

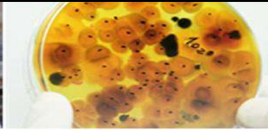



Instituto Nacional de Saúde
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A (quick) introduction to the Unix command line interface



Ministério da Saúde




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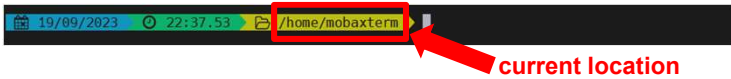
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www.insa.pt

- This introduction will help you in first steps in Unix command line
- During the course will work in our servers, but through this intro you will be using your own computer and personal files, so:
- **And as there is no “Trash bin” in Unix**, once you delete the folders/files there is no turning back... So you should only execute the commands we suggest, and **always confirm you are in the right location** (folders and files may have very similar or even equal names if they are in different locations).



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Why Unix/Linux?

Because:

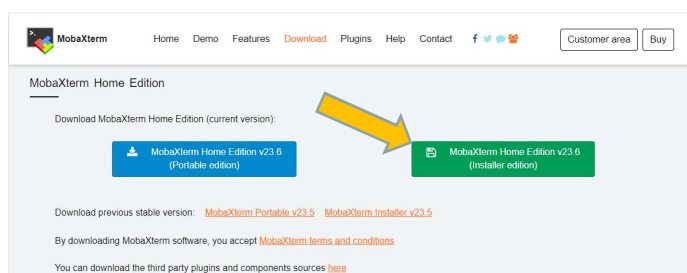
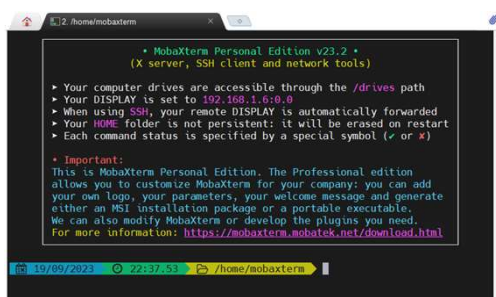
- Many tools for the analysis of genomic data only work in Unix.
- Often you need to use systems with more computational resources (high performance computing clusters), which are usually based on Unix.

Because it is a good idea:

- The Unix command line interface is a powerful tool that permits you to execute **shell scripts** to automate much of your analysis and keep accurate, detailed records of every step, facilitating reproducibility and reuse.

Help, I only have Windows! How do I begin?

- There are many ways to start using Unix-like systems in Windows
 - We're going to use **MobaXterm** because it is free and easy to install and use

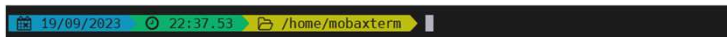


<https://mobaxterm.mobatek.net/download-home-edition.html>

OK, now I have a black screen. Now what?

After you install and run MobaXterm, you have a screen like this:

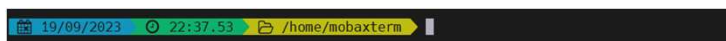
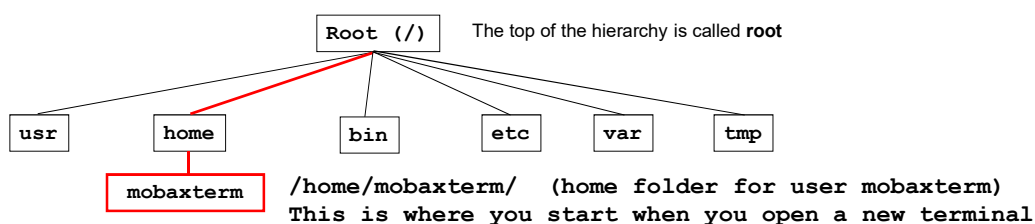
Note: You need to press the button “start local terminal”



- To run bioinformatics tools in Unix-like systems you usually run commands through a command-line interface.
 - This includes running programs, and copying/moving files around
- To run a command you type instructions and press enter for results

