2017/2018

Bioinformatics

Code: 101951
ECTS Credits: 6

Degree	Type	Year	Semester
2500890 Genetics	OB	3	1

Contact

Name: Sònia Casillas Viladerrams

Email: Sonia.Casillas@uab.cat

Use of languages

Principal working language: catalan (cat)

Some groups entirely in English: No

Some groups entirely in Catalan: No

Some groups entirely in Spanish: No

Teachers

Antoni Barbadilla Prados

Raquel Egea Sánchez

Prerequisites

It is convenient for the student to review the basic concepts acquired in the subjects of the second grade:

- The module of Databases and fundamentals of programming within the subject Instrumental Techniques
- Molecular Genetics of Eukaryotes
- Molecular Genetics of Prokaryotes
- Population Genetics
- The content on structure and function of proteins of the subject of Biochemistry

Also, this subject is complemented by the Genomics, proteomics and interactomics course that is done during the same semester, so taking both together is recommended.

Knowledge of English is highly recommended for reading information.

A basic level of any programming language (e.g. Perl or Python) will be essential to be able to follow the sessions, both theoretical and practical, and complete the proposed activities.

Objectives and Contextualisation

Bioinformatics -the treatment, computer analysis and the interpretation and modeling of molecular and genomic data- has acquired a fundamental role in genetics nowadays. The subject taught during this course constitutes an introductory vision to bioinformatics. The main objectives are:

- To provide students with the basic bioinformatics knowledge that will allow them both to use a variety of tools to perform information searches in the databases and to approach the computational analysis of sequences of nucleic acids, proteins and genomes
- To apply scripting for the automation of repetitive bioinformatic tasks

- To give a perspective of the potential of this discipline both in the research and professional shperes

Content

Topic 1. Introduction to bioinformatics. Bioinformatics in genomic research. The three corners of bioinformatic analysis. The bioinformatic challenges of data integration.

Topic 2. Databases of interest for biosciences. Bibliographic databases. Construction of search strategies. Molecular databases. Search engines.

Topic 3. Sequence formats. Extraction of sequences from the primary databases. Sequence Formats. Tools for conversion between formats.

Topic 4. Sequence statistics. Sequence visualization, editing and analysis tools. Sequence statistics.

Topic5. Sequence alignment. Comparison of sequences. Local and global alignment for dynamic programming. Scoring matrices: identity and similarity. Penalties for gaps. Dot-plots.

Topic 6. Similarity searches. Heuristic algorithms for similarity searching against databases: BLAST. Applications of BLAST. Search for remote counterparts using PSI-Blast. Tools for the automation of similarity searches.

Topic 7. Multiple alignment. Multiple sequence alignment. Progressive alignments. Distance matrices. The CLUSTAL package. Applications of multiple alignment. Tools for the automation of multiple alignment. Matrices of position (weight) and LOGOS.

Topic 8. Molecular phylogenetic reconstruction. The molecular phylogeny. Methods of phylogenetic inference. Tools for phylogenetic reconstruction. Examples of phylogenetic reconstruction.

Topic 9. Genome assembly. Mapping against reference genomes. De novo assembly algorithms. Formats and tools.

Topic 10. Genome annotation. Annotation of genes. Annotation of regulatory regions. Visualization of annotations through genome browsers.

Topic 11. Comparative and functional genomics. Different levels of comparison. Synthenic blocks. Rearrangement hotspots. Comparative view using genome browsers.