Bacterial WGS training : Exercise 1

Title	**Linux command line.**
Training dataset:	None
Questions:	• How do I use the command line? • How do I navigate the file system?
Objectives:	• Learn/Remember how to use the command line. • Learn/Remember how to navigate through the Linux file system.
Time estimation:	30 min
Key points:	• Remeber the shell basic commands: *pwd cd ls mkdir rmdir mv nano cat less more head tail rm*

:bangbang: Important things to remnenber:

- Use Tab to automatically complete file names and paths, so it can be easiert to write in the terminal
- Use keyboard arrows (:arrow_up: :arrow_down:) to move through your terminal's history, so you don't have to write the commands again.
- Try not to use spaces, accents or special characters like "Ñ" letter, when writting directory of file names.
- Basic commands you should always remember: *pwd cd ls mkdir mv rm rmdir less nano*

Answering to main questions

How do I use the command line?

Open a terminal by clicking in the icon or typing **Ctrl+Alt+T**. Now you can type in the prompt.

How do I navigate the file system?

Let's remember the basics: *pwd cd ls mkdir mv rm rmdir less nano* . We are going to use those commands to:

Checking the working directory (pwd)

Check our working directory:

```
pwd
#Output: /home/alumno
```

Moving between directories (cd)

Move to our Desktop folder:

```
cd ~/Escritorio
pwd
#Output: /home/alumno/Escritorio
```

Move to the course folder:

```
cd
pwd
#Output: /home/alumno
cd wgs
pwd
#Output: /home/alumno/wgs
cd bacterial_wgs_training_dataset/RAW/FULL_DATA
pwd
#Output: /home/alumno/wgs/bacterial_wgs_training_dataset/RAW/FUL
cd .
pwd
#Output: /home/alumno/wgs/bacterial_wgs_training_dataset/RAW/FUL
cd ..
#Output: /home/alumno/wgs/bacterial_wgs_training_dataset/RAW/
cd ../..
#Output: /home/alumno/
```

Questions:

▶ Which is the meaning of the "~" symbol?

▶ What does de `cd` command without arguments do?

▶ What does "." mean?

▶ What does ".." mean?

Listing directories (ls)

```
cd wgs
cd bacterial_wgs_training_dataset
ls
#Output: ANALYSIS RAW  REFERENCES  RESULTS
```

This is the folder structure we will use for this training. Now we are going to list the files in the `REFERENCE` folder:

```
ls REFERENCES
```

This command will output a big list of files, which are the files that we will usea as REFERENCE through the different exercises of the training. Now wi will run this other command:

```
ls /home/alumno/wgs/bacterial_wgs_training_dataset/REFERENCES/
```

Questions:

▶ What does ".." mean?

▶ Which is the difference between this last command and the previous one?

▶ Do they display the same information?

▶ Which one is relative path?

▶ Which one is absolute path?

Let's see different parameters for the `ls` command. Write:

```
ls REFERENCES
ls -l REFERENCES
ls -a REFERENCES
ls -la REFERENCES
```

Questions:

▶

What does de different arguments of `ls` do?

▶ What does the new file special?

⚠ **REMINDER:** ⚠ EVERY TIME YOU CHANGE DIRECTORY (cd) YOU HAVE TO CHECK YOUR PATH (pwd) AND LIST THE FILES INSIDE (ls) TO CHECK YOU DIDN'T MAKE MISTAKES

Creating and removing directories (mkdir & rmdir)

Now we are going to move to the ANALYSIS folder which is the folder were we will run all the exercises

```
cd ANALYSIS
pwd
#Output: /home/alumno/wgs/bacterial_wgs_training_dataset/ANALYSI
ls
```

As you can see the folder is empty, so now we will fill this folder. Create a directory for this handson: **Remember:** Linux is case sensitive and does not like white spaces in names

```
mkdir 01-handsonLinux
ls
#Output: 01-handsonLinux
```

Now type:

```
mkdir 01-handsonlinux 01-HandsOnLinux
ls
#Output: 01-handsonlinux 01-handsonLinux 01-HandsOnLinux
```

Questions:

▶ Is it possible to create more than one directory at the same time?

▶ If the names of the folders are the same, why it creates three different directories?

Now we will remove the extra directories:

```
rmdir 01-handsonLinux 01-HandsOnLinux
ls
#Output: 01-handsonlinux
```

Moving and renaming files (mv)

Move to the new folder

```
cd 01-handsonlinux
pwd
#Output: /home/alumno/wgs/bacterial_wgs_training_dataset/ANALYSI
```

We are going to move the hidden file in REFERENCE folder to this directory and then rename it:

```
mv ../../REFERENCES/.ThisIsAHiddenFile .
ls
ls -a
ls -a ../../REFERENCES/
mv .ThisIsAHiddenFile NowImNotHidden
ls -a
ls
```

Questions:

▶ Which is the difference between the two `mv` commands?

▶ Do you remember what "." mean from the first questions?

▶ And ".."?

⚠ **REMINDER:** ⚠ LINUX DOES NOT REQUIRE FILE EXTENSIONS

Editing files and displaying them (nano & cat)

We are going to read the file and edit it:

```
cat NowImNotHidden
#Output: I'm a hidden file.
```

This is not true, so we are going to edit it:

```
nano NowImNotHidden
```

Write: I'm not a hidden file.

And **save** it: *Ctrl + O Intro*

Close the new file: *Ctrl + X*

Now read the new file:

```
cat NowImNotHidden
#Output: I'm not a hidden file.
ls
#Output: NowImNotHidden
cd ../../
```

Read files other ways (less & more & head & tail)

And now we will read this file:

```
cat REFERENCES/bacterial_wgs_training_initial.tree
less REFERENCES/bacterial_wgs_training_initial.tree
#Remember: To close less press "q"
```

```
more REFERENCES/bacterial_wgs_training_initial.tree
#Remember: To close more press "q"
```

```
head REFERENCES/bacterial_wgs_training_initial.tree
tail REFERENCES/bacterial_wgs_training_initial.tree
```

```
head -n4 REFERENCES/bacterial_wgs_training_initial.tree
tail -n3 REFERENCES/bacterial_wgs_training_initial.tree
```

Questions:

▶

Which is the difference between `head` and `tail`?

▶

What does the argument `-nX` do to `tail` and `head`?

Removing a file (rm)

Now we will learn how to remove files:

```
cd ANALYSIS/01-handsonlinux/
pwd
ls
#Output: NowImNotHidden
mv ../../REFERENCES/bacterial_wgs_training_initial.tree .
ls
#Output: bacterial_wgs_training_initial.tree NowImNotHidden
rm NowImNotHidden
ls
#Output: bacterial_wgs_training_initial.tree
```

cd ANALYSIS/01-handsonlinux/
pwd
ls
#Output: NowImNotHidden
mv ../../REFERENCES/bacterial_wgs_training_initial.tree .
ls
#Output: bacterial_wgs_training_initial.tree NowImNotHidden
rm NowImNotHidden
ls
#Output: bacterial_wgs_training_initial.tree