Course Unit Title	Bioinformatics
Course Unit Code	BME435
Type of Course Unit	Compulsory
Level of Course Unit	Bachelor of Science, 4th Year
National Credits	3
Number of ECTS Credits Allocated	5
Theoretical (hour/week)	3
Practice (hour/week)	-
Laboratory (hour/week)	2
Year of Study	4
Semester when the course unit is delivered	5
Course Coordinator	Dr. Mahmut Çerkez
Name of Lecturer (s)	Fatih Veysel Nurçin
Name of Assistant (s)	-
Mode of Delivery	Face to Face, lab works
Language of Instruction	English
Prerequisites	
Recommended Optional Program Components	

Course description:

This course is a 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 generating biological knowledge to better understand living systems, for the 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.

Objectives of the Course:

- Learn basic aspects of bioinformatics.
- Develop an understanding of the engineering approach toward understanding biological databases and analysis.

Learning Outcomes,

At the end of the course the student should be able to

- Describe biological databases and how they are used.
- How to choose an appropriate biological database for a given problem.
- Define bioinformatics of a Genome Wide analysis.
- How to design and use database systems for data mining.
- Decide which probabilistic method is the best for sequence alignment.
- Apply the bioinformatics principles discussed in the design of genome comparison and pattern recognition problems.

Critically review bioinformatics research studies and new technologies.

		Assessment
1	Describe biological databases and how they are used. .	1
2	How to choose an appropriate biological database for a given problem.	1, 2

3	How to design and use database systems for data mining.	1, 2
4	How to analyze functional data	1, 2
5	Define bioinformatics of a Genome Wide analysis.	1, 2
6	Decide which probabilistic method is the best for sequence alignment.	1, 2
7	Apply the bioinformatics principles discussed in the design of genome comparison and pattern recognition problems. Critically review bioinformatics research studies and new technologies	1, 2

Assessment Methods: 1. Written Exam, 2. Assignment, 3. Project/Report, 4. Presentation, 5. Lab. Work

Course's Contribution to Program

		CL
1	Apply knowledge of mathematics, natural science with relevant to life science and multidisciplinary context of engineering science.	4
2	Analyze, design and conduct experiments, as well as to analyze and interpret data.	4
3	Design a system, component or process to meet desired needs within realistic constraints such as economic, environmental, social, political, ethical, health and safety, manufacturability and sustainability.	4
4	Function on multidisciplinary teams.	4
5	Control in design work, by using simulation, modelling and tests and integration in a problem solving oriented way.	4
6	Display an understanding of professional and ethical responsibility.	4
7	Communicate effectively aware of the non-technical effects of engineering.	2
8	Search technical literature and other information sources.	3
9	Recognize of the need for, and an ability to engage in life-long learning.	4
10	Exhibit a knowledge of contemporary issues.	3
11	Use the techniques, skills and modern engineering tools necessary for engineering practice to develop marketable products for the global market.	4

CL: Contribution Level (1: Very Low, 2: Low, 3: Moderate, 4: High, 5: Very High)

Course Contents

Week	Chapter	Topics	Exam
1		General Discussions and Introduction	
2		Genomic Era	
3		The anatomy of genome	
4		Probabilistic models of genome sequences	
5		Introduction to Biological Databases	
6		Sequence Alignment (All in the family)	
7		Multiple Sequence Alignment	
8		MIDTERM	Midterm
9		Gene and Promoter Prediction	
10		Molecular Phylogenetics	

11		SARS-a post-genomic epidemic	
12		Structural Bioinformatics	
13		Whole genome comparison	
14		Genomics and Proteomics	
15		Project Presentations	Final

Recommended Sources

Textbook:

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

Attendance	10%	Less than 25% class attendance results in NA grade
Quiz	20%	Written Quiz
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

- Attendance to the course is mandatory.
- Late assignments will not be accepted unless an agreement is reached with the lecturer.
- Students may use calculators during the exam.
- 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)	15	4	60
Labs and Tutorials			
Assignment	5	4	20
Project/Presentation/Report	-	-	-
E-learning activities	-	-	-
Quizzes	2	2	4
Midterm Examination	1	15	15
Final Examination	1	15	15
Self Study	14	3	42
Total Workload			156
Total Workload/30(h)			5.3
ECTS Credit of the Course			5