

## **Bioinformatics – lecture (30 h , ECTS 2, written exam)**

The lecture will address various databases and algorithms used in bioinformatics, genetics, genomics, molecular biology and biotechnology, and the linkage between types of data. Basic operations on a single and multiple sequences or three-dimensional biomolecular structures will be discussed along with methods allowing pair comparison and searching databases with nucleotide, amino acid sequences and protein structures. During the lecture we will assess the concept of protein families, sequence motifs related to function, cell compartments segregation of signals, comparison of genomes for different organisms, population genetics and system level modeling of a single cell. Advanced methods for finding sequence-level and structural similarity and assessing both sequence and structural variability between proteins, genes and whole genomes will also be presented. The lecture will further describe methods for genome sequencing, distinguishing between coding and noncoding DNA sequences (ab initio methods and homology based methods), genome annotations, and comparative and functional genomics at the genomic level. Finally the lecture will address theories of protein and genome folding, tools exercised by molecular graphics, modeling of protein structures and genomic domains, structure of biopolymers, protein-protein interaction networks, types of biological networks, functional motifs in proteins and genomes, and the analysis of various omics data taken from -omics experiments data, with basic concepts in systems biology.