Course guide
200630 - FBIO - Fundations of Bioinformatics

Unit in charge: School of Mathematics and Statistics
Teaching unit: 1004 - UB - (ENG)Universitat de Barcelona.
Degree: MASTER'S DEGREE IN STATISTICS AND OPERATIONS RESEARCH (Syllabus 2013). (Optional subject).
Academic year: 2022 ECTS Credits: 5.0 Languages: Spanish

LECTURER

Coordinating lecturer: ESTEBAN VEGAS LOZANO
Others: Primer quadrimestre: ESTEBAN VEGAS LOZANO - A

REQUIREMENTS

Knowledge of statistical software R.
References:

DEGREE COMPETENCES TO WHICH THE SUBJECT CONTRIBUTES

Specific:
5. CE-1. Ability to design and manage the collection of information and coding, handling, storing and processing it.
6. CE-2. Ability to master the proper terminology in a field that is necessary to apply statistical or operations research models and methods to solve real problems.
7. CE-3. Ability to formulate, analyze and validate models applicable to practical problems. Ability to select the method and/or statistical or operations research technique more appropriate to apply this model to the situation or problem.
8. CE-5. Ability to formulate and solve real problems of decision-making in different application areas being able to choose the statistical method and the optimization algorithm more suitable in every occasion.

Translate to english
9. CE-6. Ability to use appropriate software to perform the necessary calculations in solving a problem.
10. CE-9. Ability to implement statistical and operations research algorithms.

Transversal:
1. ENTREPRENEURSHIP AND INNOVATION: Being aware of and understanding how companies are organised and the principles that govern their activity, and being able to understand employment regulations and the relationships between planning, industrial and commercial strategies, quality and profit.

2. SUSTAINABILITY AND SOCIAL COMMITMENT: Being aware of and understanding the complexity of the economic and social phenomena typical of a welfare society, and being able to relate social welfare to globalisation and sustainability and to use technique, technology, economics and sustainability in a balanced and compatible manner.

3. TEAMWORK: Being able to work in an interdisciplinary team, whether as a member or as a leader, with the aim of contributing to projects pragmatically and responsibly and making commitments in view of the resources that are available.

4. EFFECTIVE USE OF INFORMATION RESOURCES: Managing the acquisition, structuring, analysis and display of data and information in the chosen area of specialisation and critically assessing the results obtained.
TEACHING METHODOLOGY

Theory sessions:
In the theory sessions, the professor will present the problems that are tackled in each topic and will provide a summary of the principle concepts and problematic points of each topic. The student should complete the professor’s explanations by consulting the reference texts and complementary materials.

Practical Sessions:
The practical sessions will be conducted with the computer, where instruction will take place regarding the use of bioinformatics tools pertinent to each topic and the problems that are posed.

LEARNING OBJECTIVES OF THE SUBJECT

Upon completing the course, the student must be able to:

* Identify the bioinformatics domain of study.
* Know the large group of problems that bioinformatics poses.
* Be familiar with the most typical methods and models in bioinformatics.
* Be familiar with the basic components of organisms.
* Understand the coding and transmission mechanisms of biological information.
* Know the processes of gene expression and its regulation.
* Know the existence and availability of diverse information resources, both basic (nucleic acids, proteins, etc.) and more complex (patterns, genomes, etc.).
* Know the principle tools for recovering information such as SRS or Entrez.
* Know how to access these resources and make queries for obtaining information.
* Understand and differentiate distinct types of problems related to the alignment of sequences: in pairs, multiples and data search.
* Know the algorithms for aligning two sequences in optimum form.
* Know how to perform and interpret the alignment of two sequences.
* Understand the problem of Multiple Sequence Alignment (MSA).
* Know how to perform and interpret an MSA.
* Know how to conduct a sequence search in a database and how to interpret the results.
* Know the principle methods for representing an MSA and understand the relationships (hierarchical) between them.
* Understand the basic components of Markov models and their application toward sequence analysis.
* Know the basic components of a hidden Markov model and understand its advantages and uses for biological problems.
* Understand the problem of gene prediction and the difficulties (alternative splicing, non-coding genes, etc.) that are involved in their complete resolution.
* Know the principle methods for gene prediction.
* Know how to use gene prediction tools and their basic limitations.
* Be familiar with and know how to use genome browsers.
* Know the approach to systems biology as a comparison to traditional approaches.
* Know the study process based on microarrays.
* Conduct a microarray analysis in simple situations.
* Know the different types of biological networks.

STUDY LOAD

<table>
<thead>
<tr>
<th>Type</th>
<th>Hours</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hours large group</td>
<td>30,0</td>
<td>24.00</td>
</tr>
<tr>
<td>Self study</td>
<td>80,0</td>
<td>64.00</td>
</tr>
<tr>
<td>Hours small group</td>
<td>15,0</td>
<td>12.00</td>
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</tbody>
</table>
Total learning time: 125 h

CONTENTS

1. Introduction to Bioinformatics

2. Basic Concepts of Molecular Biology

3. Biological Databases: Concepts, Types and Applications

4. Sequence Alignment.

5. Probabilistic models of biological sequences.


7. Functional and systems genomics.

GRADING SYSTEM

The evaluation will be based on four components:

*Completion of short test exercises (2) during class hours (25%)
*Class participation and completion of assigned exercises during practice sessions (25%)
*Presentation of assigned work throughout the course (50%)

BIBLIOGRAPHY

Basic:

Complementary:
RESOURCES

Hyperl ink:
- Libres Electrònics. Online lectures in Bioinformatics
  [http://lectures.molgen.mpg.de/online_lectures.html]
- Organismes i Institucions. The European Bioinformatics Institute
  [http://www.ebi.ac.uk/]
- The National Center for Biotechnology Information
- Instituto Nacional de Bioinformática
  [http://www.inab.org/]
- Portals temàtiques. BIOINFORMATICS.CA
  [http://bioinformatics.ca/]
- 123Genomics
  [http://www.123genomics.com/]
- Revistes. Bioinformatics
  [http://bioinformatics.oxfordjournals.org/]
- Briefings in Bioinformatics
  [http://bib.oxfordjournals.org/]
- BMC Bioinformatics
  [http://www.biomedcentral.com/bmcbioinformatics/]
- Webs. International Society for Computational Biology (ISCB)
  [http://www.iscb.org/]
- The Gene Discovery Page
  [http://www.biowriters.com/bioinformatics/gdp.html]
- Curs d’introducció a la Bioinformàtica.
  [http://www.ub.edu/stat/docencia/Biologia/introbioinformatica/]
  [http://es.wikipedia.org/wiki/Bioinform%C3%A1tica]
- Documents electrònics. Complete Online Bioinformatics Courses/Tutorials
  [http://www.med.nyu.edu/rcr/rcr/btr/complete.html]

Other resources:
Bioinformatics notes, available on the intranet or supplied by the professor in pdf.