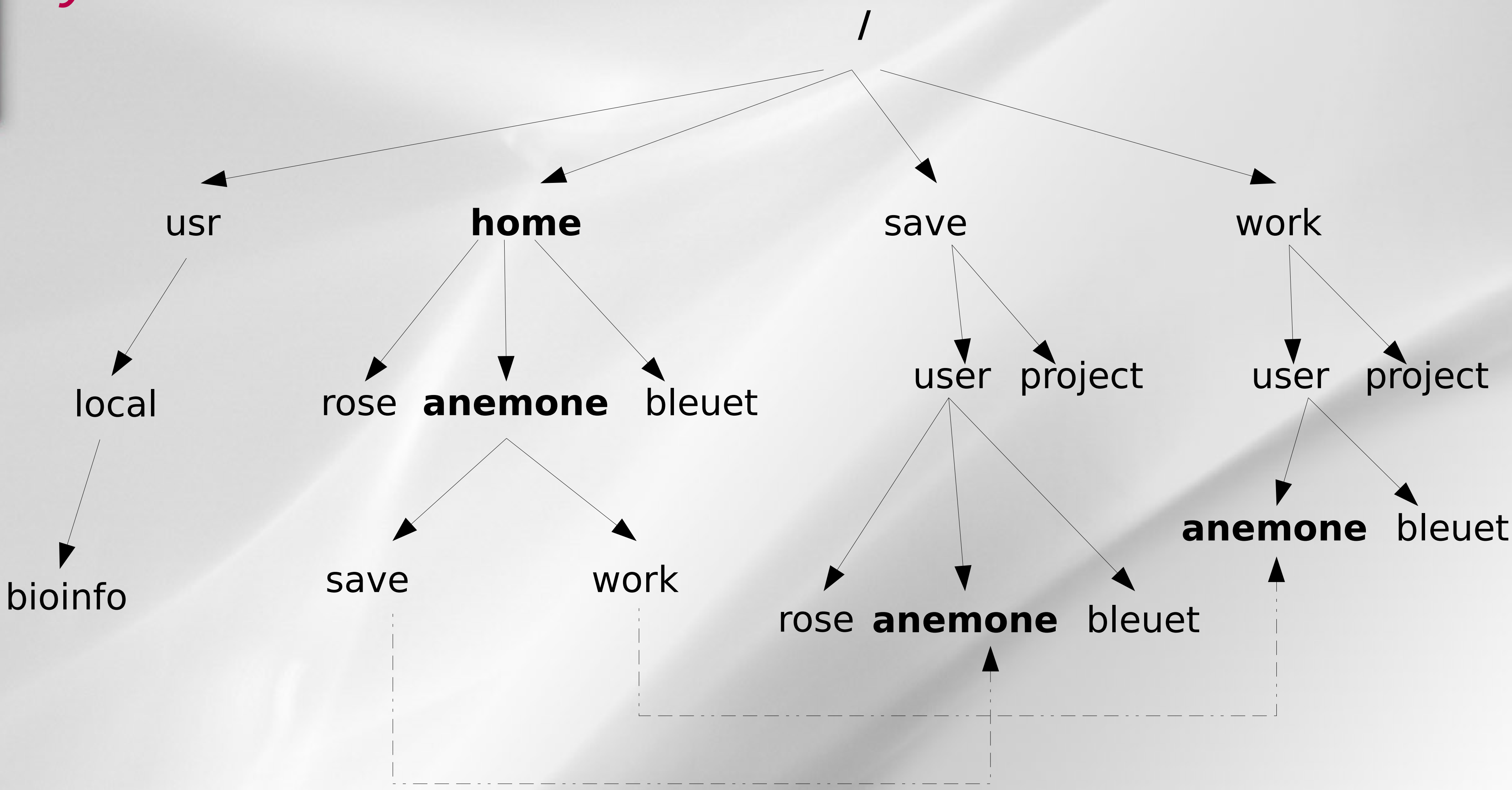
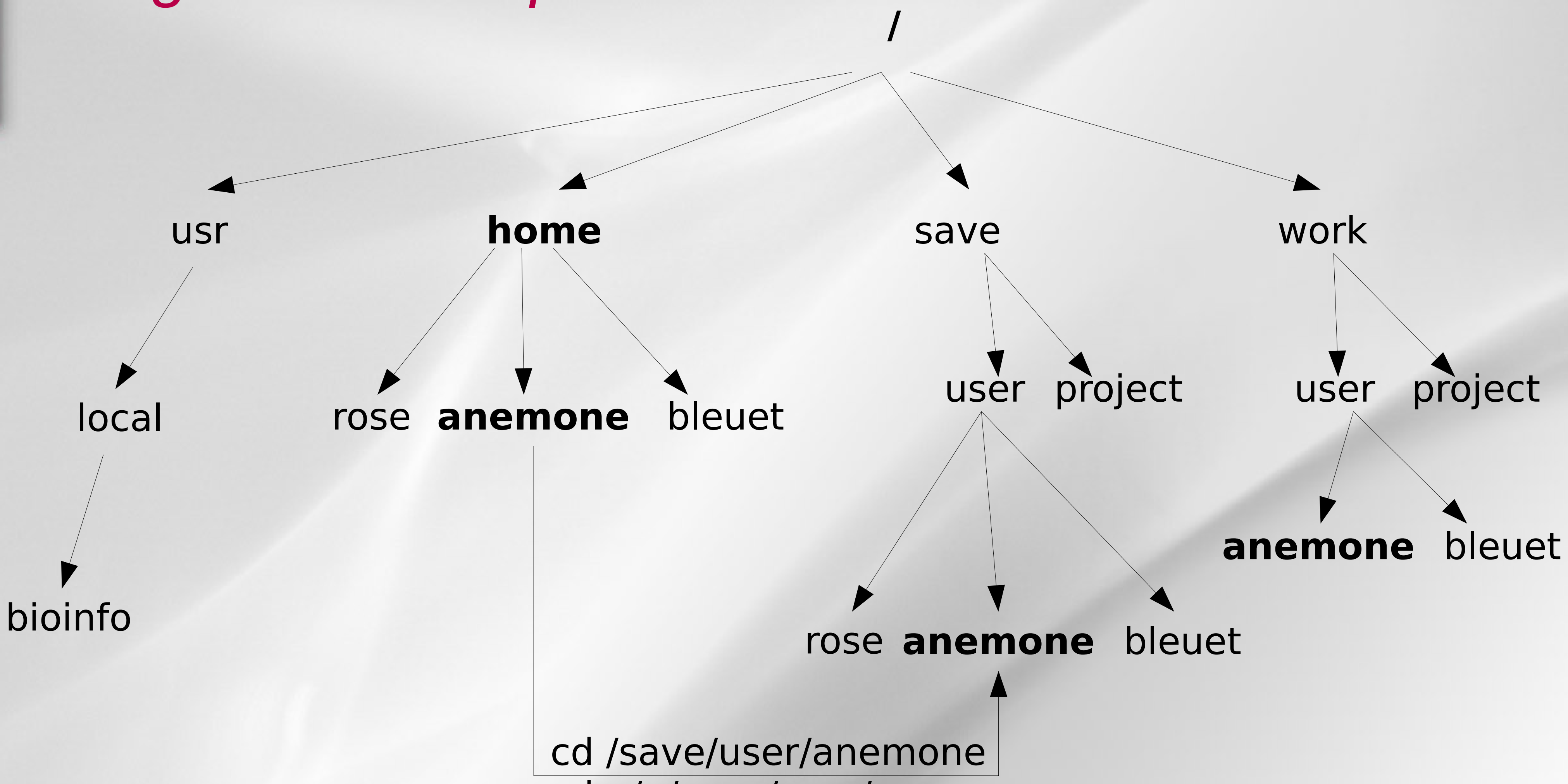
The tree structure

