

## MSc program, Biomedical Engineering Department

<b>Course Unit Title</b>	Advance Bioinformatics
<b>Course Unit Code</b>	BME503
<b>Type of Course Unit</b>	Elective
<b>Level of Course Unit</b>	
<b>National Credits</b>	3
<b>Number of ECTS Credits Allocated</b>	10
<b>Theoretical (hour/week)</b>	4
<b>Practice (hour/week)</b>	-
<b>Laboratory (hour/week)</b>	-
<b>Year of Study</b>	-
<b>Semester when the course unit is delivered</b>	-
<b>Course Coordinator</b>	Assist. Prof. Dr. Mahmut Çerkez
<b>Name of Lecturer (s)</b>	Assist. Prof. Dr. Mahmut Çerkez
<b>Name of Assistant (s)</b>	-
<b>Mode of Delivery</b>	Face to Face.
<b>Language of Instruction</b>	English
<b>Prerequisites</b>	-
<b>Recommended Optional Programme Components</b>	
<b>Course description:</b>	
<p>This course is graduate level bioinformatics course, which emphasizes as a basis for understanding bioinformatics and their applications. The course focuses on a general introduction to the uses of biological databases in the generating biological knowledge to better understand living systems, for purposes of aiding healing of diseases. Topics include Genomic Era, the anatomy of genome, probabilistic models of genome sequences, biological databases, sequence alignment, gene and promoter prediction, molecular phylogenetics, post-genomic epidemic, structural bioinformatics and proteomics. This course covers the fundamental concepts molecular biology, database management systems, and probabilistic models.</p>	
<b>Objectives of the Course:</b>	
<ul style="list-style-type: none"> <li>• Students will exhibit depth and breadth of knowledge by demonstrating a well-developed understanding of biological sciences.</li> <li>• Student will be able to critically analyse and solve problems in biotechnology by gathering, synthesizing and critically evaluating information from a range of sources.</li> </ul>	
<b>Learning Outcomes</b>	
<p>At the end of the course the student should be able to:</p> <ul style="list-style-type: none"> <li>• Understand the theoretical basis behind bioinformatics</li> <li>• Search databases accessible on the internet for literature relating to molecular biology and biotechnology.</li> <li>• Manipulate DNA and protein sequences using stand-alone PC programs and programs available on the internet.</li> <li>• Find homologues, analyse sequences, construct and interpret evolutionary trees.</li> <li>• Analyse protein sequences, identify proteins, and retrieve protein structures from</li> </ul>	

databases. View and interpret these structures.			
<ul style="list-style-type: none"> <li>Query biological data, interpret and model biological information and apply this to the solution of biological problems in any arena involving molecular data.</li> </ul>			
		Assessment	
1	Describe biological databases and how they are used.	1,2	
2	How to choose an appropriate biological database for a given problem.	1, 2	
3	Define bioinformatics of Genome Wide analysis.	1, 2	
4	How to design and used database systems for data mining.	1, 2	
5	Decide which probabilistic method is the best for sequence alignment.	1, 2	
6	Apply the bioinformatics principles discussed in the design of genome comparison and pattern recognition problems.	1, 2	
7	Critically review bioinformatics research studies and new technologies.	1, 2	
Assessment Methods: 1. Written Exam, 2. Project/Report			
<b>Course's Contribution to Program</b>			
		CL	
1	Apply the rules of scientific research and ethics	5	
2	Discuss complex biomedical engineering issues as well as own research results comprehensively and in the context of current international research and present these in writing and orally	5	
3	Solve problems by systems analytical thinking both in subject specific and interdisciplinary concepts	5	
4	Combine specialized knowledge of various component disciplines	5	
5	Carry out independent scientific work and organize (capacity of teamwork), Conduct and lead more complex projects	5	
6	To assess the social and environment-related effects of their actions	4	
CL: Contribution Level (1: Very Low, 2: Low, 3: Moderate, 4: High, 5: Very High)			
<b>Course Contents</b>			
Week	Chapter	Topics	Assessment
1		General Discussions and Introduction	

2		Genomic Era	1 <sup>st</sup> Homework is Assigned
3		The anatomy of genome	
4		Probabilistic models of genome sequences	Projects start.
5		Introduction to Biological Databases	Assignment I (Due)
6		Sequence Alignment (All in the family)	
7		Multiple Sequence Alignment	
8		Midterm	Midterm Exam, Assignment II
9		Gene and Promoter Prediction	
10		Molecular Phylogenetics	
11		SARS-a post-genomic epidemic	
12		Structural Bioinformatics	Assignment II (Due)
13		Whole genome comparison	
14		Genomics and Proteomics	
15		Project Presentations	Project submission
16		Finals	

### Recommended Sources

#### Textbook:

1. Jin Xiong, Essential Bioinformatics, Cambridge University Press, 2006 ISBN-13: 978-0-521-60082-8. Nello Cristianini, Matthew W. Hahn, Introduction to Computational Genomics, A Case studies Approach, Cambridge University Press, 2006, ISBN-0-521-67191-4.

### Assessment

Project	30%	
Midterm Exam	30%	Written Exam
Final Exam	40%	Written Exam
Total	100%	

**Assessment Criteria**

Final grades are determined according to the Near East University Academic Regulations for Undergraduate Studies

**Course Policies**

1. Attendance to the course is mandatory.
2. Late assignments will not be accepted unless an agreement is reached with the lecturer.
3. Students may use calculators during the exam.
4. Cheating and plagiarism will not be tolerated. Cheating will be penalized according to the Near East University General Student Discipline Regulations

**ECTS allocated based on Student Workload**

Activities	Number	Duration (hour)	Total Workload(hour)
Course duration in class (including Exam weeks)	16	4 h	64
Labs and Tutorials	10	10	100
Assignment	4	3	12
Project/Presentation/Report	3	10	30
E-learning activities	-	-	-
Quizzes	-	-	-
Midterm Examination	1	5	5
Final Examination	1	3	3
Self Study	-	100	100
Total Workload			312
Total Workload/30(h)			10.1
ECTS Credit of the Course			10