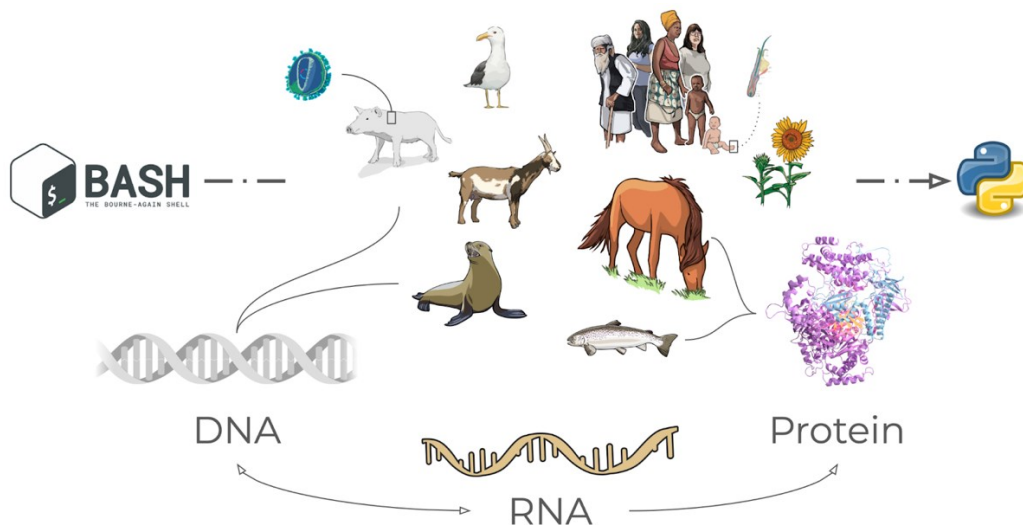


Programming for Biologists – 3 credits

This course introduces research students to programming as a natural part of problem-solving. Students will learn to navigate a Unix-based terminal, write scripts in Bash and Python, and leverage computational tools to handle large data sets. The course emphasises human-machine interplay, showing how coding knowledge enhances the effective use of AI tools.



Any student that wants to improve their efficiency in doing research is welcome to join. It will be tailored to all levels and the students can choose their engagement by completing more/less advanced tasks. **Seats are limited to 15 participants.**

The course is running from **Nov 17 till Jan 15** and is structured around lectures with connecting practical sessions in pairs (labs), followed by a final project.

Structure:

- **Lectures:** 5 x 2-hour sessions (theory, concepts, and live coding examples)
- **Labs:** 5 x 3-hour sessions (practical exercises in pairs)
- **Project:** individual task for final evaluation

Modules:

1. **Introduction to the Terminal and Bash**
 - Paths, file management, and shell scripting basics
 - Customising the environment (`.bashrc`)
 - Lab: File manipulation and text searches
2. **Version Control with GitHub**
 - Repository creation, commits, and collaboration
 - Lab: Managing and sharing code via GitHub
3. **Python Fundamentals**
 - Writing and running scripts
 - Parsing PDB files and comparing sequences to UniProt
 - Lab: Extracting and analysing protein sequences
4. **Bash-Python Integration**

- Calling Python scripts from Bash with `argparse`
 - Processing large data sets (e.g. 1000 PDB files)
 - Lab: Automating file processing with Python and Bash
- 5. External Tool Integration**
- Using subprocesses to call external programs (e.g. TM-align)
 - Generating sequence logos for structurally similar regions
 - Lab: Analysing protein structural similarity with TM-align and visualising results.

Requirements:

- Computer with Unix-based OS (MacOS or Linux)
- AI tools can be used for learning, but submitted code for the final project must be original (checked for plagiarism).

For registration or if you have any questions contact:

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