Symbolic link



The tree structure

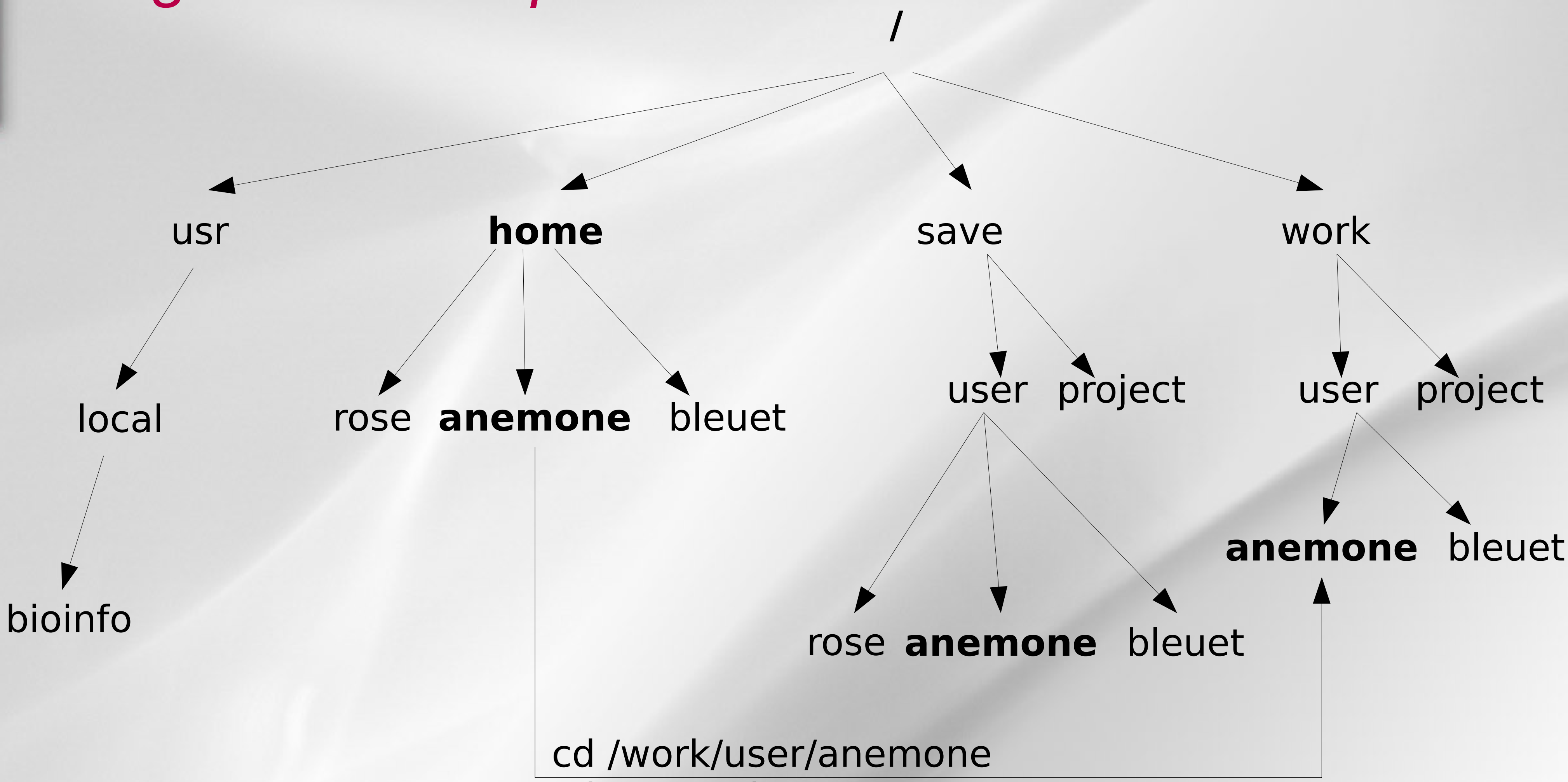
Navigation: exemple



cd /save/user/anemone
cd ../../save/user/anemone
cd save *(symbolic link)*

The tree structure

Navigation: exemple



/

usr
home
save
work

local
rose
anemone
bleuet
user
project
user
project

bioinfo
rose
anemone
bleuet
anemone
bleuet

cd /work/user/anemone
cd ../../work/user/anemone
cd work *(symbolic link)*

The command line : syntax

command_name [-option] [parameter]

