Course guide
34960 - MMB - Mathematical Models in Biology

Last modified: 01/06/2023

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: 2023 **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
ADRIÁN FERNANDO PONCE ÁLVAREZ - 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

Type	Hours	Percentage
Hours large group	60,0	32.00
Self study	127,5	68.00

Total learning time: 187.5 h

CONTENTS

Models of Population Dynamics

Description:
1. One dimensional models in ecology. A single species dynamics. One-dimensional discrete models.
2. Modelling interactions between populations with differential equations. Stability and bifurcations.
3. Epidemiology.

Full-or-part-time: 12h 30m
Theory classes: 2h
Laboratory classes: 2h
Self study : 8h 30m

Mathematical Models in Neuroscience

Description:
1. Membrane biophysics.
2. Excitability and action potentials: the Hodgkin-Huxley model, the Morris-Lecar model, integrate & fire models.
3. Bursting oscillations.
4. Synaptic transmission and dynamics.
5. Neuronal networks. Firing rate models. Wilson-Cowan equations.
6. Applications to cognitive tasks (working memory, decision making and visual perception).
7. Recurrent Neural Networks.
8. Statistical Models.

Full-or-part-time: 100h
Theory classes: 16h
Laboratory classes: 16h
Self study : 68h

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...), evolutionary distances, phylogenetic trees.
3. Phylogenetic tree reconstruction: distance and character-based methods.
4. Genomics: Markov chains and Hidden Markov models for gene prediction. Tropical arithmetics and Viterbi algorithm. Forward and Expectation-Maximization algorithms. Multiple sequence alignment.

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 perfomance 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.

UNIVERSITAT POLITÈCNICA DE CATALUNYA
BARCELONATECH

BIBLIOGRAPHY

Basic:

- Murray, J.D. Mathematical biology, vol. 1 [on line]. 3rd ed. Berlin: Springer, 2002 [Consultation: 10/07/2023]. Available on: https://link-springer-com.recursos.biblioteca.upc.edu/book/10.1007/b98868. ISBN 9780387952239.
- Izhikevich, Eugene M. Dynamical systems in neuroscience : the geometry of excitability and bursting. Cambridge: MIT Press, 2007. ISBN 0262090430.
- Ermentrout, Bard G.; Terman, David H. Mathematical foundations of neuroscience [on line]. New York: Springer, 2010 [Consultation: 10/07/2023]. Available on: https://link-springer-com.recursos.biblioteca.upc.edu/book/10.1007/978-0-387-87708-2. ISBN 9780387877082.
- Keeling, Matthew J.; Rohani, Pejman. Modeling infectious diseases in humans and animals. Princeton: Princeton University Press, cop. 2008. ISBN 9780691116174.
- Allman, Elizabeth S.; Rhodes, John A. Mathematical models in biology : an introduction. Cambridge: Cambridge University Press, 2004. ISBN 9780521819800.
- Istas, Jacques. Mathematical modeling for the life sciences [on line]. Berlin: Springer, 2005 [Consultation: 10/07/2023]. Available on: https://link-springer-com.recursos.biblioteca.upc.edu/book/10.1007/3-540-27877-X. ISBN 354025305X.

Complementary:

- Bacaër, N.; Bravo de la Parra, R.; Ripoll, J. Breve historia de los modelos matemáticos en dinámica de poblaciones [on line]. [Consultation: 10/07/2023]. Available on: https://rafaelbravodelaparra.web.uah.es/Breve%20historia%20de%20los%20modelos%20matem%C3%A1ticos%20en%20din%C3%A1mica%20de%20poblaciones-N%20Bacaer.pdf. ISBN 9791034365883.
- Stein, William A. [et al.]. Sage mathematics software (Version 4.4.2) [on line]. 2010 [Consultation: 10/07/2023]. Available on: http://www.sagemath.org/.
- Pachter, Lior; Sturmfels, Bernd. Algebraic statistics for computational biology. Cambridge: Cambridge University Press, 2005. ISBN 0521857007.
- Keener, James P.; Sneyd, James. Mathematical physiology. Vol 1 [on line]. 2nd ed. New York: Springer Verlag, 2009 [Consultation: 10/07/2023]. Available on: https://link-springer-com.recursos.biblioteca.upc.edu/book/10.1007/978-0-387-75847-3. ISBN 9780387758473.
- Durbin, Richard [et al.]. Biological sequence analysis : probabilistic models of proteins and nucleic acids [on line]. Cambridge: Cambridge University Press, 1998 [Consultation: 10/07/2023]. Available on: https://ebookcentral-proquest-com.recursos.biblioteca.upc.edu/lib/upcatalunya-ebooks/detail.action?pq-origsite=primo&docID=320915. ISBN 0521629713.
- Feng, Jianfeng. Computational neuroscience : a comprehensive approach [on line]. Boca Raton: Chapman & Hall/CRC, 2004 [Consultation: 10/07/2023]. Available on: http://nba.uth.tmc.edu/homepage/cnjclub/2007summer/renart_chapter.pdf. ISBN 1584883626.
- Steel, Mike. Phylogeny: Discrete and random processes in evolution. CBMS-NSF Regional conference series in Applied Mathematics, SIAM, 2016. ISBN 9781611974478.
- Miller, Paul. An Introductory course in computational neuroscience. Cambridge, Masachusetts: The MIT Press, [2018]. ISBN 9780262038256.
- Felsenstein, Joseph. Inferring phylogenies. Sunderland, Massachusetts: Sinauer Associates, cop. 2004. ISBN 9780878931774.