Study programme(s): Applied Mathematics – Data Science

Level: Master studies

Course title: Big Data in Medicine and Biology

Lecturer: Dušan Jakovetić, Mirjana Ivanović

Status: elective

ECTS: 5

Requirements: Pattern analysis and machine learning, Introduction to digital signal processing

Learning objectives

- Understanding basic principles and use of computer vision in medicine, image registration, shape and appearance modelling
- Understanding decision support analysis, pattern recognition and predictive model construction and evaluation in the context of medical applications.
- Understanding basic computational methods for analysis and interpretation of Big Data in bioinformatics

Learning outcomes

Experience in analysis and processing of medical images using advanced algorithms such as image registration, active shape and appearance modelling.
Experience in using decision support, knowledge-based and learning systems in computer-based diagnosis, planning and monitoring of therapeutic interventions.
Experience in using algorithms for sequence analysis and alignment, microarray data analysis, biological networks.

Syllabus

Introduction to medical imaging: basic notions, modalities, resolution, interpolation, optimization
Shape and appearance modelling - shape determinants, registration, texture and appearance, statistical modelling of shape and texture variations, dimensionality reduction, classification of image populations, active shape and appearance models: for object parametrization in images
Image registration - establishing structural and geometric correspondence between medical images, normalization and objective measures, transformations and deformations
Introduction to biomedical signals (1D, multichannel), application of basic time and/or frequency analysis procedures, and feature representation and parametrization. Signal analysis and pattern recognition algorithms for efficient noninvasive diagnostics, on-line monitoring and rehabilitation. Basics of computational neuroscience and big data perspectives.
Introduction to genomic data (sequences, gene expression, protein-protein interactions), finding information in biological databases (GenBank, Swiss-Prot, MIPS, GEO, ArrayExpress).
Integration of heterogeneous data. Methods for inferring information from genomic data in gene function prediction, linking genes and diseases, phylogenetic analysis, drug-protein interactions, metagenomics analysis.

Literature

1. Rangaraj M. Rangayyan Biomedical Signal Analysis a Case-Study Approach IEEE Press, Willey Interscience 2002
2. Jure Leskovac, Anand Rajaraman, Jeffrey D. Ullman, Mining of Massive Datasets, Cambridge University Press,2010
3. Vivien Marx, Biology: The big challenges of big data, 2013.
4. Phillip Compeau, Pavel Pevzner, Bioinformatics Algorithms: An Active Learning Approach, Active Learning Publishers, 2014.

Weekly teaching load	Other: 0

Lectures: 2	Exercises: 2	Other forms of teaching: 0	Student research: 0	
Teaching methodology Lectures; revisions of the material; active students' participation in problem solving; lab reports, application of the taught material on real-world examples from one of the three major topics within the course project				
Grading (maximum number of points 100)				
Pre-exam obligations	**Points**	**Final exam**	**points**	
Lab reports	10	Final project	90	