



Course Specification

(Bachelor)

Course Title: **Bioinformatics**

Course Code: **BIOL_455**

Program: **Bachelor of Science**

Department: **Biology**

College: **College of Science**

Institution: **Majmaah University**

Version: **4th**

Last Revision Date: **26 December 2023**



Table of Contents

| | |
|---|---|
| A. General information about the course: | 3 |
| B. Course Learning Outcomes (CLOs), Teaching Strategies and Assessment Methods | 4 |
| C. Course Content | 6 |
| D. Students Assessment Activities | 7 |
| E. Learning Resources and Facilities | 7 |
| F. Assessment of Course Quality | 8 |
| G. Specification Approval | 9 |



A. General information about the course:

1. Course Identification

1. Credit hours: 3 (2+1)

Equivalent to ECTS Credit point: 4.5

2. Course type

A. University College Department Track Others

B. Required Elective

3. Level/year at which this course is offered: (Level 8)

4. Course General Description:

This course focuses on bioinformatics, covering biological databases and computational tools for genome, sequence, and structure analysis. Students will learn to use software packages and access public biological databases, enhancing their interdisciplinary understanding.

5. Pre-requirements for this course (if any):

Molecular Biology (BIOL_352)

6. Co-requisites for this course (if any): None

7. Course Main Objective(s):

The course objective is to train the students with advanced skills in bioinformatics. They'll learn to use various DNA and protein sequence databases, conduct effective database searches, analyze DNA sequences, design PCR primers, predict structure, compare sequences, and explore gene expression patterns.

2. Teaching mode (mark all that apply)

| No | Mode of Instruction | Contact Hours | Percentage |
|----|--|---------------|------------|
| 1 | Traditional classroom | 60 | 80 |
| 2 | E-learning | 15 | 20 |
| 3 | Hybrid <ul style="list-style-type: none"> • Traditional classroom • E-learning | | |
| 4 | Distance learning | | |



3. Contact Hours (based on the academic semester)

| No | Activity | Contact Hours |
|--------------|-------------------|---------------|
| 1. | Lectures | 30 |
| 2. | Laboratory/Studio | 30 |
| 3. | Field | |
| 4. | Tutorial | |
| 5. | Others (specify) | |
| Total | | 60 |

Workload (based on academic semester)

| No | Activity | Contact Hours |
|---|--|---------------|
| 1. | Contact hours | 60 |
| 2. | Self –study hours or Academic learning hours (Assignments, quizzes, reports, discussions, library , research....) | 60 |
| Total Workload | | 120 |
| Equivalent to ECTS Credit Pionts | | 4.5 |

B. Course Learning Outcomes (CLOs), Teaching Strategies and Assessment Methods

| Code | Course Learning Outcomes | Code of PLOs aligned with the program | Teaching Strategies | Assessment Methods |
|------------|--|---------------------------------------|--|---|
| 1.0 | Knowledge and understanding | | | |
| 1.1 | Acquire fundamental understanding of the content and characteristics of vital bioinformatics databases. Conduct searches based on text and sequences, and analyze and interpret the outcomes within the context of bioinformatics expertise. | K3 | Lecture, Videos, Group discussion | Midterm 1 Midterm 2 Final exam Quizzes. Class exercises E exam |
| 1.2 | Explore the database analyses at the DNA, RNA and protein level | K3 | Lectures , online course on future X (the national elearning platform) | Quizzes. Class exercises E exam |
| 1.3 | To understand the methods for predicting the | K3 | Lecture, Videos, Group discussion | Midterm 1 Midterm 2 |





