

Course Description					
Name	Code	Semester	T+A Hour	Credit	ECTS
BIOINFORMATICS	EEE4110345	Fall Semester	3+0	3	6
<b>Prerequisites Courses</b>	OLASILIK VE RASSAL DEĞİŞKENLER				
<b>Recommended Elective Courses</b>	Consent of Department				
<b>Language of Instruction</b>	English				
<b>Course Level</b>	First Cycle (Bachelor's Degree)				
<b>Course Type</b>	Elective				
<b>Course Coordinator</b>	Prof.Dr. Reda ALHAJJ				
<b>Name of Lecturer(s)</b>	Prof.Dr. Reda ALHAJJ				
<b>Assistant(s)</b>					
<b>Aim</b>	The course provides an introduction to the field of bioinformatics including key concepts, algorithms, structures and databases, the development of the field historically, its applications and relevant developments in the field. The course covers the basics of bioinformatics sequence analysis and related tools and databases. Topics covered include pairwise alignment, score matrices, sequence database search, biological networks, network analysis and machine learning techniques, and visualization. The course also an overview of basics of molecular biology, including the concepts of genomes and genes and includes an introduction to genome browsers and central biological databases and knowledge-bases. □□□□				
<b>Course Content</b>	This course contains; Introduction to the course material, what is bioinformatics, and why to study bioinformatics, Building the background: Basic concepts in bioinformatics, suffix trees and arrays, Sequence Alignment basics, pairwise sequence alignment, multiple sequence alignment, Databases and database search, Microarray data analysis, Presentations by students lecture/ articles / tools , Presentations by students lecture/ articles / tools , Phylogenetic Trees, Machine learning, Network model and graph analysis, Biological networks, visualization and analysis, Project Presentations.				
<b>Course Learning Outcomes</b>			<b>Teaching Methods</b>	<b>Assessment Methods</b>	
Has a general understanding of central topics and concepts within the field of bioinformatics				A, E, F, G	
Understands dynamic programming algorithms for alignment of biological sequences □□□□				A, E, F, G	
Understands and be able to explain basics of molecular biology and evolution pertaining to sequence alignment and connect them with the various algorithms				A, E, F, G	
Is able to compare technical aspects of pairwise local and global sequence alignment algorithm				A, E, F, G	
Is able to use biological databases and knowledgebases, machine learning and network analysis				A, E, F, G	
Understanding of basic approaches to biological networks and visualize			5	A, F, G	
<b>Teaching Methods</b>	5: Cooperative Learning				
<b>Assessment Methods</b>	A: Traditional Written Exam, E: Homework, F: Project Task, G: Quiz				
<b>Lecture Schedule</b>					
Sequence	Topics	Preliminary Preparation			
1	Introduction to the course material, what is bioinformatics, and why to study bioinformatics				
2	Building the background: Basic concepts in bioinformatics				
3	suffix trees and arrays				
4	Sequence Alignment basics				
5	pairwise sequence alignment				
6	multiple sequence alignment				
7	Databases and database search				
8	Microarray data analysis				
9	Presentations by students lecture/ articles / tools				
10	Presentations by students lecture/ articles / tools				
11	Phylogenetic Trees				
12	Machine learning, Network model and graph analysis				
13	Biological networks, visualization and analysis				
14	Project Presentations				
<b>Evaluation Methods</b>		<b>Weight(%)</b>			
Midterm Exam		30			
General Exam		70			

**Resources**

"No specific text book, notes will be made available, including in class notes, (sometimes) slides, research papers, book chapters, etc.  
Recommended Reference: Understanding Bioinformatics Marketa Zvelebil & Jeremy O. Baum"

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