- Command_name : what you want to do ?
- Option : how to do it ?
- Parameter : on which ?

```
ls

ls -l /home

ls -a

ls -l -a
ls -a -l      } same thing
ls -la
ls -al
```

The help on command

command_name [--help / - help / -h]

man command_name

```
ls --help
blastn --help

man ls
man cd
```

Some basics commands

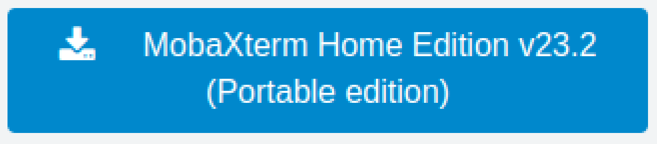
- Examples

```
cd : change directory
pwd : print working directory
ls [nom_répertoire]: 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 Windows

- **MobaXterm**



- **Other tools : wsl / openssh**

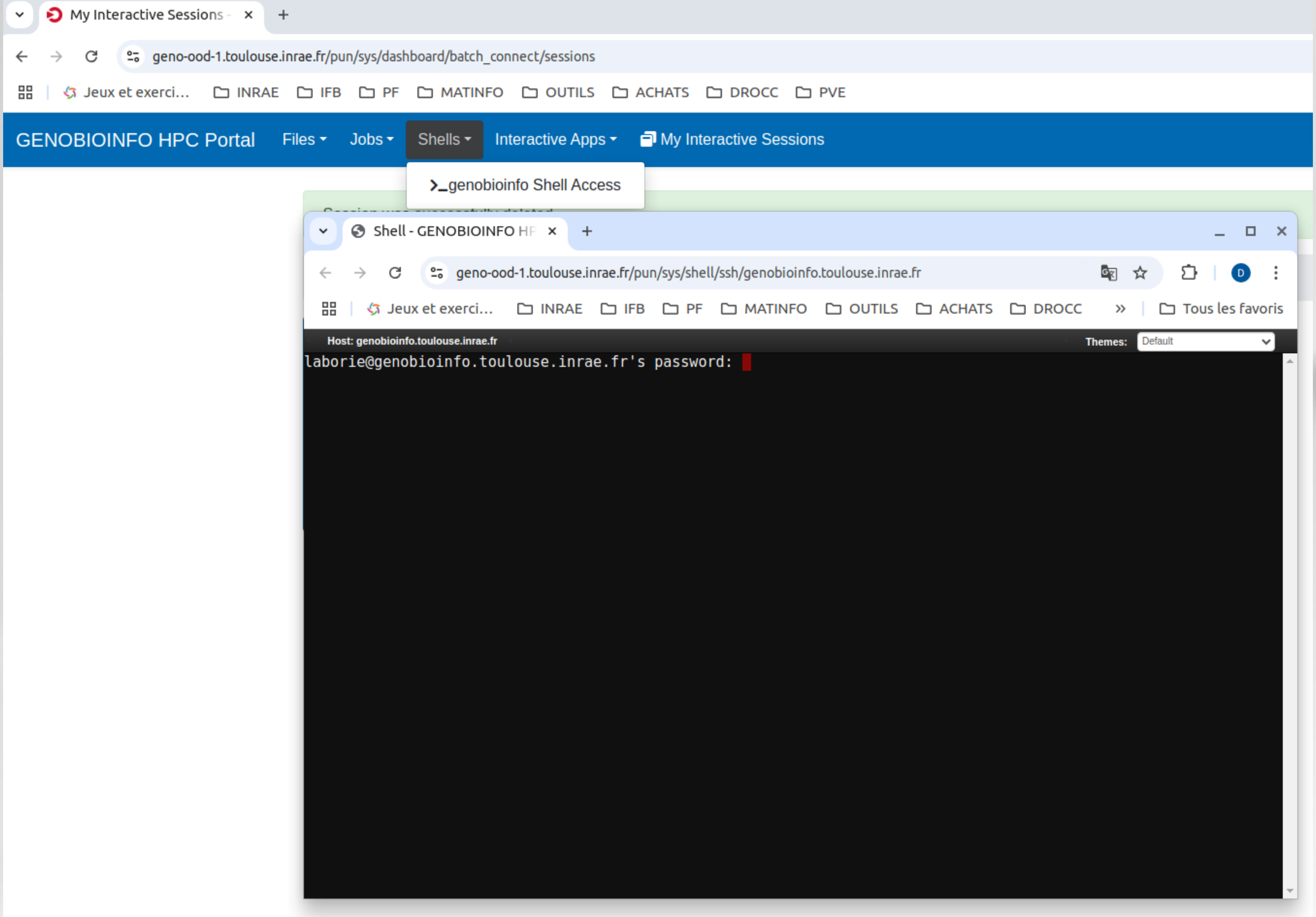
From Linux / Mac

- **Open command line tool (terminal)**

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

How to connect to genobioinfo ?

https://geno-ood-1.toulouse.inrae.fr/