| Code | Course Learning Outcomes | Code of PLOs aligned with the program | Teaching Strategies | Assessment Methods |
|------------|---|---------------------------------------|--|--|
| | three-dimensional structures of protein sequences. | | | Final exam |
| 1.4 | Acquire foundational knowledge to perform DNA alignment, comparison, and phylogenetic analysis. | K3 | Lectures , online course on future X (the national elearning platform) | Quizzes' Midterm and final exams |
| 2.0 | Skills | | | |
| 2.1 | Explain the ability to search for genes and organisms in the Gene Bank Database and proficiently design primers utilizing various bioinformatics software tools. | S3 | Lectures, Videos, Group discussion, Brain storming, Critical thinking | Midterm 1 Midterm 2 Final exam |
| 2.2 | Explore to know how to construct phylogenetic trees based on biological sequence data. | S3 | Lectures, Videos, Group discussion, Brain storming, Critical thinking | Short answer, Fill in the blanks, Diagram |
| 2.3 | Explain how to use biological knowledge to construct algorithms (DNA & protein sequence databases, Sequence similarity, alignment, & assembly, Sequence patterns/motifs, Phylogenetic, Protein structure prediction, Mapping metabolic and regulatory pathways. | S3 | Lectures, Videos, Group discussion, Brain storming, Critical thinking | Short answer, Matching, Diagram |
| 2.4 | Carry out the experiments how to use computers to construct algorithms, Phylogenetic, Protein structure prediction. | S4 | Lab experiment, videos, diagrams Labs reports | Practical exams, Lab reports, Group research |
| 3.0 | Values, autonomy, and responsibility | | | |
| 3.1 | Exhibit responsibilities to accomplish individual activities and effectively plan and prepare the scientific reports. | V2 | Homework, and group discussion | Assignments, Homework, Presentation, Rubrics of behavior and performance in the lab. |
| 3.2 | Communicate, manage tasks and participate the activities related to | V2 | Group discussion | Oral Presentation |



| Code | Course Learning Outcomes | Code of PLOs aligned with the program | Teaching Strategies | Assessment Methods |
|------|------------------------------|---------------------------------------|---------------------|--------------------|
| | training and community work. | | | |
| ... | | | | |

C. Course Content

| No | List of Topics | Contact Hours |
|----|---|---------------|
| 1 | Introduction to Bioinformatics: This topic begins with an overview of bioinformatics, which is the intersection of biology and computational science. It explores how computational tools and techniques are used to analyze biological data. | 3 |
| 2 | Nucleic acid sequence databases: nucleic acid sequence databases are fundamental resources for biological research. They store genetic information, enable comparisons across species, and support various genetic and genomic analyses, contributing significantly to our understanding of genetics, evolution, and the molecular basis of life | 3 |
| 3 | Protein sequence databases: Protein sequence databases are repositories of amino acid sequences of proteins from diverse organisms. These databases serve as critical resources for researchers in molecular biology, bioinformatics, and structural biology. | 3 |
| 4 | Structure classification database, Protein-Protein interaction database and pathway database: Each of these database types plays a vital role in biological research by organizing and providing access to data that helps scientists uncover the intricacies of biomolecular structures, interactions, and cellular processes. | 3 |
| 5 | The central dogma: It states that genetic information flows from DNA to RNA to protein. | 3 |
| 6 | Database searching (e.g., FASTA and BLAST algorithms): Both FASTA and BLAST are essential tools for researchers seeking to identify similar sequences in large genomic or proteomic databases. These algorithms play a critical role in various biological research applications, including gene annotation, protein function prediction, evolutionary analysis, and the discovery of potential drug targets. | 3 |
| 7 | Sequence alignment - pairs, multiple sequence alignment and identifying similar sequences including basic statistical approaches | 3 |
| 8 | Sequence alignment - pairs, multiple sequence alignment and identifying similar sequences including basic statistical approaches | 3 |
| 9 | Structure and prediction. Sequence Based Secondary Structure Prediction. Visualization of structures using Rasmol or SPDBV. Fundamentals of the methods for 3D structure prediction. | 3 |
| 10 | Phylogenetic relationships: A comprehensive understanding of how scientists reconstruct evolutionary histories, interpret phylogenetic trees, and apply this knowledge to diverse scientific disciplines. | 3 |
| 11 | (Total theory) | 30 |
| 12 | Literature Search and Usage of PubMed | 4 |
| 13 | Sequence retrieval | 4 |
| 14 | Pair wise sequence alignment | 4 |





| | | |
|--------------|--|-----------|
| 15 | Databases search for homologous sequence using (BLAST) and (FASTA) | 4 |
| 16 | MSA: (Clustal W, Clustal X, PILE UP) etc. | 4 |
| 17 | Protein structure prediction tools | 5 |
| 18 | PCR Primer Designing | 5 |
| 19 | (Total practical's) | 30 |
| Total | | 60 |

