

Syllabus of BI 7623

- **Course Objectives**

The aim of the course is to provide practical bioinformatical skills in genomics, transcriptomics, proteomics and metabolomics, knowledge of the major web-resources and understanding of how these methods are applied in real-life scientific research. The introductory material about each of the -omics fields is provided. The explanation of how the methods are applied in research, what practical advantages and limitations they have and what challenges they allow to address is provided through review and research articles. Practical skills are provided through the use of open-access databases and data analysis software tools.

After this course students should recognize the scientific problems in the post-genomic biology, know where to access the large volumes of -omics data, understand how to perform simple analyses of these data, and know examples of how these research tools were applied in published investigations.

Course Description

Week 1. Introduction to -omes and -omics. Course overview.

Weeks 2, 3, 4. Gene, Genome and Genomics. Online genomics databases and tools.

Standalone bioinformatics analysis of genomic data. Applications of genomics.

Genome sequencing projects (technology of sequencing and assembly, bioinformatics of genome annotation, current status of genome sequencing projects)

Genomic browsers and databases

Orthology prediction (comparative genomics)

Search for transcription factor binding sites (TFBS)

Computational prediction of miRNA target genes

De novo prediction of regulatory motifs in genome

Single nucleotide polymorphisms (SNP) in medical genetics and basic research

Weeks 5, 6, 7. Transcriptomics. Microarrays, EST, SAGE. Bioinformatical methods in transcriptomics. Application of transcriptomics.

Experimental techniques: microarrays, EST, SAGE.

Microarray data: normalization and analysis.

Genevestigator and OncoMine - browsing microarray-derived gene expression profiles, tissue and stage-of-development-specific patterns of expression, coexpression of genes, pre-computed lists of differentially expressed genes.

Standalone analysis of publicly available microarray expression data: GEO database, TM4 analysis suite.

Assembly of EST: CAP3 program

Examples of basic research in transcriptomics

Weeks 8, 9. Proteomics. Aims, strategies and methods. Bioinformatics tools in proteomics.

Application of proteomics.

Aims, strategies and challenges in proteomics. Proteomics technologies: 2D-electrophoresis, MALDI-TOF mass spectrometry, yeast 2-hybrid system.

Protein-protein interactions: experimental and computational methods, databases.

Weeks 10, 11, 12. Metabolomics. Technologies in metabolomics. Nutrigenomics. Other omics.

Nuclear Magnetic Resonance Spectroscopy and Mass Spectrometry in metabolomics.

Metabolic pathways resources: KEGG, Biocarta. Nutrigenomics and metabolic health.

Solved problems and future challenges.

Week 13. Final project

Grading Policy

In the course there are the two major sources of grades:

1. the weekly tasks (maximum of 6 points per week, maximum of 72 points for the 12 weeks);
2. the individual final project and the group discussion of the complete projects (maximum of 28 points).

The weekly tasks may include questions to articles and practical assignments. The proportions of these types of tasks may differ from week to week, however the total maximum number of points is constant: 6 points. '6' - 'excellent', '5' - 'good', '4' - 'satisfactory', '3-0' - 'unsatisfactory'. For a creative approach to the tasks one bonus point can be granted.

Answers received later than 2 weeks after the beginning of the week are graded based on the maximum of '4.0' points (e.g., the task for week 1 should be submitted before week 3 begins).

Individual projects are offered to the students several weeks before the end of the course. The students should submit their complete projects, discuss and evaluate them in a group.

Good performance in the regular tasks is required but not sufficient to obtain the 'A' grade.

Both the regular work and fulfillment of the project are necessary.

Textbook(s)

The course is mainly based on lecture texts and scientific articles. Additionally, it uses selected sections of the open-access textbooks: Genomes 2, Sequence-Evolution-Function, Human Molecular Genetics 2 (NCBI Bookshelf).

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