```
laborie@genobioinfo.toulouse.inrae.fr's password:
```

Tricks & Tips

- **Copy / Paste with the mouse**
  - Select a text (it is automatically copied)
  - Click on the mouse wheel (the text is pasted where the cursor is located)
- **Stop a process :**
  - Use the CTRL <C> keys
- **Command and path completion :**
  - Use the TAB key (tab tab)
- **Back to the previous used commands :**
  - Use the « up » and « down » keys

TP1

- Connect yourself to genobioinfo server with your (training) login/password

- Do the exercices (TP1)
  https://genotoul-bioinfo.pages.mia.inra.fr/linux-cluster/linux-initiation/tp1/
  or (if it doesn’t work)
  http://vm-genoword.toulouse.inrae.fr/Training/linux-initiation/tp1/

Part II

Plan

- File types
- Manipulating files
- TP 2.1
- File permissions
- wild card characters
- TP 2.2

File types

The « ls » command

List the content of a directory

ls [-options] [dir_name]

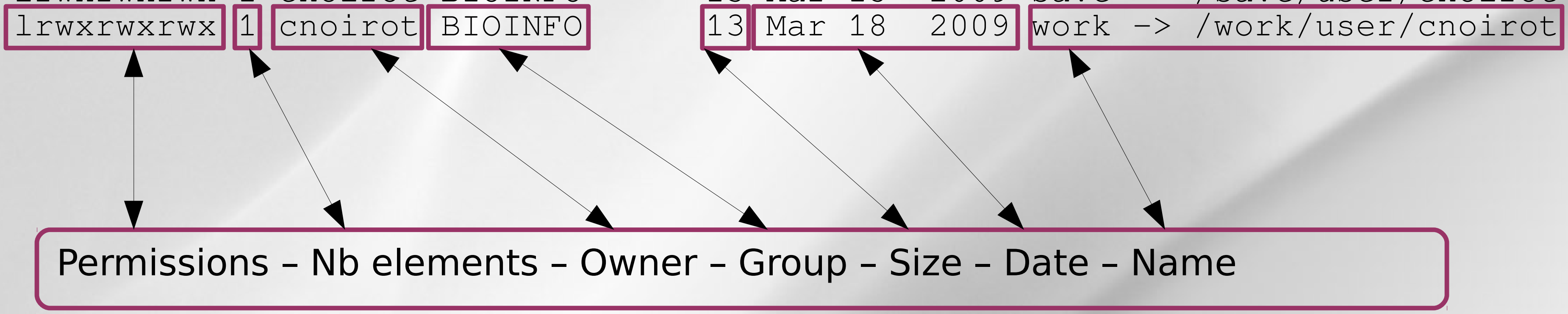
- **-a** : display hidden files/dir
- **-l** : use the long format
- **-t** : sort the content
- **-r** : reverse the sort order
- **-h** : human readable

```
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
```

File types

“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
```



Permissions – Nb elements – Owner – Group – Size – Date – Name

Manipulating files

File/Dir. Creating and removing

mkdir / rmdir [dir_name] : create/remove an empty directory

```
mkdir dir_name
```

touch / rm [file_name] : create/remove a file

```
touch file_name
```

Manipulating files

Copying files/dir

cp src_filename dest_filename

=> copy source file to destination file

```
cp file1 file2
```

cp -r src_dirname dest_dirname

=> copy source dir. to destination dir.

```
cp -r dir1 dir2
```

Manipulating files

Moving / renaming a file

mv source destination

- **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
```

Manipulating files

Wild cards characters

? replace any (one) character

```
ls bov?.seq
```

***** replace 0, 1 ou any character

```
ls *.seq

rm bacterie*
```

[ ] replace any character between a selection

```
ls [123]*

ls f[a-c]*
```

Symbolic link

A kind of shortcut

ln -s nom_fic_source nom_fic_destination

create a symbolic link

```
    ln -s file_name link_name
```

```
    ls -l link_name
      link_name -> file_name
```

Part II

TP

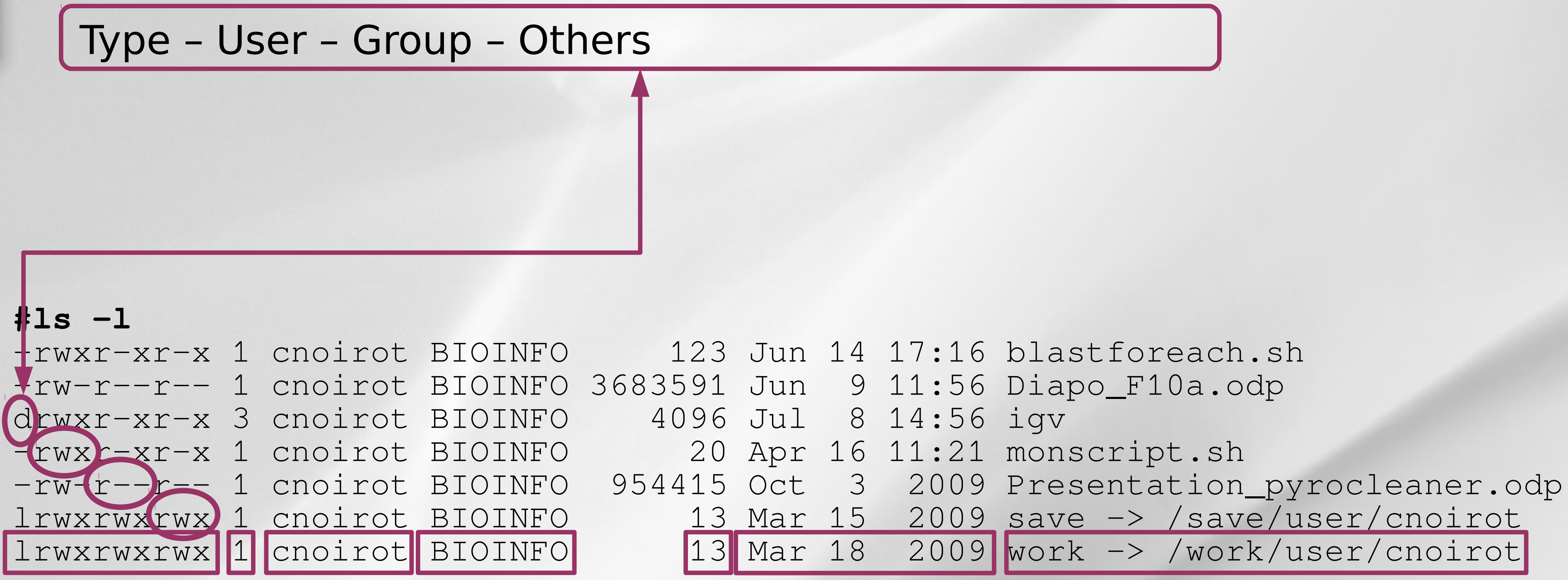
- Do the exercises (TP 2.1) https://genotoul-bioinfo.pages.mia.inra.fr/linux-cluster/linux-initiation/tp2.1/

  or (if it doesn't work)

  http://vm-genoword.toulouse.inrae.fr/Training/linux-initiation/tp2.1/

File types

Read, write,execute



Type – User – Group – Others