D. Students Assessment Activities

| No | Assessment Activities * | Assessment timing (in week no) | Percentage of Total Assessment Score |
|----|-------------------------------------|--------------------------------|--------------------------------------|
| 1. | Quiz-1 | 4 th Week | 5 |
| 2. | Mid-term exam-1 | 6 th Week | 10 |
| 3. | Mid-term exam-2 | 8 th Week | 10 |
| 4. | E-Exam-2 | 10 th Week | 10 |
| 5. | Homework, Assignment, Presentation, | 12 th Week | 5 |
| 6. | Practical's, | 13 th Week | 20 |
| 7. | Final exam | 15 th Week | 40 |

*Assessment Activities (i.e., Written test, oral test, oral presentation, group project, essay, etc.).

E. Learning Resources and Facilities

1. References and Learning Resources

| | |
|------------------------------|--|
| Essential References | <ol style="list-style-type: none"> 1. Introduction to Bioinformatics, Teresa Attwood, David Parry-Smith, 1st edition, May 2001, Pearson Education. ISBN: 978-8178085074. 2. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Second Edition, Andreas D. Baxevanis, B. F. Francis Ouellette. 2nd edition, October 2004, A John Wiley & Sons, Inc., Publication. ISBN: 978-0471478782. |
| Supportive References | <ul style="list-style-type: none"> • Bioinformatics: Sequence, Structure and Databanks: A Practical Approach (The Practical Approach Series, 236), Des Higgins (Editor), Willie Taylor. 1st edition, October 2000, Oxford University Press. ISBN: 978-0199637904. |





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|---------------------------------|--|
| | <ul style="list-style-type: none"> • Bioinformatics: Sequence and Genome Analysis, David W. Mount. 2nd edition, June 2004, Cold spring harbor laboratory press. ISBN: 978-0879697129. • Higgins, D & Taylor, W 2000, Bioinformatics: sequence, structure and databanks: a practical approach, Oxford University Press, Oxford (ISBN 0 19 963790 3.) |
| Electronic Materials | <ul style="list-style-type: none"> • http://www.aun.edu.eg/molecular_biology/Procedure%20Bioinformatics22.23-4-2015/Xiong%20-%20Essential%20Bioinformatics%20send%20by%20Amira.pdf • https://www.ncbi.nlm.nih.gov/ • http://www.rcsb.org/ • https://web.expasy.org/docs/swiss-prot_guideline.html • http://bioinfo.ut.ee/primer3-0A.0/primer3/ • http://en.bio-soft.net/primer.html |
| Other Learning Materials | Computer-based programs with professional standards or and virtual software's |

2. Required Facilities and equipment

| Items | Resources |
|---|--|
| facilities (Classrooms, laboratories, exhibition rooms, simulation rooms, etc.) | Classroom |
| Technology equipment (projector, smart board, software) | Smart board and e podium available |
| Other equipment (depending on the nature of the specialty) | Library and seminar room Wi-Fi internet connections |

F. Assessment of Course Quality

| Assessment Areas/Issues | Assessor | Assessment Methods |
|---|----------------|---------------------|
| Effectiveness of teaching | Students | Direct Assessment |
| Effectiveness of Students assessment | Program leader | Direct Assessment |
| Quality of learning resources | Students | Indirect Assessment |
| The extent to which CLOs have been achieved | Faculty | Direct Assessment |
| Other | | |

Assessors (Students, Faculty, Program Leaders, Peer Reviewers, Others (specify))

Assessment Methods (Direct, Indirect)





G. Specification Approval

| | |
|-------------------------------|--------------------|
| COUNCIL /COMMITTEE | DEPARTMENT COUNCIL |
| REFERENCE NO. | #7 |
| DATE | 07/10/2024 |

