1.	Course	*Bioinformatics*
2.	Code	KNI_E3
3.	Study programme	Computer Science and Engineering PhD study programme
4.	Study programme organized by	FCSE
5.	Cycle	Third - PhD
6.	Academic year / semester winter/summer/elective	7. ECTS credits 7,5
8.	Teacher	Prof. d-r Slobodan Kalajdziski
9.	Prerequisites	none
10.	Course programme goals (competences): Enabling the students to use advanced design techniques together with bioinformatics algorithms. Gained knowledge on design and development of algorithms for solving various bioinformatics problems.	
11.	Course syllabus: In this course the computational techniques and algorithms used in computer technologies that can be applied in biology and medicine will be studied. The course structure is build upon: basic and advanced algorithms (greedy algorithms, dynamic programming, divide and conquer algorithms, graph algorithms, combined pattern recognition, clustering and trees, hidden Markov models, probability algorithms, global/local adjustment of sequence pairs, multiple sequence adjustment, replacement matrices, etc.) Application of these techniques and algorithms in database searches with sequences, structural PDB files, protein interaction, active parts and motifs. Structural-classification schemes (CATH, SCOP, Gene Ontology), foreseeing and adjustment by structure, determining the protein function. Proteomics and analysis of protein sequences. Experimental and computational methods for determining the protein interaction. Topological and modular analysis of protein interaction networks. GeneOntology – standard ontology used for describing processes in bioinformatics.	
12.	Teaching methods: Classes supported with slide presentations, interactive teaching, lab equipment and other software packages, teamwork, case studies, invited guest lecturers, presentations of project works, e-learning materials, forums and consultations.	
13.	Total fund of work hours	7,5 EKTC x 30 h = 225 h
14.	Available hours distribution	45+30+150 = 225

15.	Teaching activities	15.1.	Theoretical classes	45 h
		15.2.	Practical classes (labs, exercises), seminars, team work	30 h
16.	Other activities	16.1.	Project tasks	50 h
		16.2.	Self study	50 h
		16.3.	Homework	50 h

17.	Grading		
	17.1.	Tests	40 points
	17.2.	Seminar work/ project (presentation: written and oral)	50 points

	17.3.	Active participation	10 points
18.	Grading criteria (points/grade)	to 59 points	5 (five) (F)
		from 60 to 68 points	6 (six) (E)
		from 69 to 76 points	7 (seven) (D)
		from 77 to 84 points	8 (eight) (C)
		from 85 to 92 points	9 (nine) (B)
		from 93 to 100 points	10 (ten) (A)
19.	Conditions for attending the final exam	Successful completion of activities 15.1 and 15.2	
20.	Language	Macedonian or English	
21.	Quality assessment	Internal evaluation and student pools	

22.	Literature					
	22.1.	Compulsory				
		No.	Author	Title	Publisher	Year
		1.	Ingvar Eidhammer, Inge Jonassen, William R. Taylor	Protein Bioinformatics: An Algorithmic Approach to Sequence and Structure Analysis,1 edition	Wiley	2004
		2.	David W. Mount	Bioinformatics: Sequence and Genome Analysis,2 edition	Cold Spring Harbor, Laboratory Press	2004
		3.	N.C.Jones, P.A.Pevzner	An introduction to bioinformatics algorithms	MIT Press	2004
	22.2.	Additional				
		No.	Author	Title	Publisher	Year
		1.	Philip E. Bourne, Helge Weissig	Structural Bioinformatics, 1 edition	Wiley-Liss	2003
		2.	Arthur M. Lesk	Introduction to Protein Architecture: The Structural Biology of Proteins, 1st edition	Oxford University Press	2001
		3.	Aidong Zhang	Protein Interaction Networks: Computational Analysis	Cambridge University Press	2009