```
#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
```

Permissions

File permission modification

chmod [options] filename

modifies the permissions of a file

- **u** :user, **g** : group, **o** : other, **a** : all
- **r** : read, **w** : write, **x** : execute

```
chmod g+w file_name
```

Manipulating files

Finding files/dir

find dirname [-option] [parameter]

```
find /home/formation -name "*.seq"
find . -type d
find . -type f
find / -size +1000k
```

Kind of files

file command

file file_name

```
file find_result.txt:          ASCII text
file create_account             symbolic link

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

Part II

TP

- Do the exercises (TP 2.2)

  https://genotoul-bioinfo.pages.mia.inra.fr/linux-cluster/linux-initiation/tp2.2/

  or (if it doesn't work)

  http://vm-genoword.toulouse.inrae.fr/Training/linux-initiation/tp2.2/

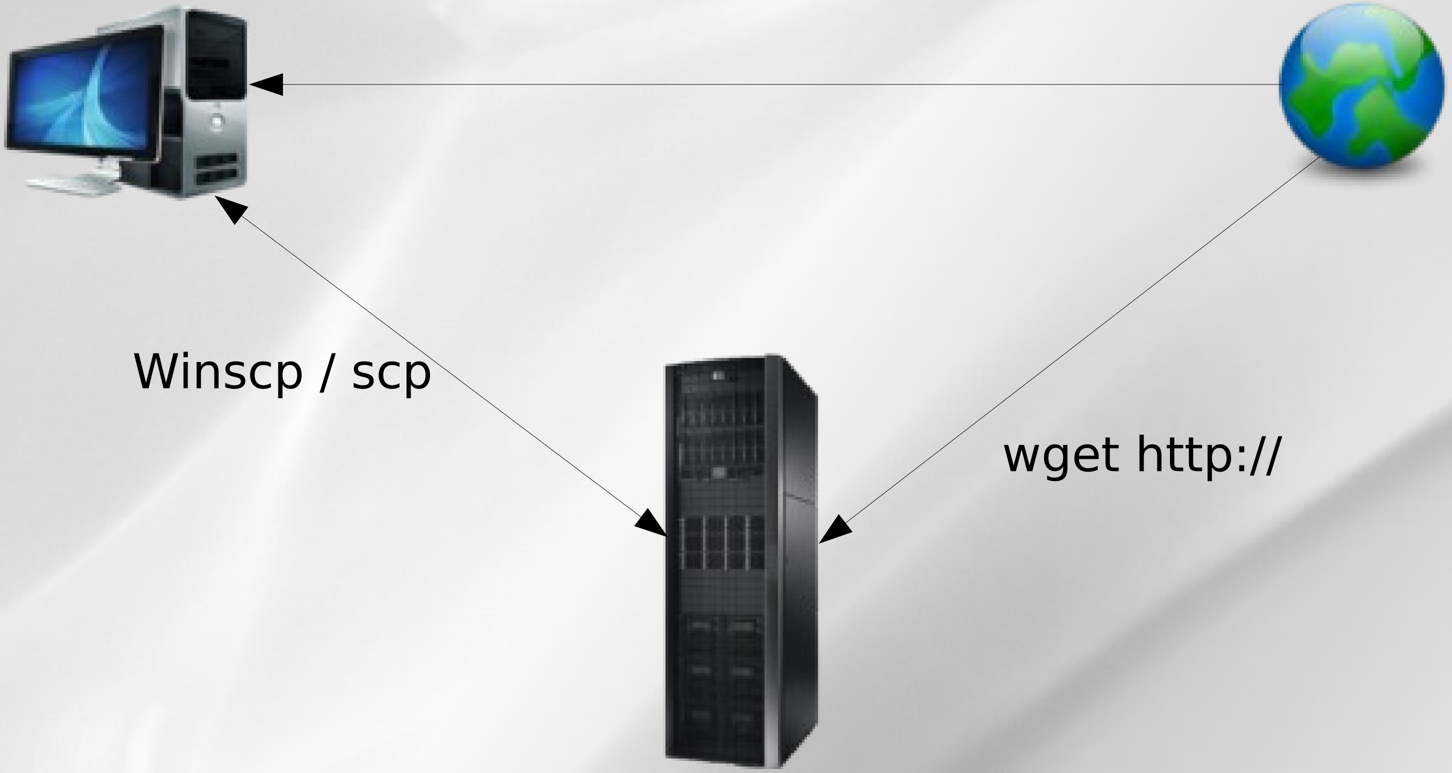
Part III

Plan

- 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

Several possible cases



Internet browser (http:// + save as)

Winscp / scp

wget http://

« genobioinfo » server

Downloading / transferring

Directly from internet to genobioinfo

File download from Internet to « genobioinfo server »:

- Copy the URL of the file to download

```
wget http://url.a.telecharger/nom_fichier
```

