MSc in Bioinformatics for Health Sciences
PGB. Principles of Genome Bioinformatics

Syllabus Information

Academic Course: 2018/19

Academic Center: 804 - Official Postgraduate Programme in Biomedicine

Study: 8045 – Bioinformatics for Health Sciences - MSc

Subject: 30167 – PGB. Principles of Genome Bioinformatics

Credits: 5.0

Course: 1st

Teaching languages: English

Teachers: Maria del Mar Albà Soler, Cedric Notredame and Roderic Guig

Teaching Period: 1st term

Presentation

The subject Principles of Genome Bioinformatics (PGB) provides the foundations of DNA/RNA and protein sequence comparisons, molecular evolution, genome sequencing, gene annotation and large scale analysis of mRNAS.

Associated skills

General:

1. Using scientific English.

2. Ability to work in a team.

3. Ability to solve by yourself a given problem.

4. Ability to use programming in Perl to perform simple sequence analyses

5. Ability to search and manage information from different sources

Specific competences:

1. To understand the dynamic programming algorithm for pairwise sequence alignment.

2. To understand multiple sequence alignments, and how to compute sequence distance matrices.

3. To understand basic concepts of sequence evolution, natural selection and substitution rates.

4. To understand the most commonly used algorithms to identify similar sequences in databases.

5. To know how to use genome databases to extract sequence and functional information.

6. To understand the basic procedures involved in genome assembly and annotation.

7. Ability to work with next generation sequencing data for transcript assembly and gene expression quantification.

8. Ability to understand and communicate research in the area of computational genomics.

Contents

Contents section 1: Protein and DNA sequence

- Homology: orthology and paralogy. Mechanisms of sequence evolution. Algorithms for pairwise and multiple sequence alignment.

- Amino acid substitution matrices. Estimation of genetic distance and evolutionary rate on sequence alignments. Database sequence similarity searches. Representation and search of sequence motifs.

Contents section 2: Genome and transcriptome analysis

- Sequence repositories. Genome projects. Transcriptomics and high throughput sequencing technologies. Comparative genomics and genome evolution. Comparison of large sequence datasets.

Teaching methods

Approach and general organization of the subject:

Combining theory and hands-on. The subject coordinator gives most lectures and exercises. Other experts may participate in specific lessons. Final project is presented in class, team work and communication skills are also evaluated.

Training activities:

Solving problems in class using programming (Perl) and statistical packages (R). Making questions and promoting discussions in the class.

Evaluation

Assessment system:

Written exam, final subject project, participation in class.

Grading system:

On a system where 10 is the maximum mark, exam gives a maximum of 6 points, final project 4 points, attitude/participation in class may add another 0.5 points.

Bibliography and Information Resources

David W. Mount. Bioinformatics - Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press, New York