



Universitat de Lleida

DEGREE CURRICULUM
**METHODS IN SYSTEMS
BIOLOGY**

Coordination: FERREZUELO MUÑOZ, FRANCISCO

Academic year 2023-24

Subject's general information

Subject name	METHODS IN SYSTEMS BIOLOGY			
Code	14705			
Semester	1st Q(SEMESTER) CONTINUED EVALUATION			
Typology	Degree	Course	Character	Modality
	Master's Degree in Biomedical Research	1	OPTIONAL	Attendance-based
Course number of credits (ECTS)	4			
Type of activity, credits, and groups	Activity type	PRALAB	PRAULA	TEORIA
	Number of credits	0.2	1.7	2.1
	Number of groups	1	1	1
Coordination	FERREZUELO MUÑOZ, FRANCISCO			
Department	BASIC MEDICAL SCIENCES			
Important information on data processing	Consult this link for more information.			
Language	English			

Teaching staff	E-mail addresses	Credits taught by teacher	Office and hour of attention
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Learning objectives

Learning:

After the course, students should know about:

1. What Systems Biology is.
2. The paradigm shift underlying the current surge in Systems Biology.
3. The methods that are available for Systems Biology studies and how they work.
4. The different types of problems that can be solved with those methods.

Capacities:

After the course, students should be able to:

1. Critically analyze Systems Biology research.
2. Identify the best methods to solve a given problem.
3. Plan research using Systems Biology methods.

Competences

CB1 Knowledge and understanding that provide a basis or opportunity for originality in developing and / or applying ideas, often within a research context

CB2 Being able to apply the acquired knowledge and have the ability to solve problems in new or unfamiliar environments within broader (or multidisciplinary) contexts related to their field of study

CB3 Being able to integrate knowledge and handle complexity, and formulate judgments based on information that was incomplete or limited, include reflecting on social and ethical responsibilities linked to the application of their knowledge and judgments (*)

CB5 Acquiring learning skills to enable them to continue studying in a way that will be largely self-directed or autonomous

CG1 Knowing how to select and apply different analytical methods at the molecular, biochemical, cellular, genetic and phenotypic level for the diagnosis and study of the diseases.

CG5 Ability to prepare, process and interpret the results rigorously and applying appropriate technologies

CG6 Knowing to address research projects towards medical and translational interests (diagnosis and therapy)

CE4 Recognize high performance techniques (high throughput) and be able to use bioinformatics tools for data analysis.

CT2 Mastering a foreign language

CT3 Mastering ICT

Subject contents

SYSTEMS BIOLOGY: A PARADIGM

Evolving paradigms in Biology. Reductionism vs. holism vs. neo-reductionism. Modularity in living organisms.

What is needed to study the systems biology of an organism? Eukaryotes vs. prokaryotes.

GENOMICS:

DNA microarrays.

Next-generation sequencing technologies.

Variomic approach in Systems Biology.

A case study of exome sequencing and/or RNAseq analysis

PROTEOMICS:

Protein identification by mass spectrometry.

Gel-free approaches.

Quantitative proteomics.

METABOLOMICS:

Basic concepts on metabolomics.

Differential treatment of biological samples.

Metabolites databases.

SYSTEMS BIOLOGY:

Network representations.

Mathematical models of biological systems.

Development plan

1. SYSTEMS BIOLOGY: A PARADIGM

1.1 Evolving paradigms in Biology. Reductionism vs. holism vs. neo-reductionism. Modularity in living organisms. (1h Seminar)

1.2 What is needed to study the systems biology of an organism? Eukaryotes vs. prokaryotes. (1h Seminar)

2. GENOMICS:

2.1 DNA microarrays. Concepts in DNA microarray data analysis. (3h Seminar)

2.2 Next-generation sequencing (NGS) platforms. (3h Seminar)

2.3 Applications of microarray and NGS technologies. (2h Seminar)

2.4 Variomic approach in Systems Biology: a case study (4h Practice)

3. PROTEOMICS:

3.1 Protein identification by mass spectrometry. (2h Seminar)

3.2 Gel-free approaches. (2h Seminar)

3.3 Quantitative proteomics. (2h Seminar)

3.4 Analysis of a selected problem by proteomic approaches. (2h Practice)

4. METABOLOMICS:

4.1 Basic concepts on metabolomics: applications. (1h Seminar)

4.2 Equipments and software: chromatography, QTOF, TripleQ. (2h Seminar)

4.3 The HMDB, MADISON and MASSTRIX databases. (1h Seminar / 2 h Practice)

4.4 Analysis of a selected problem. (2h Practice)

5. SYSTEMS BIOLOGY:

5.1 Network representations. (1h Practice)

5.2 Mathematical models of biological systems. (1h Seminar / 1h Practice)

5.3 Analyzing mathematical models of biological systems. (1h Seminar / 2h Practice)

Evaluation

Five evaluation activities. Each corresponding to the different parts of the subject. Genomics (NGS/microarrays), genomics (variomics), proteomics, metabolomics, and systems biology. For each evaluation there will be a written test and/or oral presentation counting up to 16 % of the global grading plus 4 % for attendance and active participation in class.