Using commands to navigate the file system

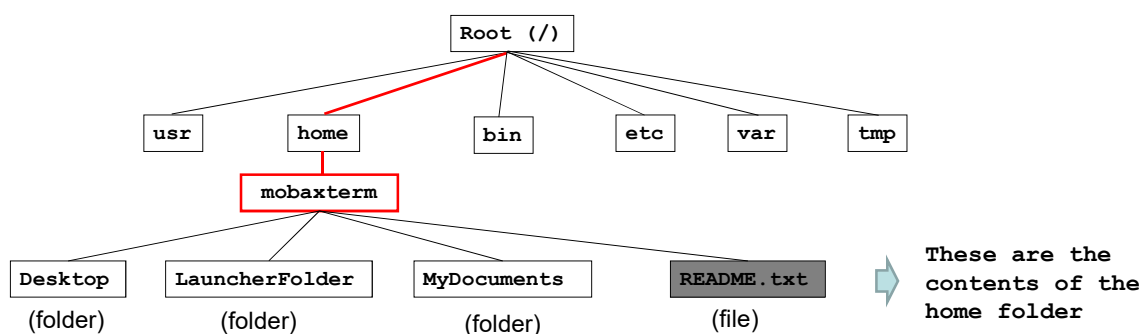
The file-system is arranged in a hierarchical structure, like an inverted tree



Using commands to navigate the file system

- How do I know the contents of the current folder?
 - Type 'ls' (command to list files), and press enter

```
19/09/2023 23:05.08 /home/mobaxterm ls
Desktop LauncherFolder MyDocuments README.txt
```

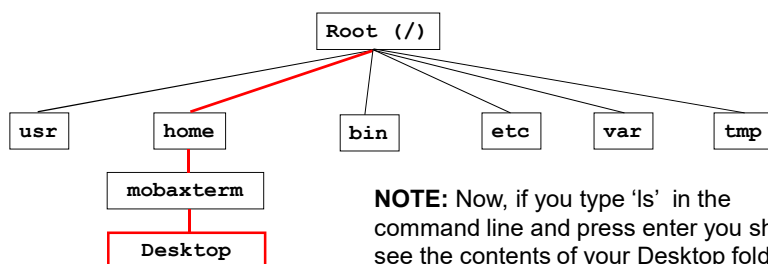


Using commands to navigate the file system

- How do I move to a folder (within my current folder) eg. Desktop?
 - Type 'cd Desktop' (command to change directory), and press enter

```
19/09/2023 23:18.26 /home/mobaxterm cd Desktop
19/09/2023 23:20.46 /home/mobaxterm/Desktop
```

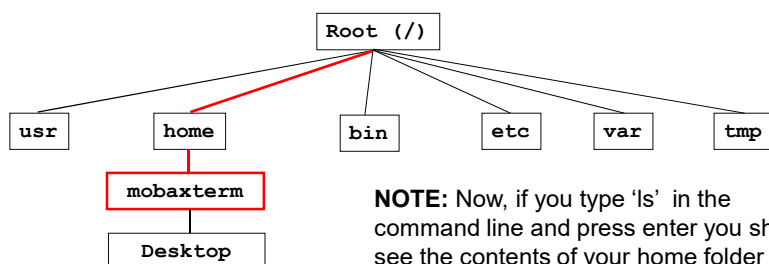
- The terminal says that your new current folder is /home/mobaxterm/Desktop



Using commands to navigate the file system

- How do I go back to the previous folder?
 - Type 'cd ..', and press enter (Note: there is a space between 'cd' and '..')

```
19/09/2023 23:44.44 /home/mobaxterm/Desktop cd ..
19/09/2023 23:44.47 /home/mobaxterm
```

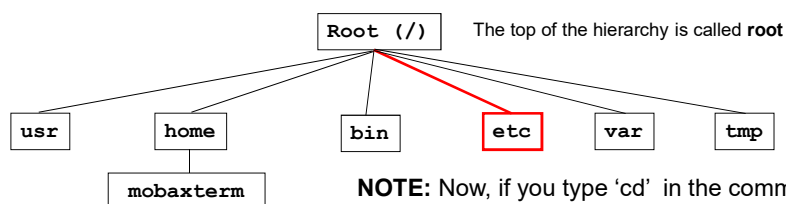


NOTE: Now, if you type 'ls' in the command line and press enter you should see the contents of your home folder