Downloading / transferring

Transfer between genobioinfo and desktop computer

We recommend to use « scp » command (secure copy)

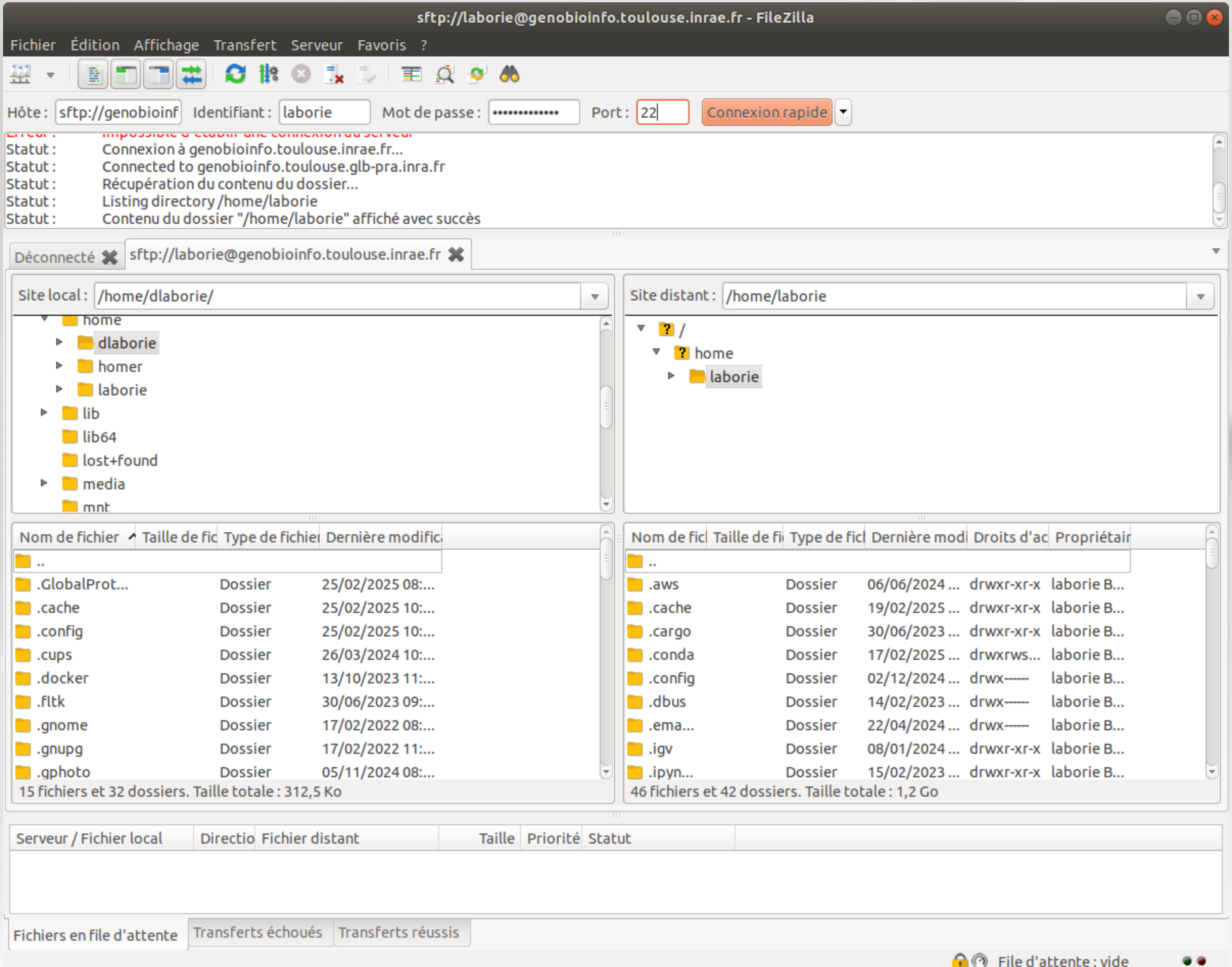
scp [user@host1:]file1 [user@host2:]file2

copy file from the network

```
scp source_name
  bleuet@genobioinfo.toulouse.inrae.fr:/destination_name
  (copy from desktop to "genobioinfo server")
```

Downloading / transferring

FileZilla : copy via graphical interface



sftp://laborie@genobioinfo.toulouse.inrae.fr - FileZilla

Hôte : sftp://genobioinf
Identifiant : laborie
Mot de passe : ••••••••••••••
Port : 22

```
Statut :	Connexion à genobioinfo.toulouse.inrae.fr...
Statut :	Connected to genobioinfo.toulouse.glb-pra.inra.fr
Statut :	Récupération du contenu du dossier...
Statut :	Listing directory /home/laborie
Statut :	Contenu du dossier "/home/laborie" affiché avec succès
```

Site local : /home/dlaborie/

- home
  - dlaborie
  - homer
  - laborie
- lib
- lib64
- lost+found
- media
- mnt

Site distant : /home/laborie

- /
  - home
    - laborie

Nom de fichier	Taille de fic	Type de fichier	Dernière modific
..			
.GlobalProt...		Dossier	25/02/2025 08:...
.cache		Dossier	25/02/2025 10:...
.config		Dossier	25/02/2025 10:...
.cups		Dossier	26/03/2024 10:...
.docker		Dossier	13/10/2023 11:...
.fltk		Dossier	30/06/2023 09:...
.gnome		Dossier	17/02/2022 08:...
.gnupg		Dossier	17/02/2022 11:...
.gphoto		Dossier	05/11/2024 08:...

