



Bioinformatics analysis of biological sequences

Lecturers: Teresa Nogueira (external collaborator at cE3c-FCUL)

Calendar: February 6 -10, 2017

Duration: 36 hours

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

Overview: There are thousands of totally sequenced genomes freely available in 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. One of the most used tools for data mining is the software for the analysis and comparison of amino acids and nucleotide sequences that allow the identify and search for similarity. This course is aimed at researchers, molecular biology students, and health professionals who want to learn how to perform data mining of nucleic acids and proteins sequences to discover biological knowledge, or to implement new laboratory techniques in molecular biology, research or diagnostics.

Objectives: Provide the participants with knowledge about the biological sequences from reliable databases, as well as with autonomy and critical attitude in the use of bioinformatics software freely available in the Internet.

General Plan:

1. DNA sequencing technologies
2. Sequencing complete genomes
3. Sequencing metagenomes
4. Biological sequences databases
5. Biological meaning of sequence alignment
6. Aligning nucleotide sequences
7. Local similarity search of nucleotide sequences
8. Local similarity search of protein sequences and domains
9. Analysis and discussion of case studies

This course can have recognition of 6 ECTs for FCUL PhD students enrolling in it as part of their first doctoral year. For FCUL PhD students only requiring 5 ECTs recognized in their specific PhD programs the last 6 hours of the course are not mandatory and the certificate will be on 'Topics in bioinformatics analysis of biological sequences'.

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 the Doctoral program in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL; UP) and Biology and Ecology of Global Changes (BEAG UL, UA) when the course counts credits for their formation, in which case the delivery of a final report done after the course is mandatory; 25 € for PhD students from institutions of the PEERS network (cE3c, 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: 1) cE3c students; 2) BIODIV students (not from cE3c); 3) FCUL students (not from cE3c); 4) BEAG students (not from FCUL).

Deadline for applications: January 20th, 2017

Candidates should send a short CV and motivation letter to Teresa Nogueira (teresainogueira@gmail.com).