

Study programmes: Master studies - Informatics				
Course name: R309 - Introduction to bioinformatics				
Lecturers: Gordana Pavlović-Lažetić and other lecturers of the Department of Computer science and informatics				
Status: Optional				
ECTS: 8				
Attendance prerequisites: No prerequisites				
Course aims: Acquiring knowledge about types and sources of data available to computational biology, and about mathematical methods and algorithms used for solving substantial informatical problems in molecular biology.				
Course outcome: After the course, a student is capable of further studying and individual scientific work in bioinformatics.				
Course content:				
<ul style="list-style-type: none"> - Basic concepts of molecular biology; - String comparison algorithms. - Phylogenetics trees. - Genome sequencing and assembly. - Mathematical apparatus as basis for string analysis. - Data mining in bioinformatics. 				
Literature:				
1. Biological sequence analysis: Probabilistic models of proteins and nucleic acids, R. Durbin, S. Eddy, A. Krogh, G. Mitchison, Cambridge University Press, 1998				
2. Algorithms on Strings, Trees, and Sequences, Computer Science and Computational Biology, Dan Gusfield, Cambridge University Press, 1997				
3. Algorithmic Aspects of Bioinformatics, Hans-Joachim Böckenhauer, Dirk Bongartz, Springer, 2007 (lecturer may opt for other suitable current literature)				
Number of hours: 7	Lectures: 2	Tutorials: 3	Laboratory: -	Research: 2
Teaching and learning methods: Frontal, group, individual and practical.				
Assessment (maximal 100 points)				
Course assignments	points	Final exam		points
Lectures	-	Written exam		-
Exercises / Tutorials	-	Oral exam		%ispit_us meni%
Colloquia	40	Written-oral exam		40
Essay / Project	20			