15 fichiers et 32 dossiers. Taille totale : 312,5 Ko

Nom de fic	Taille de fi	Type de fic	Dernière mod	Droits d'ac	Propriétair
..					
.aws		Dossier	06/06/2024 ...	drwxr-xr-x	laborie B...
.cache		Dossier	19/02/2025 ...	drwxr-xr-x	laborie B...
.cargo		Dossier	30/06/2023 ...	drwxr-xr-x	laborie B...
.conda		Dossier	17/02/2025 ...	drwxrws...	laborie B...
.config		Dossier	02/12/2024 ...	drwx------	laborie B...
.dbus		Dossier	14/02/2023 ...	drwx------	laborie B...
.ema...		Dossier	22/04/2024 ...	drwx------	laborie B...
.igv		Dossier	08/01/2024 ...	drwxr-xr-x	laborie B...
.ipyn...		Dossier	15/02/2023 ...	drwxr-xr-x	laborie B...

46 fichiers et 42 dossiers. Taille totale : 1,2 Go

Serveur / Fichier local	Directio	Fichier distant	Taille	Priorité	Statut

File d'attente : vide

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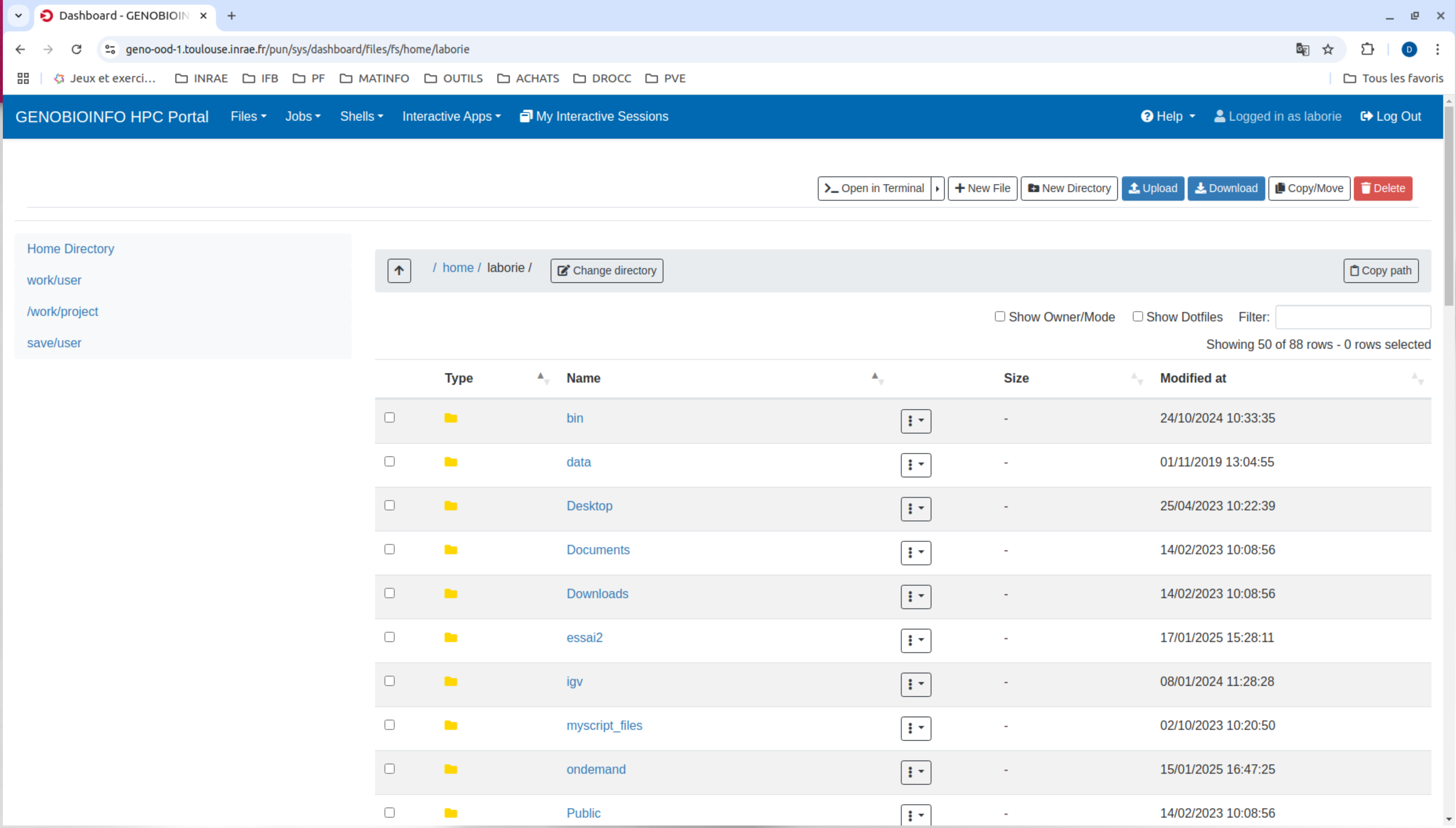
Downloading / transferring

OpenOnDemand : Upload / Download



☐ Show Owner/Mode ☐ Show Dotfiles Filter:

Showing 50 of 88 rows - 0 rows selected

	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 space control

df [-option] [partition_name] :

Show the differences disk spaces

```
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 control

du [-option] [dir_name] :

Show the disk usage

```
du -csh /home/formation/*
483K    /home/formation/bin
26K     /home/formation/comptes.txt
242K    /home/formation/last.txt
1.5K    /home/formation/public_html
1.5K    /home/formation/save
26K     /home/formation/tgicl.cfg
1.5K    /home/formation/work
780K    total
```

Compressing / uncompressing

Several formats

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

```
gzip  file_to_compress
            =>gz file creation
```

gunzip : uncompress a file **.gz**

```
gunzip file_to_uncompress.gz
```

<u>Other formats</u> : bz2, zip, rar, Z, 7z

Archiving

Tar command

tar -cvf : archive a file tree

```
tar -cvf formation.tar /home/formation
         => .tar file creation
```

tar -xvf : deploy a file tree

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

<u>Tips</u>: combination of tar + gzip (.tgz)

tar -cvzf : archive + compression

tar -xvzf : uncompress-ion + deploy

Part III

TP3

- Do the exercises (TP 3.1) https://genotoul-bioinfo.pages.mia.inra.fr/linux-cluster/linux-initiation/tp3.1/

  or (if it doesn’t work)

  http://vm-genoword.toulouse.inrae.fr/Training/linux-initiation/tp3.1/

Looking into files

Display a file content

cat file_name : display the file content

```
cat /bank/ncbi/genbank/genbankRelease/current/fasta/gbphg1.seq.fasta

>AB000833.1 Bacteriophage Mu DNA for ORF1, sheath protein gpL,
   ORF2, ORF3, complete cds.

