

ETS Ingeniería Agronómica, Alimentaria y de Biosistemas	
Program	20BT– Degree in Biotechnology

Course number and name	
Number	20504323
Name	Biomics
Semester	S2 [(February - June)], 3 rd Year

Credits and contact hours	
ECTS Credits	4
Contact hours	48

Coordinator's name	Stephan Pollmann stephan.pollmann@upm.es
Professors' name	

Specific course information
<p>Description of course content</p> <p>The main objective is the student to acquire up-to-date knowledge of 'omics' technologies, focusing in transcriptomics, proteomics, and metabolomics. The syllabus includes the main aspects of the design and experimental development. Knowledge of how to analyze the massive data obtained is also imparted.</p> <p>Likewise, workshops are given on both the generation and analysis of functional networks as mapping networks.</p> <p>The student will acquire knowledge on the main techniques currently used in research in this field and will be in a position to critically evaluate the scientific literature on this theme.</p>
<p>List of topics to be covered</p> <p>1. Introduction</p> <p>1.1. Concept of genome, transcriptome, proteome and metabolome</p> <p>1.2. Structure and function of the main groups of biomolecules: nucleic acids, proteins, carbohydrates, lipids. Other biomolecules and secondary metabolites</p> <p>1.3. Technological advances in the global analysis of biomolecules. Meta-analysis and bioinformatics</p> <p>2. Transcriptomics</p> <p>2.1. Gene expression. Tools for the quantification of RNAs. Low and medium technologies coverage: Northern-blot, RT-qPCR, AFLP and SAGE.</p> <p>2.2. Microarrays</p> <p>2.3. RNAseq</p> <p>2.4. Experimental design. Standardization. Differentially expressed genes. Clustering analysis. Gene ontologies. Atlas of expression. Integration in metabolic fluxes.</p> <p>3. Proteomics</p>

<p>3.1. Definition of proteome and proteomics. Cell homogenization. Preparation of sample. Electrofocus. Two-dimensional (2D) electrophoresis of proteins. Visualization and analysis.</p> <p>3.2. MALDI-TOF MS. Intact protein extraction. Peptide mass footprint (PMF). LC-ESI MS/MS. Peptide Fragment Footprint (PFF). De novo sequencing.</p> <p>3.3. Differential isotope labeling (ICAT). Use of labels for relative and absolute quantification (iTRAQ). Absolute protein quantification (AQUA).</p> <p>3.4. Multidimensional protein identification technology. (MudPIT). NanoLC-ESI MS/MS.</p> <p>3.5. Protein microarrays. Two-hybrid system in yeast.</p> <p>4. Metabolomics</p> <p>4.1. Definition of metabolome and metabolomics. Total and selective extraction of metabolites.</p> <p>4.2. Chromatographic resolution. Isotopic distribution. Liquid Chromatography - Mass Spectrometry (LCMS). Derivatization. Fragmentation. Gas chromatography. Mass Spectrometry (GC MS). Head space GC-MS (HS/GC-MS).</p> <p>4.3. Quantitative (targeted) metabolomics. Chemometric profiles (untargeted)</p> <p>4.4. Principal component analysis (PCA). Partial Least Squares (PLS) by using projections of latent structures.</p> <p>5. Systems Biology</p> <p>5.1. Networks and interactions of macromolecules. Interaction between levels of organization. Bioinformatics tools in network analysis.</p>	
Prerequisites or co-requisites	
- Bioinformatics	
Course category in the program	
Mandatory	

Specific for course objectives
<p>Specific learning outcomes</p> <p>RA85 - Know the products of transcription (transcriptome), their regulation and expression (proteome), as well as the interaction of these products with each other (interactome) and their effect on cellular metabolic fluxes</p> <p>RA83 - Know the methodological bases of transcriptomic, proteomic and metabolomics for the understanding, management and production of this type of information.</p> <p>RA84 - Know the databases related to the global analysis of organisms</p> <p>RA87 - Interpret the results from the analysis of transcriptomic, proteomic and metabolomics, and know the possibilities of this discipline in science and biotechnology</p> <p>RA86 - Know the structure and function of the main types of biomolecules and their relevance in biotechnology</p>

Further reading and supplementary materials
<p>Bioanalytics for Beginners Reinhard Renneberg. Springer-Verlag New York Inc, 2012. ISBN: 978-1-4614-0922-9</p> <p>http://www.genome.gov/10000464</p> <p>http://www.swissproteomicsociety.org/links.html</p> <p>http://www.bmrp.wisc.edu/metabolomics/external_metab_links.html</p> <p>www.metazome.net</p>



www.phytozome.net
www.genevestigator.com
<http://bar.utoronto.ca>
<https://xcmsonline.scripps.edu>

Teaching methodology			
-- lectures	-- problem solving sessions	-- collaborative actions	-- laboratory sessions
Other:			

Evaluation Criteria
<p>Progressive Evaluation :</p> <p>A) Individual work. 15% of the final mark of the course The delivery of solved problems and the resolution of evaluation tests, being essential for accounting the delivery/completion of at least 50% of them.</p> <p>B) Practices of bioinformatic tools: 15% of the final mark of the course. Participation and delivery to the date/time communicated in the course regulations is mandatory.</p> <p>C) Two partial exams: 70% (35% + 35%) of the final grade for the course. It is mandatory to pass the partial exams (5/10). Students who do not pass the first part or who have not performed it, goes automatically to the final exam in the ordinary call.</p> <p>For the extraordinary evaluation, final exam accounts for 100% of the final grade. This final exam will include theoretical and practical aspects.</p>