Last update: 03/10/2011

34960 - MMB - Mathematical Models in Biology

Coordinating unit:	200 - FME - Faculty of Mathematics and Statistics
Teaching unit:	725 - MA I - Department of Applied Mathematics I 726 - MA II - Department of Applied Mathematics II
Academic year:	2011
Degree:	MASTER IN ADVANCED MATHEMATICS AND MATHEMATICAL ENGINEERING (Syllabus 2010). (Teaching unit Optative)
ECTS credits:	7,5
Teaching languages:	English

Teaching staff

Coordinator: JOAQUIM PUIG SADURNI

Others:

JESUS FERNANDEZ SANCHEZ - A
ANTONI GUILLAMON GRABOLOSA - 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 analyize 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.
* Courses and all the bibliography will be in English.

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.

Generical:

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 INFORMATI0N 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 consist of lectures, problem sessions and practical computer sessions. Lectures will consist of expositions about the contents of this subject following a biological problem.

Both practical sessions and problem sessions will be in a PC room and will help the student to develop part of the subject with extensions to the lectures, practical problems with real or simulated data and algorithms to perform these operations. 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	Self study:	127h 30m	68.00%
	Theory classes:	60h	32.00%

Content

Models of Population Dynamics	Learning time: 56h 20m Theory classes: 9h Practical classes: 9h Self study : 38h 20m

Description:

1. Differential equations models. Stability and Bifurcations. Applications to population dynamics.
2. One-dimensional discrete models. Chaos in biological systems.
3. Introduction to stochastic models. Branching processes
4. Simulation with SAGE

Mathematical models in Genomics	Learning time: 62h 30m Theory classes: 12h Practical classes: 8h Self study : 42h 30m

Description:

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

Mathematical Models in Physiology	Learning time: 56h 20m Theory classes: 11h Practical classes: 7h Self study : 38h 20m

Description:

1. Enzymatic reactions and Michaelis-Menten theory.
2. Neuronal activity: transmembranic diffusion, Hodgkin-Huxley models and variations.
3. Pancreatic Beta cells and bursting models.
4. Models in systems physiology: hormone physiology, respiration, cardiac activity.

Biological networks	Learning time: 12h 20m Theory classes: 3h Practical classes: 1h Self study : 8h 20m

Description:

1. Complex networks in biology.
2. Networks of neurons: synapse modelling, connectivity and synchronization.
3. Firing rate models and mean field techniques in cell networks.

Qualification system

The course has three parts and each of these parts will give a part of the qualification, based on practical problems to be delivered. Besides, students will be asked to write a report on a specialized subject (from a list of suggested topics) and deliver it 2 days before presenting it in front of the students and teachers . The contents and the clarity of explanations and exposition.

The final qualification will be given by the formula 0.6*NP+0.4*NT where:

- NP=NP1+NP2+NP3 practice qualification: this is the qualification of 3 practical qualifications.

- NT=report qualification.

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Bibliography

Basic:

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.* Berlin: Springer, 2005. ISBN 354025305X.

Murray, J.D. *Mathematical biology*. 3rd ed. Berlin: Springer, 2002. ISBN 978-0-387-95223-9.

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*. 2nd ed. New York: Springer Verlag, 2009. ISBN 9780387758466.

Izhikevich, Eugene M. *Dynamical systems in neuroscience : the geometry of excitability and bursting.* Cambridge: MIT Press, 2007. ISBN 0262090430.

Pikovsky, Arkady; Rosenblum, Michael; Kurths, Jürgen. *Synchronization : a universal concept in nonlinear sciences.* Cambridge: Cambridge University Press, 2001. ISBN 0521592852.

Complementary:

Stein, William A. [et al.]. *Sage mathematics software (Version 4.4.2)* [on line]. 2010 [Consultation: 11/05/2010]. Available on: <http://www.sagemath.org/>.

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

Renart Alfonso; Brunel, Nicolas; JingWang, Xiao. "Mean-field theory of irregularly spiking neuronal populations and working memory in recurrent cortical networks". Feng, Jianfeng. *Computational neuroscience : comprehensive approach* [on line]. Boca Raton: Chapman & Hall/CRC, 2004. p. 432-490Available on: <http://nba.uth.tmc.edu/homepage/cnjclub/2007summer/renart_chapter.pdf>.

Rolls, Edmund T.; Deco, Gustavo. *The noisy brain : stochastic dynamics as a principle of brain function.* Oxford: Oxford University Press, 2010. ISBN 9780199587865.

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

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