Using commands to navigate the file system

- How do I go to a specific folder from any other folder?
 - Eg. type 'cd /etc/' and press enter to go to the /etc folder from anywhere

```
20/09/2023 00:21.20 /home/mobaxterm cd /etc/
20/09/2023 00:21.39 /etc
```



NOTE: Now, if you type 'cd' in the command line and press enter you should go back home 'cd' is equivalent to 'cd /home/mobaxterm/'

Using commands to navigate the file system

- Some useful tips:
 - It is frequent to get the spelling incorrectly. Also, Unix is case-sensitive!
 - If you get an error, check spelling, case, and spaces. Eg. avoid file names with spaces
 - If you press the up↑ and down↓ keys you navigate the history of commands
 - It can be useful to repeat a command, or to review parameters, etc...
 - Pressing tab while writing a command will perform autocompletion
 - Eg. after writing 'cd /e', pressing tab will complete to 'cd /etc/'

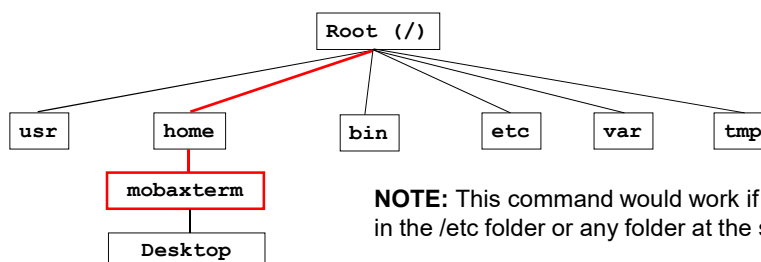
Using commands to navigate the file system

- How do I go to a specific folder relative to my current folder?
 - Eg. type 'cd ../home/mobaxterm' and press enter to go back home

```

20/09/2023 08:58:07 /etc > cd ../home/mobaxterm/
20/09/2023 11:11:02 /home/mobaxterm >

```

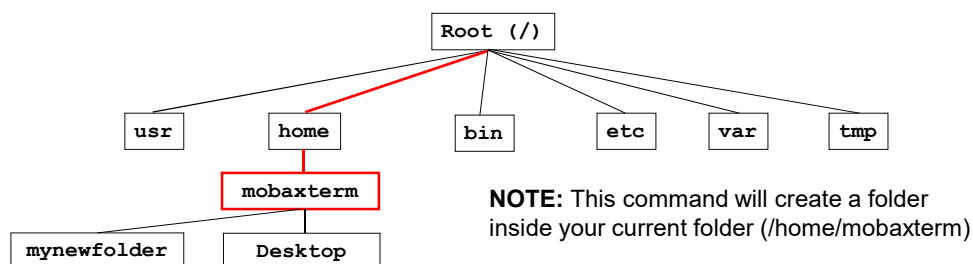


NOTE: This command would work if you were in the /etc folder or any folder at the same level

Using commands to navigate the file system

- How do I create a new folder?
 - Eg. type 'mkdir mynewfolder' and press enter to create a new folder 'mynewfolder'

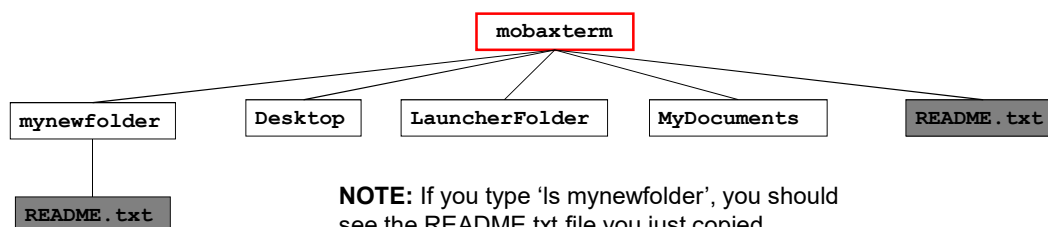
```
20/09/2023 11:11:02 /home/mobaxterm mkdir mynewfolder
20/09/2023 11:47:45 /home/mobaxterm
```



Using commands to navigate the file system

- How do I copy a file from one folder to another?
 - Eg. type 'cp README.txt mynewfolder' and press enter to copy the file to the new folder

