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A Unix competency framework for learning bioinformatics

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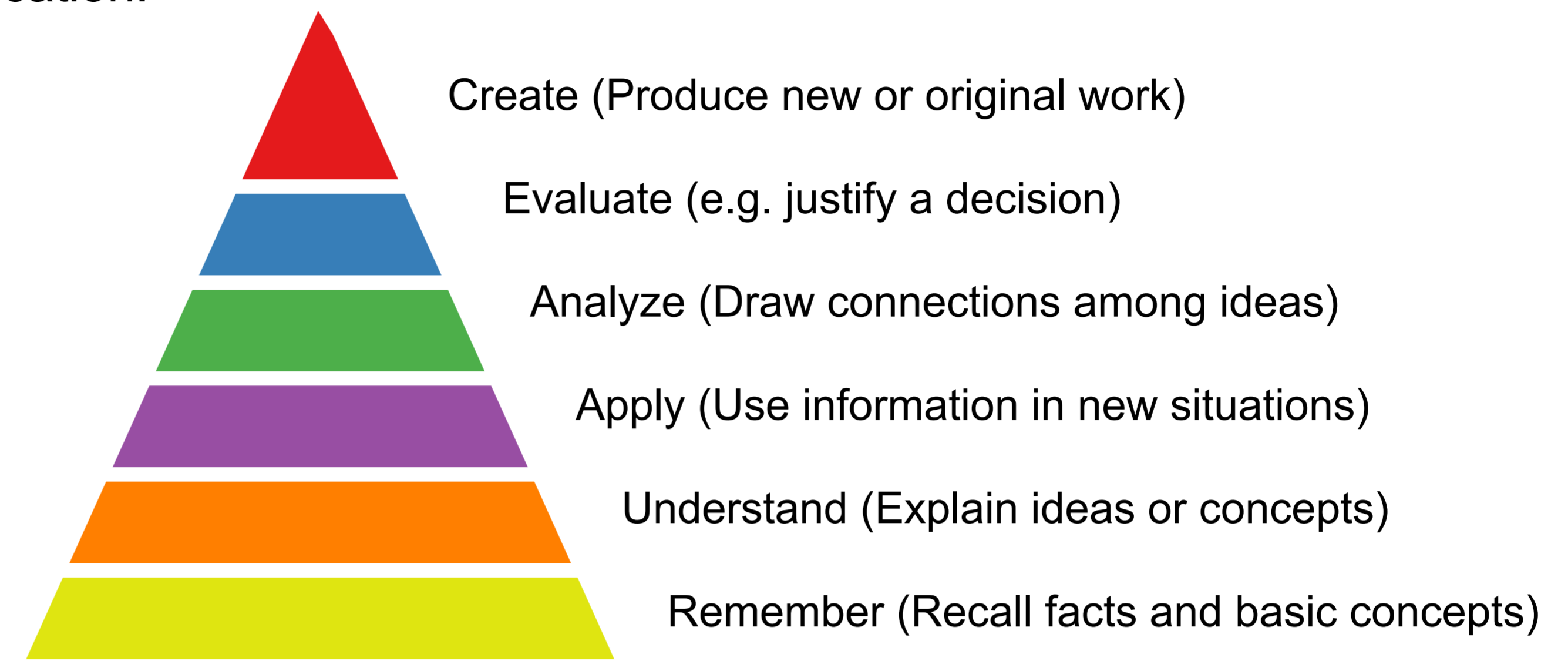
Introduction

- 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 !**

IFB sandbox.bio hosted by IFB

Basics of the Unix command line interface
 U1 U2

Unix file system
 U2 U3

Manipulating files and directories
 U3 U4

Combining bash commands
 U4



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 ?

