



# Course Specification

— (Bachelor)

**Course Title:** Bioinformatics

**Course Code:** CIT 1405

**Program:** Bachelor in Information Technology

**Department:** Department of Information Technology

**College:** Faculty of Computers and Information Technology

**Institution:** University of Tabuk

**Version:** 1.0

**Last Revision Date:** 12 Nov. 2023



## Table of Contents

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



## A. General information about the course:

### 1. Course Identification

1. Credit hours: ( 3 )

#### 2. Course type

A.  University  College  Department  Track  Others

B.  Required  Elective

3. Level/year at which this course is offered: (Level 10 or 11/4th Year)

4. Course general Description: This course is an introduction to the application of bioinformatics. It focuses on computational tools to solve biological problems. The topics include concepts of molecular genetics, biological databases, database searching, sequence alignments, protein structure prediction, motif discovery, metagenomics, phylogenetic trees, hierarchical clustering, etc.

5. Pre-requirements for this course (if any): **CIT1305**

6. Co-requisites for this course (if any):

7. Course Main Objective(s): Upon the completion of this course, the students will be able to:

- Understand the principles of bioinformatics and tools for solving computational problems.
- Become familiar with a variety of currently available biological databases (GenBank, Pubmed, PDB).
- Search and retrieve information from databases (e.g., NCBI, GenBank and Swiss-Prot) and use software available on their website (BLAST, MAFFT) to analyze the search results.
- How to compare, align and analyze biological sequences.
- How to construct and visualize phylogenetic trees.





## 2. Teaching mode (mark all that apply)

No	Mode of Instruction	Contact Hours	Percentage
1	Traditional classroom	45	100%
2	E-learning		
3	Hybrid <ul style="list-style-type: none"> <li>• Traditional classroom</li> <li>• E-learning</li> </ul>		
4	Distance learning		

## 3. Contact Hours (based on the academic semester)

No	Activity	Contact Hours
1.	Lectures	45
2.	Laboratory/Studio	
3.	Field	
4.	Tutorial	
5.	Others (specify)	
<b>Total</b>		45

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

Code	Course Learning Outcomes	Code of PLOs aligned with program	Teaching Strategies	Assessment Methods
<b>1.0</b>	<b>Knowledge and understanding</b>			
1.1	Identify and define concepts, principles, models and issues in bioinformatics.	K2, K4		
1.2	How the human genome DNA is sequenced.	K2, K3		



Code	Course Learning Outcomes	Code of PLOs aligned with program	Teaching Strategies	Assessment Methods
1.3	Understand the common file formats used in bioinformatics and the information it holds.	K2, K3, K4	Lectures. Textbooks and References. Supplemental materials. In class discussions. Office hours.	First and Final exams. Assignments. Quizzes. Projects.
1.4	Define DNA sequences can be analyzed to identify genes.	K3, K4		
1.5	Demonstrate both classical and modern techniques to detect/discover patterns/motifs in sequence data.	K2, K3, K4		
<b>2.0</b>	<b>Skills</b>			
2.1	To use genome databases to extract sequence and functional information.	S1, S3, S4	Lectures. Textbooks and References. Supplemental materials. In class discussions.	First and Final exams. Assignments. Quizzes. Projects.
2.2	To apply leading existing bioinformatics tools to address biological questions (e.g., PyMol tool to visualize and analyze protein structures, iTOL tool to display, annotate and managing phylogenetic trees).	S2, S3, S4, S5		





Code	Course Learning Outcomes	Code of PLOs aligned with program	Teaching Strategies	Assessment Methods
3.0	Values, autonomy, and responsibility			
3.1	Acquire and demonstrate the professional and ethical issues in the bioinformatics area.	V1	In class discussions. Assignments/Projects. Presentations.	Evaluating students' work (in the class discussions, Projects Assignments, & Presentations).
3.2	Communicate and work (effectively, ethically, and professionally) (Individually and in groups/teamwork) to accomplish the assigned tasks.	V2		

