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A Unix competency framework for learning bioinformatics

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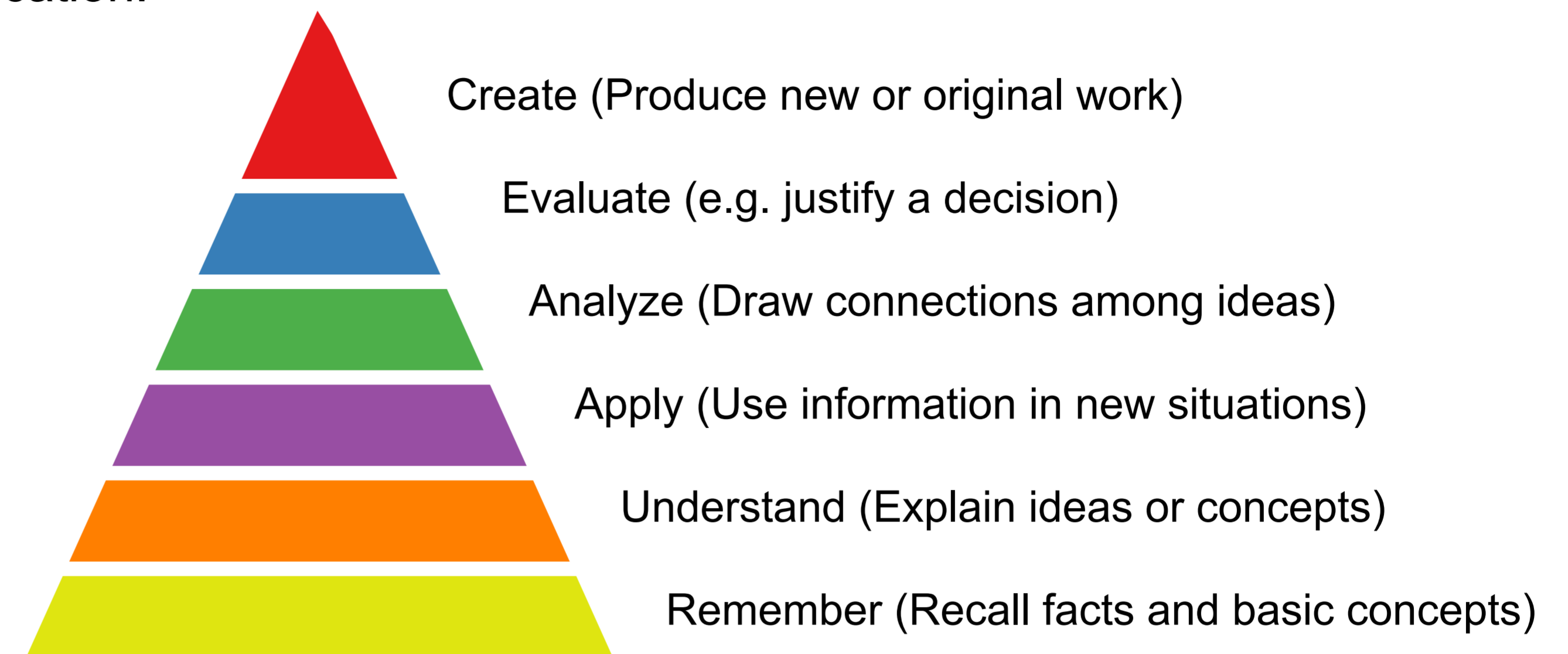
Introduction

- Bioinformatics relies on core tasks running on Unix computing infrastructures such as the IFB NNCR
- There is a need to correlate these bioinformatics tasks with required Unix skills (e.g., navigation, file manipulation, basic scripting, etc.)
- We propose a Unix competency framework that provides a thematic grouping and a rating system to classify the skills required (e.g., beginner, intermediate, advanced) using the Bloom taxonomy

Aim: formalise the competencies in Unix for bioinformatics, indepently of learning approach

The Bloom Taxonomy

- Bloom's taxonomy is a hierarchical classification of the key stages in the learning process. Today, it is used by trainers in professional development, particularly within instructional design strategies. Below is a diagram that summarizes the principle of this classification.



The competency framework

This version 1 presents four levels of competencies:

- U1** Terminal, shell and Unix command
- U2** Structure and operation of a command in the file system
- U3** Advanced exploration of the file system, and workspace
- U4** Motifs, redirection, pipe, flux



Download the competency framework
<https://zenodo.org/doi/10.5281/zenodo.12104693>

Terminal, shell and Unix command U1

- Explain the differences between a terminal and a shell
- Give examples of Unix shells
- Describe the three possible parts constituting the structure of a Unix command
- Explain the importance of space in a Unix command
- Name the command that displays the date
- Indicate the key to use to execute a command written in the terminal
- Name the command that displays the contents of a directory

Example for the first level

Associated pedagogical content : **sandbox.bio** server with 4 tutorials to learn the competency skills - **no installation required !**

sandbox.bio hosted by IFB

Basics of the Unix command line interface
 by French Institute of Bioinformatics

unix shell terminal

Welcome!

During this course, you will discover the Unix system and run some Bash commands.

U1 U2

Basics of the Unix command line interface
 IFB Scenario 1

Launch

U2 U3

Unix file system
 IFB Scenario 2

Launch

U3 U4

Manipulating files and directories
 IFB Scenario 3

Launch

U4

Combining bash commands
 IFB Scenario 4

Launch



Sandbox.bio@IFB
<https://sandboxbio.franc e-bioinformatique.fr/>

Targeted audiences

- Bioinformatics teachers and trainers**
 - evaluate Unix skills of their students/trainees before a bioinformatics course/hand-on session
 - clarify the Unix pre-requisites for a course/training
- Bioinformatics students, learners and trainees**
 - help them to evaluate their level and learning needs
- Biologists, researchers unfamiliar with Unix** and command line usage
 - inform and encourage them to acquire core graduated Unix competencies

We encourage all bioinformatics learners and users to assess their current Unix skills using the matrix

Use cases

- Example for trainers and teachers (ex. EBAll training)**

Prerequisites/Before training



Biologist who does not use the command line

Unix U1 U2 U3 U4



Learning outcomes/After training



Biologists who can construct a command line

Unix U1 U2 U3 U4



- Example for trainees and students**

Evolution of a student's skills during his university studies

Unix	U1	U2	U3	U4	U5	U6	U7
Early in L3	✓	✗	✗	✗	✗	✗	✗
Early in M1	✓	✓	✓	✗	✗	✗	✗
Early in M2	✓	✓	✓	✓	✓	✓	✗



We need your feedback !

If you wish to contribute to this work, please contact

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How do you plan to use it ?
 Suggestion for improvement ?

