

34960 - MMB - Mathematical Models in Biology

Coordinating unit:	200 - FME - School of Mathematics and Statistics
Teaching unit:	749 - MAT - Department of Mathematics
Academic year:	2017
Degree:	MASTER'S DEGREE IN ADVANCED MATHEMATICS AND MATHEMATICAL ENGINEERING (Syllabus 2010). (Teaching unit Optional)
ECTS credits:	7,5
Teaching languages:	English

Teaching staff

Coordinator:	JESUS FERNANDEZ SANCHEZ
Others:	Primer quadrimestre: MARTA CASANELLAS RIUS - A JESUS FERNANDEZ SANCHEZ - A GEMMA HUGUET CASADES - A JOAQUIM PUIG SADURNI - 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

34960 - MMB - Mathematical Models in Biology

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. The SAGE computing environment will be used, with interfaces to Python, R and C if necessary.

Learning objectives of the subject

This course is an introduction to the most common mathematical models in biology: in populations dynamics, ecology, physiology, 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

Total learning time: 187h 30m	Hours large group:	60h	32.00%
	Self study:	127h 30m	68.00%

34960 - MMB - Mathematical Models in Biology

Content

<p>Mathematical models in Genomics</p>	<p>Learning time: 75h Theory classes: 12h Laboratory classes: 12h Self study : 51h</p>
<p>Description:</p> <ol style="list-style-type: none"> 1. Brief introduction to genomics (genome, gen structure, genetic code...). Genome databases online. 2. Phylogenetics: Markov models of molecular evolution (Jukes-Cantor, Kimura, Felsenstein hierarchy...), phylogenetic trees, branch lengths. Phylogenetic tree reconstruction (distance and character based methods). 3. Genomics: Markov chains and Hidden Markov models for gene prediction. Tropical arithmetics and Viterbi algorithm. Forward and Expectation-Maximization algorithms. 4. Multiple sequence alignment: dynamical programming, tropical arithmetics and Pair-HMMs 	
<p>Mathematical Models in Neurophysiology</p>	<p>Learning time: 56h 15m Theory classes: 9h Laboratory classes: 9h Self study : 38h 15m</p>
<p>Description:</p> <ol style="list-style-type: none"> 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. 	
<p>Models of Population Dynamics</p>	<p>Learning time: 37h 30m Theory classes: 6h Laboratory classes: 6h Self study : 25h 30m</p>
<p>Description:</p> <ol style="list-style-type: none"> 1. Modelling interactions among populations with differential equations. Stability and bifurcations. 2. One-dimensional discrete models. Chaos in biological systems. 3. Paradigms of population dynamics in current research. 	



34960 - MMB - Mathematical Models in Biology

Biological networks	Learning time: 18h 45m Theory classes: 3h Laboratory classes: 3h Self study : 12h 45m
Description: 1. Complex networks in biology. 2. Networks of neurons.	

Qualification 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.

34960 - MMB - Mathematical Models in Biology

Bibliography

Basic:

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Istas, Jacques. *Mathematical modeling for the life sciences* [on line]. Berlin: Springer, 2005. Available on: <<http://dx.doi.org/10.1007/3-540-27877-X>>. ISBN 354025305X.

Murray, J.D. *Mathematical biology* [on line]. 3rd ed. Berlin: Springer, 2002. Available on: <<http://link.springer.com/book/10.1007/b98868> (v. 1) <http://link.springer.com/book/10.1007/b98869> (v. 2)>. ISBN 978-0-387-95223-9.

Pachter, Lior; Sturmfels, Bernd. *Algebraic statistics for computational biology*. Cambridge: Cambridge University Press, 2005. ISBN 0521857007.

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*. New York: Springer, 2010. ISBN 978-0-387-87708-2.

Keeling, Matthew James; Rohani, Pejman. *Modeling infectious diseases in humans and animals*. Princeton: Princeton University Press, cop. 2008. ISBN 9780691116174.

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/>>.

Keener, James P.; Sneyd, James. *Mathematical physiology*. Vol 1. 2nd ed. New York: Springer Verlag, 2009. ISBN 9780387758466.

Durbin, Richard [et al.]. *Biological sequence analysis : probabilistic models of proteins and nucleic acids*. Cambridge: Cambridge University Press, 1998. ISBN 0521629713.

Feng, Jianfeng. *Computational neuroscience : a comprehensive approach* [on line]. Boca Raton: Chapman & Hall/CRC, 2004 [Consultation: 23/11/2012]. Available on: <http://nba.uth.tmc.edu/homepage/cnjclub/2007summer/renart_chapter.pdf>.

Felsenstein, J. *PHYLIP* [on line]. [Consultation: 23/11/2012]. Available on: <<http://evolution.genetics.washington.edu/phylip.html>>.

European Bioinformatics Institute; Wellcome Trust Sanger Institute. *Ensembl project* [on line]. [Consultation: 23/11/2012]. Available on: <<http://www.ensembl.org>>.