### C. Course Content

No	List of Topics	Contact Hours
1.	Part 1: Introduction to class Part 2: Introduction to bioinformatics, history, terminology, basic molecular biology	3
2.	Part 1: Human genome project-HGP Part 2: First generation sequencing, Next generation sequencing (NGS)	3
3.	Part 1: Third generation sequencing Part 2: File formats, FASTA, FASTQ, Quality Score	3
4.	Part 1: Biological database (Primary, secondary, Derived database) Part 2: Using the NCBI's Bioinformatics Tools and Databases	3
5.	Part 1: Sequence alignment foundations: basic Idea Part 2: Sequence changes (mutations, deletions, and insertions), optimal alignments.	3
6.	Part 1: Optimal alignments, dot plots. Part 2: Alternative alignments, scoring alignments	
7.	Part 1: Dynamic programming algorithm, Needleman and Wunsch algorithm (global alignment) Part 2: Smith & Waterman algorithm (local alignment)	3
8.	Part 1: BLAST (Basic Local Alignment Search Tool): BLAST output Part 2: Statistical significance of results, BLAST scores and E-values	3





9.	Part 1: Multiple sequence Alignment (MSA) Part 2: Tools involved in MSA, practical database searching with BLAST	3
10.	Part 1: Phylogenetic tree construction, phylogeny terminologies, distance matrix methods (UPGMA, Neighbor-joining) Part 2: Phylogenetic tree formats visualization, iTOL Interactive Tree of Life tool.	3
11.	Part 1: Structural bioinformatics Part 2: Structural databases	3
12.	Part 1: Genome Assembly, de novo whole-genome shotgun assembly, first law of assembly Part 2: Second law of assembly, directed graph review, overlap graph	3
13.	Part 1: Shortest common superstring Part 2: Greedy shortest common superstring	3
14.	Part 1: Third law of assembly, De Bruijn graph assembly Part 2: Eulerian walk definitions and statements	
15.	Part 1: Advanced topics in bioinformatics I Part 2: Advanced topics in bioinformatics II	3
<b>Total</b>		<b>45</b>

#### D. Students Assessment Activities

No	Assessment Activities *	Assessment timing (in week no)	Percentage of Total Assessment Score
1.	Three Assignments	4, 6, 8	15 %
2.	Midterm I	7 or 6	15 %
3.	Midterm II	11 or 12	15%
4.	Project	12 or 13	15%
5.	Final Exam	15	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

- Pevsner, Jonathan. Bioinformatics and functional genomics. John Wiley & Sons, 2015.
- Xiong, Jin. Essential bioinformatics. Cambridge University Press, 2006.





<b>Supportive References</b>	<ul style="list-style-type: none"> <li>• Claverie, Jean-Michel, and Cedric Notredame. <b>Bioinformatics for dummies</b>. John Wiley &amp; Sons, 2006.</li> <li>• Masulli, Francesco. "Understanding Bioinformatics, Marketa Zvelebil, Jeremy Baum, Garland Science—Taylor &amp; Francis Group (2007), 800 pp., Paperback, ISBN: 0-8153-4024-9/ISBN-13: 978-0-8153-4024-9, 111.00 US \$(Amazon. com), 41.99£(amazon. UK), 64.99 EUR (amazon. de)." (2008): 182.</li> </ul>
<b>Electronic Materials</b>	Detailed Slides when necessary
<b>Other Learning Materials</b>	TBD

## 2. Required Facilities and equipment

Items	Resources
<b>facilities</b> (Classrooms, laboratories, exhibition rooms, simulation rooms, etc.)	<b>Classrooms and LABs</b>
<b>Technology equipment</b> (projector, smart board, software)	<b>Data Show</b>
<b>Other equipment</b> (depending on the nature of the specialty)	<b>Each student should have a laptop with the required Software</b>

## F. Assessment of Course Quality

Assessment Areas/Issues	Assessor	Assessment Methods
Effectiveness of Teaching	Faculty	Direct
Effectiveness of Students Assessment	Students	Indirect
Quality of Learning Resources	Students	Indirect
The Extent to which CLOs have been Achieved	Faculty	Direct (as in section B)
	Students	Indirect
Other	-	-

**Assessors** (Students, Faculty, Program Leaders, Peer Reviewer, Others (specify))

**Assessment Methods** (Direct, Indirect)

## G. Specification Approval

<b>COUNCIL /COMMITTEE</b>	
<b>REFERENCE NO.</b>	





DATE

