Bioinformatics analysis of biological sequences — from sequence to structure

Lecturers: Teresa Nogueira (cE3c;INIAV- Instituto Nacional de Investigação Agrária e Veterinária) and Eva Pinho (INIAV- Instituto Nacional de Investigação Agrária e Veterinária)

Note: This course will be given remotely

Calendar: January 17th-21th 2022

Duration: 36 hours

Schedule: 9h-12h30 and 14h-17h30, Monday-Thursday; 9h-13h and 14h-18h Friday

Objectives: Acquire knowledge regarding bioinformatic tools available to predict nucleic acid (RNA, DNA or Nucleic Acids Mimics) and protein three-dimensional structure, as well as autonomy and critical thinking in the use of those tools.

Develop skills on the use of bioinformatics software freely available on the Internet and to interpret the biological meaning of the results.

Overview

Nucleic acids are the molecular base of life through their unique ability to store and proliferate genetic information from DNA to proteins, through RNA. Besides storing genetic information, nucleic acids are also involved in other biological functions such as enzymatic catalysis and transcriptional regulation. Computational tools for prediction of nucleic acid structures are used for the identification and modelling of biologically important nucleic acid structures. The recent successes in predicting RNA three-dimensional structure directly from sequence and in designing

sequences that self-assemble into predefined DNA and RNA nanostructures show that nucleic acid structure is predictable and controllable. The prediction and design approaches deal with reverse problems of relating sequence and structure, but share the main computational principles, visual representations and modelling approaches. This course will introduce the nucleic acid and protein structure prediction tools together with an overview of their current capabilities and deficiencies. There are thousands of totally sequenced genomes freely available on the Internet. The number keeps on growing as at least one genome sequence is released every day. Large-scale sequencing requires bioinformatics analysis, whose algorithms will be the aim of this course, and that underlie the generation of reliable databases. Algorithms are also the basis of reliable sequence databases generation. An intelligent analysis of these databases allows the extraction of information and scientific knowledge.

At the end of this course, researchers, molecular biology students, or health professionals will be able to predict the three-dimensional structure of nucleic acid and proteins from their sequence and use the acquired knowledge to improve or create new methodologies in molecular biology research and diagnostics. They will also learn how to perform different analyses of nucleic acids and proteins sequences to discover biological knowledge.

General Plan:

- Nucleic acids unique characteristics
- Bioinformatic tools to predict nucleic acids secondary structure
- Towards nucleic acid tertiary structure prediction
- Molecular evolution and biological meaning of sequence alignment
- Aligning nucleotide and protein sequences
- Local similarity search nucleotide and protein sequences
- Functional and structural analysis of protein sequences
- Analysis and discussion of case study plan

This course can have a recognition of 6 ECTs for FCUL PhD students enrolling in it as part of their first doctoral year. These students need to deliver two reports after the course. For students only requiring 5 ECTs recognized in their specific PhD programmes the last 3.5 hours of the course are not mandatory, they need to deliver only the main report and the certificate will be on **'Topics in bioinformatics analysis of biological sequences'. Such report(s) are also advised for other students requesting creditation of the course in their institutions.**

Location: Faculdade de Ciências da Universidade de Lisboa

Nº (min, max) students: 10 – 20

Directed to: PhD or MSc students, postdocs, clinical analysts and other professionals working in Biology, Biochemistry and related topics.

Minimal formation of students: bachelor degree in Biology, Biochemistry or related areas.

Fee: Free for 1st year PhD students in Doctoral programmes at FCUL (e.g. Biologia), Biodiversity, Genetics and Evolution (BIODIV UL; UP), Biology and Ecology of Global Changes (BEAG UL, UA) and Sustainability Science (UL, several institutions), when the course counts credits for their formation,

in which case the delivery of a final report done after the course is mandatory; the course is also free for more advanced PhD students of the BIODIV programme (ULisboa or UPorto); 50 € for more advanced PhD students of cE3c; 80 € for PhD students of the PEERS network (CFE); 125 € for FCUL Master students and unemployed; 180 € for BTI, BI and other PhD students; 250 € for Professional and postdocs.

When the maximum number of students is reached, 10 vacancies will be available for non-paying 1st year PhD students mentioned above, being, by order of preference students from: 1) cE3c; 2) BIODIV (not from cE3c); 3) FCUL (not from cE3c); 4) Sustainability Science (not from cE3c or FCUL); 5) BEAG (not from cE3c or FCUL).

Deadline for applications: December 23rd 2021

To apply send an e-mail to Teresa Nogueira (teresainogueira@gmail.com) with a cv and motivation letter. The cv and letter should be named as *1st-lastNAME-CV.pdf and 1st-lastNAME-ML.pdf* (that is personalize the name of each file with your first and last name).

In the email please add the following information:

Full Name:
E-mail:
Phone:
Professional activity: Professional/Postdoc, BTI, BI (or other non-post-doc research grant),

PhD student (with/ without scholarship), Lic. (Bachelor)/Master student

PhD student of the 1st year of a Doctoral programme at FCUL, BIODIV (FCUL/FCUP), or BEAG (FCUL or UA)?

If yes to the above question, PhD student doing the Course to count credits for 1st year?:

PhD student of cE3c or CEF (Centro de Ecologia Funcional)?:

Name of the PhD programme: