

This competency framework regarding the **Unix shell** for **bioinformatic usage** was created by the **e-learning working group of the French Institute of Bioinformatics**. The objective is to define **the expected Unix competencies in bioinformatics**. These competencies are organized according to **increasing levels of difficulty** and thematic groups. The competencies are **cumulative** meaning that competencies acquired at a given level are required at the next level. Each competency has been defined operationally by following Bloom's taxonomy of learning objectives.

(Airasian, P. W. et al. A Taxonomy for Learning, Teaching, and Assessing: A Revision of Bloom's Taxonomy of Educational Objectives. (Longman, New York, NY, USA, 2001)).

This framework can be freely **reused** and serves as inspiration for defining the competencies or prerequisites of a training course, or for evaluating the level of a student. This content is made available under the terms of the Creative Commons Attribution 4.0 International License (CC BY 4.0). Version 1, July 2024.



Terminal, Shell & Unix Command

U1

Structure and Function of a Command within the Directory Tree

U2

- ☐ Explain the differences between a terminal and a shell
- ☐ Give examples of Unix shells
- ☐ Describe the three main syntactic components of a Unix command
- ☐ Explain the importance of the space in a Unix command
- ☐ Name the command that allows you to display the date
- ☐ Indicate the keyboard key used to execute a command in the terminal
- ☐ Name the command that displays the content of a directory

- ☐ Explain the structure of a filename
- ☐ Explain the difference between a directory (or folder) and a file (*ls -p* command)
- ☐ Name the character that serves as a "wildcard" to replace multiple characters, for example, the name of a file
- ☐ Explain the difference between *ls* and *ls + arguments*
- ☐ Explain the role of options in a Unix command
- ☐ Give an example of an option for a Unix command
- ☐ Describe the two forms of options for a Unix command
- ☐ Name the combination of options for the *ls* command that summarizes file sizes in a human-readable way
- ☐ Recall the command that displays the documentation of another Unix command
- ☐ Name the option of the *ls* command that displays the list of files in a detailed format
- ☐ Indicate the option of the *ls* command used to display its help message
- ☐ Name the characteristic of an absolute path in Unix
- ☐ Differentiate between an absolute path and a relative path
- ☐ Identify the root in an absolute path

- ☐ Identify the directory separator in a path (absolute or relative)
- ☐ Name the command that displays the path of the current directory
- ☐ Name the command used to navigate the directory tree
- ☐ Explain where the parent directory is located in a Unix path
- ☐ Name the command that allows you to navigate within a directory of the directory tree
- ☐ Describe the effect of the TAB key when writing a command or a path in a terminal
- ☐ Differentiate the usage of the *cd* command alone versus the *cd* command followed by an argument
- ☐ Explain what the "home" directory is
- ☐ Recognize the symbol for the "home" directory
- ☐ Use two ways to navigate to a given directory in the directory tree
- ☐ Examine your position in the directory tree after a directory change
- ☐ Name the command to display the complete content of a text file in the terminal
- ☐ Name the command that allows you to list all the Unix commands used in the shell so far
- ☐ Which keyboard keys are used to navigate through the shell command history?

Advanced Exploration, Modification of the Directory Tree and Workspace

U3

- ☐ Explain the purpose of the `-L 2` option in the command `tree -d -L 2 /shared`
- ☐ Explain the meaning of `..` in a path
- ☐ Name the command that allows you to create a directory
- ☐ Name the command that allows you to copy a file or a directory
- ☐ Explain the syntax of the `cp` command
- ☐ Explain the usefulness of `.` in the `cp` command
- ☐ Describe the effect of the `-r` option on the `cp` command
- ☐ Name the command that allows you to move a file or a directory
- ☐ Explain the syntax of the `mv` command
- ☐ Explain the difference in the result obtained with the `cp` and `mv` commands
- ☐ Name the command that allows you to delete a file
- ☐ Recognize the target file of the `rm` command
- ☐ Identify the target directory in the `rm -r` command
- ☐ Indicate the difference(s) between the `less` and `cat` commands
- ☐ Give three examples of keyboard shortcuts related to the `less` command
- ☐ Name the command that allows you to display the first lines of a file
- ☐ Indicate the option of the `head` command that allows you to display the first X lines of a file
- ☐ Indicate the command that displays the last lines of a file
- ☐ Indicate the option of the `tail` command that allows you to display the last X lines of a file
- ☐ Explain the result returned by the command `"wc filename"`
- ☐ Specify the option of the `wc` command that allows you to display the number of lines in a file
- ☐ What words is the `wc` command an abbreviation of?

Patterns, Redirection, Pipe, Streams

U4

- ☐ Name the Unix command used to display lines in a file that match a given pattern
- ☐ Explain the difference(s) between the `less` and `cat` commands
- ☐ Provide an example of using the `grep` command
- ☐ Name the option of `grep` that allows you to display the lines that do not contain the searched pattern
- ☐ Name the command that allows you to extract a column from a tab-separated text file
- ☐ Specify the behavior of `cut` in this command `"cut -f 1-3 genes.bed"`
- ☐ Explain the usefulness of the `-d` option in the `cut` command
- ☐ List the 2 output streams of a command
- ☐ Explain what the `>` sign is used for in a command
- ☐ Explain the difference between `>` and `>>`
- ☐ Name the incoming stream of a Unix command
- ☐ Name the primary use of the `stderr` output
- ☐ Give an example of redirecting the error output to a file
- ☐ Identify in this command the file that will contain the standard output and the file that will contain the standard error: `"grep tp53 /shared/data/bank/homo_sapiens 1> tp53_genes.txt 2> error.log"`
- ☐ Identify in this command the file that will contain the standard output and the standard error: `"grep tp53 genome.txt > tp53_genes.txt 2>&1"`
- ☐ Use the `cut` command to extract the first column of a file to a new file
- ☐ Name the command that allows you to sort the lines of a file
- ☐ Describe the effect of the `-u` option in the `sort` command
- ☐ Name the option that allows sorting based on numerical values

Three other levels will be proposed in a future version of this framework:

U5

Usage of a bioinformatics program

U6

Variables, script, automation

U7

Usage of a computing cluster

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