Course guides
34960 - MMB - Mathematical Models in Biology

Unit in charge: School of Mathematics and Statistics
Teaching unit: 749 - MAT - Department of Mathematics.
Degree: MASTER’S DEGREE IN ADVANCED MATHEMATICS AND MATHEMATICAL ENGINEERING (Syllabus 2010).
(Optional subject).
Academic year: 2021 ECTS Credits: 7.5 Languages: English

LECTURER

Coordinating lecturer: MARTA CASANELLAS RIUS
Others: Primer quadrimestre:
MARTA CASANELLAS RIUS - A
JESUS FERNANDEZ SANCHEZ - A
GEMMA HUGUET CASADES - A
JOSE TOMAS LAZARO OCHOA - A

PRIOR SKILLS

* Proficiency in undergraduate mathematics: calculus, algebra, probability and statistics.
* Ability to perform basic operations in linear algebra: eigenvalues and eigenvectors, computation of determinants, rank of matrices...
* Ability to analyze and solve linear differential equations and discuss the stability of simple vector fields.
* Interest towards biological applications of mathematics and/or previous working experience.

REQUIREMENTS

* Basic knowledge of undergraduate mathematics: calculus, ordinary differential equations, linear algebra, probability and statistics.
* First course in ordinary differential equations: linear differential equations, qualitative and stability theory and numerical simulation.
* Basic knowledge of computer programming for scientific purposes.

DEGREE COMPETENCES TO WHICH THE SUBJECT CONTRIBUTES

Specific:
1. RESEARCH. Read and understand advanced mathematical papers. Use mathematical research techniques to produce and transmit new results.
2. MODELLING. Formulate, analyse and validate mathematical models of practical problems by using the appropriate mathematical tools.
3. CALCULUS. Obtain (exact or approximate) solutions for these models with the available resources, including computational means.
4. CRITICAL ASSESSMENT. Discuss the validity, scope and relevance of these solutions; present results and defend conclusions.

Transversal:
5. SELF-DIRECTED LEARNING. Detecting gaps in one’s knowledge and overcoming them through critical self-appraisal. Choosing the best path for broadening one’s knowledge.
6. EFFICIENT ORAL AND WRITTEN COMMUNICATION. Communicating verbally and in writing about learning outcomes, thought-building and decision-making. Taking part in debates about issues related to the own field of specialization.
7. THIRD LANGUAGE. Learning a third language, preferably English, to a degree of oral and written fluency that fits in with the future needs of the graduates of each course.
8. TEAMWORK. Being able to work as a team player, either as a member or as a leader. Contributing to projects pragmatically and responsibly, by reaching commitments in accordance to the resources that are available.
9. EFFECTIVE USE OF INFORMATION RESOURCES. Managing the acquisition, structure, analysis and display of information from the own field of specialization. Taking a critical stance with regard to the results obtained.
TEACHING METHODOLOGY

The course will be structured in five blocks each consisting of a brief introduction through theoretical lectures, the development of a short project in groups and wrap-up sessions with oral presentations, discussion and complementary lectures. The central part intended to develop the short project will held at the computer lab.

LEARNING OBJECTIVES OF THE SUBJECT

This course is an introduction to the most common mathematical models in biology: in populations dynamics, ecology, neurophysiology, sequence analysis and phylogenetics. At the end of the course the student should be able to:

* Understand and discuss basic models of dynamical systems of biological origin, in terms of the parameters.
* Model simple phenomena, analyze them (numerically and/or analytically) and understand the effect of parameters.
* Understand the diversity of mechanisms and the different levels of modelization of physiological activity.
* Obtain and analyze genomic sequences of real biological species and databases containing them.
* Use computer software for gene prediction, alignment and phylogenetic reconstruction.
* Understand different gene prediction, alignment and phylogenetic reconstruction methods.
* Compare the predictions given by the models with real data.
* Communicate results in interdisciplinary teams.

STUDY LOAD

<table>
<thead>
<tr>
<th>Type</th>
<th>Hours</th>
<th>Percentage</th>
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<tbody>
<tr>
<td>Hours large group</td>
<td>60,0</td>
<td>32.00</td>
</tr>
<tr>
<td>Self study</td>
<td>127,5</td>
<td>68.00</td>
</tr>
</tbody>
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Total learning time: 187.5 h

CONTENTS

Mathematical Models in Neuroscience

Description:
1. Membrane biophysics.
2. Excitability and action potentials: the Hodgkin-Huxley model, the Morris-Lecar model, integrate & fire models.
4. Synaptic transmission and dynamics.
6. Applications to cognitive tasks (working memory, decision making and visual perception).

Full-or-part-time: 75h
Theory classes: 12h
Laboratory classes: 12h
Self study: 51h
Models of Population Dynamics

Description:
2. One-dimensional discrete models. Chaos in biological systems.
3. Paradigms of population dynamics in current research.

Full-or-part-time: 37h 30m
Theory classes: 6h
Laboratory classes: 6h
Self study: 25h 30m

Mathematical models in phylogenetics

Description:
1. Brief introduction to genomics and phylogenetics (genome, gen structure, alignments, evolution of species...). Retrieving genomic sequences and alignments.
2. Markov models of molecular evolution (Jukes-Cantor, Kimura, Felsenstein hierarchy...), phylogenetic trees, branch lengths.

Full-or-part-time: 75h
Theory classes: 12h
Laboratory classes: 12h
Self study: 51h

GRADING SYSTEM

50%: Each of the five blocks will give a part (10%) of the qualification, based on the performance on the short-projects.
20%: Overall evaluation of the participation, interest and proficiency evinced along the course.
30%: Final exam aiming at validating the acquisition of the most basic concepts of each block.

BIBLIOGRAPHY

Basic:

Complementary:
- Stein, William A. [et al.]. Sage mathematics software (Version 4.4.2) [on line]. 2010 [Consultation: 23/11/2012]. Available on:
http://www.sagemath.org/.