Alternative assessment:

In the event that the student cannot carry out the continuous assessment due to any of the cases included in the UdL assessment regulations, he must notify the coordinator during the first week of classes.

In this case the student will be able to carry out a single assessment at the end of the subject, delivering the five activities simultaneously.

Bibliography

Textbooks

An Introduction to Systems Biology: Design Principles of Biological Circuits (2006) U. Alon. Chapman & Hall.

Biochemical Systems Analysis (1976) M. A. Savageau, Addison & Wesley.

DNA microarrays: a molecular cloning manual (2003). Ed. by D. Bowtell and J. Sambrook. CSHL Press.

Analysis of microarray gene expression data (2004). Ed. By M.T. Lee. Kluwer Academic Publishers.

Principles of Proteomics (2004) R. M. Twyman. Garland Science/BIOS Scientific Publishing.

Mass spectrometry data Analysis in Proteomics (2007). Edited by R. Mathiesen. Humana Press Inc.

Metabolomics: Methods and Protocols (2007). Edited by Weckwerth W. Humana Press Inc.

Metabolomics: The Frontier of Systems Biology (2003). Edited by Tomita M and Nishioka T. Springer-Verlag Tokyo.

Reviews

Integrative Computational Biology: Perspectives and Possibilities for *in silico* network reconstruction in Molecular Systems Biology.

Alves R, Vilaprinyo E, Sorribas A. Current Bioinformatics. 2008; 3: 98-129.

Next-generation DNA sequencing methods.

Mardis ER. Annu Rev Genomics Hum Genet. 2008;9:387-402.

Sequencing technologies - the next generation.

Metzker ML. Nat Rev Genet. 2010 Jan;11(1):31-46.

Fabrication of DNA microarray.

Dufva M. Methods Mol Biol. 2009;529:63-79.

Introduction to microarray technology.

Dufva M. Methods Mol Biol. 2009;529:1-22.

Getting started in gene expression microarray analysis.

Slonim DK, Yanai I. PLoS Comput Biol. 2009 Oct;5(10):e1000543.

Mass spectrometry and protein analysis.

Domon B, Aebersold R. Science. 2006 Apr 14;312(5771):212-7.

Is proteomics the new genomics?

Cox J, Mann M. Cell. 2007 Aug 10;130(3):395-8.

Introducción a la espectrometría de masas para la caracterización de péptidos y proteínas en proteómica.

Abian, Carrasca, Gay. Proteómica. 2008 Diciembre; 2.

Mass-spectrometry-based metabolomics: limitations and recommendations for future progress with particular focus

on nutrition research.

Scalbert A, et al. *Metabolomics*. 2009 Dec;5(4):435-458.

Exploring disease through metabolomics.

Vinayavekhin N, Homan EA, Saghatelian A. *ACS Chem Biol*. 2010 Jan 15;5(1):91-103.

Computational approaches to metabolomics.

Wishart DS. *Methods Mol Biol*. 2010;593:283-313.

Metabolomics, a novel tool for studies of nutrition, metabolism and lipid dysfunction.

Oresic M. *Nutr Metab Cardiovasc Dis*. 2009 Dec;19(11):816-24.

Metabolomics for assessment of nutritional status.

Zivkovic AM, German JB. *Curr Opin Clin Nutr Metab Care*. 2009 Sep;12(5):501-7.

Mass spectrometry: from proteomics to metabolomics and lipidomics.

Griffiths WJ, Wang Y. *Chem Soc Rev*. 2009 Jul;38(7):1882-96.

What is metabolomics all about?

Roessner U, Bowne J. *Biotechniques*. 2009 Apr;46(5):363-5.

Systems biology approaches and pathway tools for investigating cardiovascular disease.

Wheelock CE, et al. *Mol Biosyst*. 2009 Jun;5(6):588-602.

Database resources in metabolomics: an overview.

Go EP. *J Neuroimmune Pharmacol*. 2010 Mar;5(1):18-30.

Metabolomics: moving to the clinic.

Nordström A, Lewensohn R. *J Neuroimmune Pharmacol*. 2010 Mar;5(1):4-17.

Internet Resources

http://web.udl.es/usuaris/pg193845/Courses/Bioinformatics_2009/index.htm

<http://gepas.bioinfo.cipf.es/>

<http://www.ncbi.nlm.nih.gov/geo/>

<http://www.ebi.ac.uk/microarray-as/ae/>

http://variomics.net/index.php/Main_Page

<http://hapmap.ncbi.nlm.nih.gov/>

<http://variome.kobic.re.kr/FESD/>

<http://www.peptideatlas.org/>

<http://www.matrixscience.com/>

<http://www.uniprot.org/>

<http://www.hmdb.ca/>