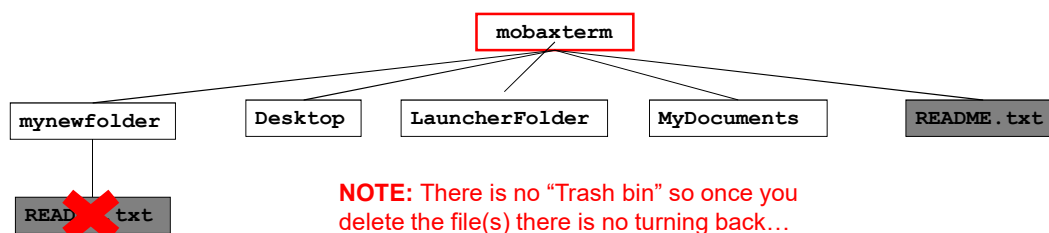
```
20/09/2023 11:47:45 /home/mobaxterm cp README.txt mynewfolder/
20/09/2023 13:13:35 /home/mobaxterm
```



Using commands to navigate the file system

- How do I delete file(s)?
 - Eg. type `rm mynewfolder/README.txt` to remove the file you just copied

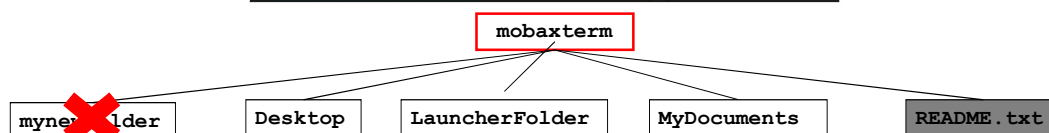
```
20/09/2023 13:13.35 /home/mobaxterm rm mynewfolder/README.txt
20/09/2023 13:16.53 /home/mobaxterm
```



Using commands to navigate the file system

- Special case: how do I delete a folder?
 - Eg. type `rmdir mynewfolder` to remove the new folder

```
20/09/2023 13:24.52 /home/mobaxterm rmdir mynewfolder/
20/09/2023 13:26.36 /home/mobaxterm
```



NOTE: `'rm mynewfolder'` will fail, as `rm` is usually just for files
 Nonetheless, `'rmdir mynewfolder'` would also fail if the folder contained anything inside
 You can do `'rm -r mynewfolder'`, to delete all files inside mynewfolder and the folder itself

Common commands:

| | |
|-----------------------------|---|
| cd <directory> | change to directory |
| pwd | display the path of the current directory |
| cd | change to home directory |
| cd .. | move one directory up |
| ls | list files and directories |

Common commands:

| | |
|--|---|
| mkdir <directory> | make a directory |
| rmdir <directory> | remove an empty directory |
| rm -r <directory> | remove a directory |
| rm <file> | remove a file |
| mv <file1> <file2> | move or rename file1 to file2 |
| cp <file> <directory> | copy file to named directory |
| cp -r <directory1> <directory2> | copy directory and its contents, to another directory |
| cat <file1> [<filen>] | display or concatenate file(s) |

Common commands:

| | |
|-------------------------------|---------------------------------------|
| more <file> | display a file a screen at a time |
| less <file> | display a file a page at a time |
| head <file> | display the first few lines of a file |
| tail <file> | display the last few lines of a file |
| wc -w <file> | count the number of words in a file |
| wc -l <file> | count the number of lines in a file |
| grep 'keyword' <file> | search a file for keywords |
| chmod [options] <file> | change access rights for named file |

Some useful resources

- https://edu.sib.swiss/pluginfile.php/2878/mod_resource/content/4/cours_elab-html/content.html
- <https://mobaxterm.mobatek.net/>
- <https://learn.microsoft.com/en-us/windows/wsl/install>
- <https://software-carpentry.org/lessons/index.html>
 - <https://swcarpentry.github.io/shell-novice/>
- <https://www.coursera.org/projects/introduction-to-bash-shell-scripting>
- Unix cheat sheet (quick reference for unix commands)
 - https://upload.wikimedia.org/wikipedia/commons/7/79/Unix_command_cheatsheet.pdf