ACGGTCAGACGTTTGGCCCGACCACCGGGATGAGGCTGACGCAGGTCAGAAATCTTTGTGACGAC
   AACCGTATCAATGCCGGTGTGG...
```

cat file_name1 file_name2 ... : display many files content

Pagers

Navigate into the file

more file_name : display more and more

less file_name : display up and down (more than **more**)

```
less my_file.txt
```

Text editors

Modify a file content

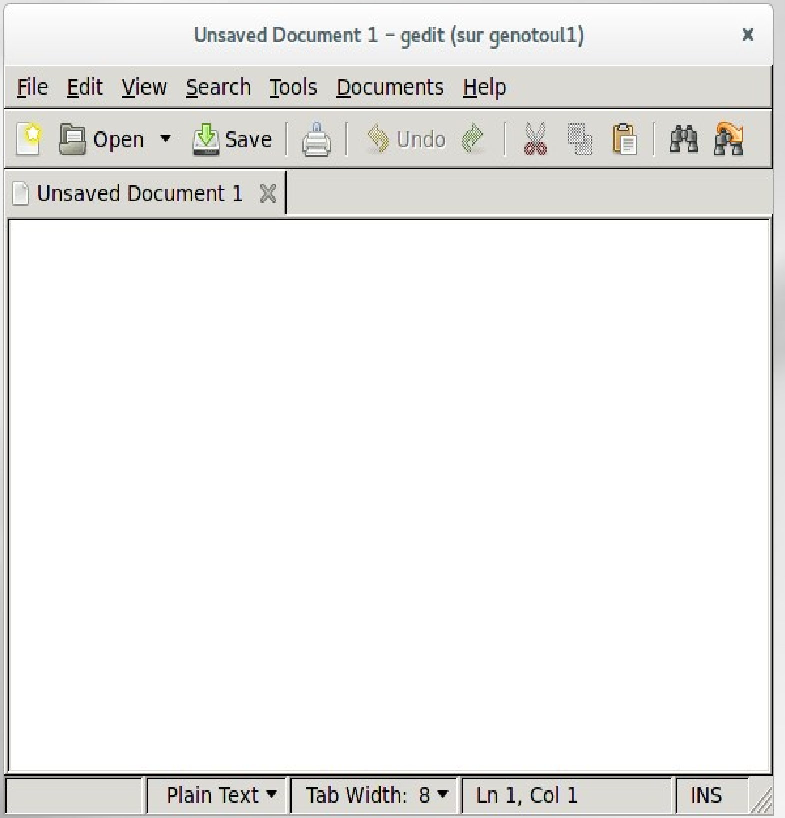
vi : standard but difficult

nano : easy to use

gedit : graphic mode, intuitive

nedit : idem as gedit

emacs : advanced features



Unsaved Document 1 – gedit (sur genotoul1)

Unsaved Document 1

Plain Text

Tab Width: 8

Ln 1, Col 1

INS

Utility commands

sort [-options] file_name : sort a file

```
    sort -n -k 1
       (num. sort, first col.)
```

wc [-options] file_name : words count

```
wc -c file_name

wc -w file_name

wc -l file_name
```

Data extraction

Filters (1)

cat [-options] file (s) name : merge files

```
cat nom_fic1 nom_fic2
```

head [-number] file_name : read the beginning of a file

```
head -100 file_name (first 100 lines)
```

tail [-f] [+/-number] file_name : read the end of a file

```
tail -n 100 file_name (last 100 lines)

tail -n +6 file_name (from the 6th line)
```

Data extraction

Filters (2)

cut [-options] file_name :

cuts the fields (vertically)

```
cut -c 1 (gets the first char.)

cut -f 2,3 (gets the #2 and #3 fields)
```

split [-options] file_name :

cuts the fields (horizontally)

```
split -l 500 file_name.txt (default size 500 lines)
```

Data extraction

File Comparison

meld file_name1 file_name2

compare two files (line per line)

```
meld fic_1 fic_2
```

Data extraction

Tex research

grep [-options] 'motif' file_name[s]

- Text research tool in the file contents
- Wild card characters may be used

```
grep SEQRES fichier_pdb (simple research)
grep -i (case insensitive)
grep -c (counts the line amount)
grep -v (all the lines except)
```

Redirections

Standard input / output

Most commands use the standard input / output :

Standard input = the keyboard

Standard output = the console

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

Redirections

Redirection

command > output_file_name

redirects the standard output to a new file

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

command1 | command2

redirects the standard output to another software

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

command >> output_file_name

redirects the standard output to an existing file and appends it

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

Part III

TP3

- Do the exercises (TP 3.2)

  https://genotoul-bioinfo.pages.mia.inra.fr/linux-cluster/linux-initiation/tp3.2/

  Or (if it doesn't work)

  http://vm-genoword.toulouse.inrae.fr/Training/linux-initiation/tp3.2/

My first script

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

```
nedit 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 langages (csh,bash...)`

My first script

- 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
```

Plateforme Bioinformatique Midi-Pyrénées

End of presentation

https://sondages.inrae.fr/index.php/84236?lang=fr

Thanks for your attention !