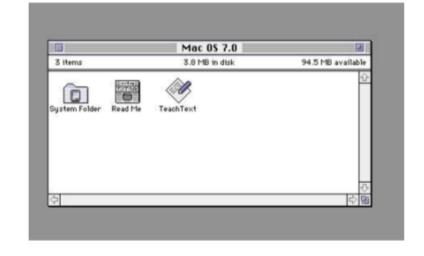
Introduzione all'uso di bash su Linux



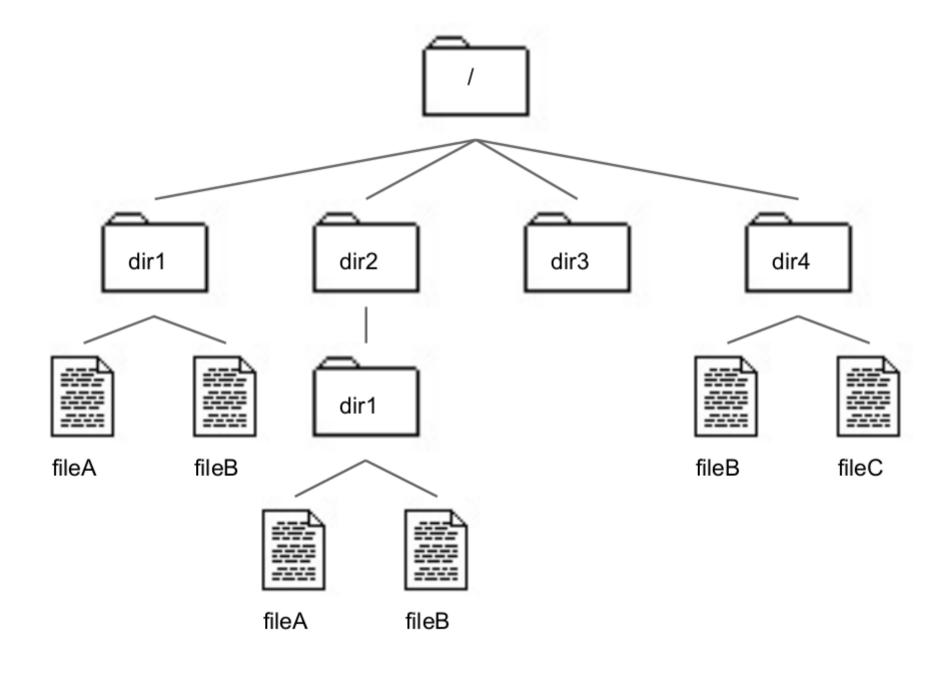
- textual shells (CLI)
 - unix shells, dos prompt



- graphic shells (GUI)
 - windows explorer, mac finder, linux desktop environments



How files are organized on disk



Browsing the filesystem

a shell always has a working directory

- you can see it with "pwd"
- you can see the files in it with "ls"
- you can change it with "cd"

at the beginning it is your home

Special names for special directories

the working (current) directory:

"."

the parent of the current directory:

'' .."

the root directory:

"/"

the home directory:

"~"



absolute path: starts from `/`

relative path: starts from the current

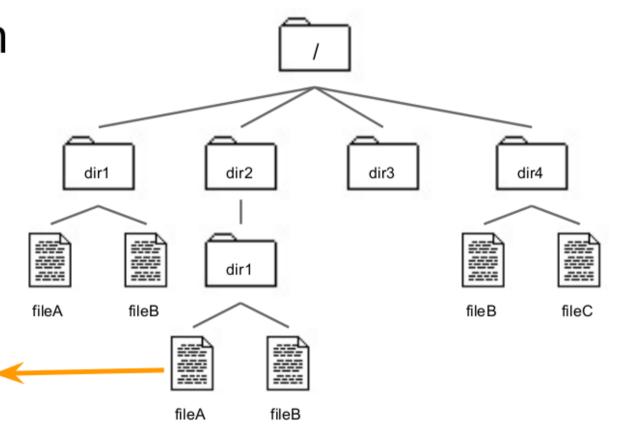
directory



Absolute paths

Always begin from the root (/)

