Program	Level		Second cycle		
	Name of the program		Theoretical Computer Science		

COURSE

Course title	**Genetic Algorithms and Bioinformatics**				
Course code	Semester	Course status		ECTS	Contact hours (L+AE+LE)
CS 545	III	Elective course		7	3+0+2
Lecturer					
Course Goals	The aim of the course is to improve the understanding of living systems through computer algorithms. The complexity of these systems presents a challenge in software and algorithms development and often requires completely new approaches in Computer Science. Through this course, students will be able to use WEB-biological databases, use of dedicated software packages and formats for search, analysis, modelling and simulation in the field of proteomics and genomics.				
Learning Outcomes	Students will be able to use WEB-biological databases, and use dedicated software packages and formats for searching, analysis, modelling and simulation in the field of proteomics and genomics.				

COURSE CONTENT

- Introductory consideration. Bioinformatics: Definition, tasks and goal of bioinformatics.
- Introduction to the basics of molecular biology: basic cell architecture, DNA structure, genes and proteins, genome, proteome, transcriptome, central dogma. Crick-Watson model.
- Classic methods and algorithms in bioinformatics: a probabilistic approach, Bayes theorem, HMM model, nearest neighbour method, clustering method, identification tree method.
- Bio-inspired methods and algorithms in bioinformatics: neural networks, evolutionary algorithms, genetic algorithms, multi-objective genetic algorithms.
- DNA sequence analysis: sequence matching, multiple sequence matching, matching visualization sequences, biological codes, manipulating sequences, statistics from sequences.
- DNA microarray analysis: microarray normalization, microarray visualization.
- Analysis and prediction of protein structures: deterministic patterns, stochastic patterns, secondary prediction structures based on neural networks, visualization of protein structures.
- Software resources: databases, data mining, computer associations with biological processes.
- Software tools: Perl, Blasta, FASTA, PDBFIND databases, MATLAB Bioinformatic Toolbox.

LITERATURE

[1] Pierre Baldi, Soren Brunak: Bioinformatics - The Machine Learning Approach, 2nd edition, (2001), MIT Press.
[2] Bryan Bergeron: Bioinformatics Computing, (2002), Prentice Hall PTR.
[3] Andrzej Polanski, Marek Kimmel: Bioinformatics, (2007), Springer-Verlag Berlin.
[4] Michael S. Waterman: Introduction to Computational Biology: Maps, Sequences and Genomes, 1st edition, (1995), Chapman&Hall/CRC.
[5] Cynthia Gibas, Per Jambeck: Developing Bioinformatics Computer Skills, (2001), O'Reilly.

STUDENT WORKLOAD (hours in a semester)

Lectures	45	Exercises	30	Individual work	100	T o t a l	175

GRADING			REMARKS	
Criterion	Maximum points	Minimum points		
Midterm exams	20	10		
Homework	10	5		
Student projects	40	20		
Seminar paper	10	5		
Final Exam	20	15		
Total	100	55		