/dir1/fileA /dir2 /dir4/fileB /dir2/dir1/fileA



Relative paths

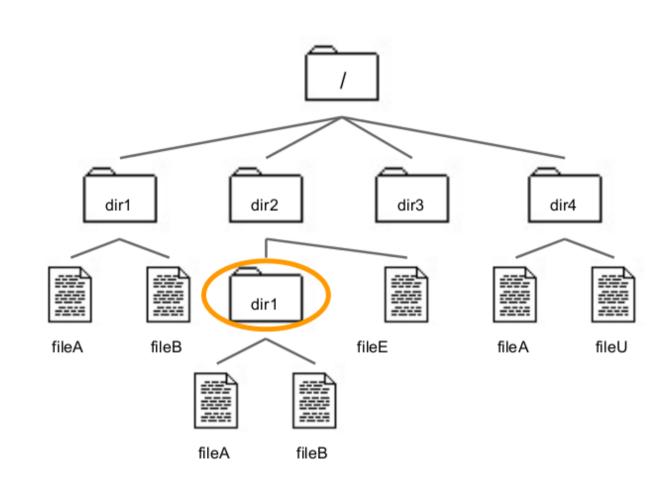
```
$ pwd
/dir2/dir1
```

Need to use fileU?

../../dir4/fileU

And fileE?

../fileE



Other commands

- Copy a file:
- \$ cp fileA copyOfFileA

- Rename a file:
- \$ mv fileA fileB

- Create a directory:
- \$ mkdir dir2



If you do not know how to use a command try:

- \$ command -h
- \$ command --help
- \$ man command
- You can Google it
- If everything fails ask us!

Command's Anatomy

Some commands are fine alone:

```
$ pwd
$ ls
```

Many require one or more arguments:

```
$ mkdir some_dir
$ mv a_file new_name
```

Most commands can have options:

```
$ ls -1 -a
```

Simple text files are your friends!

Simple text files contains text and nothing else.

- MP3 are binary files
- DOC, XLS and JPG are binary too!
- In Windows you can create text files with Notepad (not Word or Wordpad!)





Bioinformatics and Text files

- Most bioinformatics format are simple text files:
 - Fasta
 - FASTQ
 - SAM
 - VCF
 - BED

primers.fa

```
>beta_lac_FOR
ACGATCGTTACGTACTTGGGGGG
>beta_lac_REV
ACGTACGTATTTTTACGATCGATC
>ctrl_FOR
CAGCTATTATCGTATCGTACGACT
>ctrl_REV
CAGCAGCTACGTACGATCG
```

How to see the content of a file

The command
 `cat` prints the
 content of a text
 file

\$ cat primers.fa

 The command `head` prints the first lines

\$ head primers.fa

 The command `wc` prints the number of lines

\$ wc -1 primers.fa

 The command `tail` prints the last lines

\$ tail primers.fa

Redirects: do it there, not here!

- Many commands write text to the terminal:
- \$ head fileA

- Maybe the output is:
 - too long and/or
 - you want to save it on disk
- \$ head fileA > headOfFileA
- The reverse also works:
- \$ head < inputFile > headOfInputFile

"Pipes"

You can also "pipe" the output of a command into another command

 How many are the files in the current directory?

```
$ ls > listOfFiles
$ wc -l listOfFiles
```

Why bother with a file? Use a pipe:

```
$ 1s | wc -1
```

You can really do a lot of stuff with these

Grep and family

 Often you want to see only some lines in a file:

```
$ grep password secretsOfPippo
password di facebook di Pippo: 123456
password del conto in banca: qwerty
```

Can be very useful!

- Other useful command for text files:
 - sort, tr, diff, cut, sed, awk, ... (there are really many)

Don't forget...



Why bother?

The textual shell has some disadvantages:

- you need to know the commands (no hints)
- little feedback on what happens
- not very intuitive (or you are not used to it)

So why bother? Because the shell:

- handles big data much better
- GUIs take too long to write