



## Department of Life Sciences, School of Science University of Management and Technology

### BT-301: BIOINFORMATICS

<b>Lecture Schedule</b>	Tuesday / Friday – <b>Section N2</b> (11:00 AM – 12:15 PM)	<b>Semester</b>	Spring 2021
<b>Pre-requisite</b>	--	<b>Credit Hours</b>	<ul style="list-style-type: none"> <li>• 03 (<b>03 contact hours</b>) theory</li> <li>• 01 (<b>02 contact hours</b>) lab</li> </ul>
<b>Instructor</b>	Muhammad Ali	<b>Contact</b>	<a href="mailto:muhammad_ali@umt.edu.pk">muhammad_ali@umt.edu.pk</a>
<b>Office</b>	S3-37 (Ext. 3449)	<b>Office Hours</b>	03:00 – 05:00 PM ( <b>Monday - Saturday</b> )
<b>Specific Outcome</b>	The challenge facing scientists is to access and analyze genomic data to extract useful information pertaining to biological systems. This course focuses on employing existing <i>in silico</i> resources – mainly web-based programs and databases – to access the wealth of data to answer questions relevant to the average biologist, and is highly hands-on.		
<b>Learning Outcomes</b>	<p>The students will be able to:</p> <ul style="list-style-type: none"> <li>• Find structural analogs for a protein sequence</li> <li>• Describe the structure of genes and genomes</li> <li>• Distinguish between prokaryotic and eukaryotic genes</li> <li>• Find information about a specific gene</li> <li>• Interpret a GenBank entry</li> <li>• Examine whole genomes</li> <li>• Identify errors in a DNA sequence</li> <li>• Explain the significance of folding and three-dimensional protein structure</li> <li>• Perform secondary structure prediction</li> </ul>		
<b>Course Content</b>	Following topics will be included in this course ( <i>detailed week-wise breakup is</i>		

	<p><i>given at the end of the document</i>):</p> <ul style="list-style-type: none"> <li>• Biological data acquisition: the form of biological information.</li> <li>• Retrieval methods for DNA sequence, protein sequence and protein structure information; Databases – Format and Annotation: conventions for database indexing and specification of search terms, common sequence file formats.</li> <li>• Annotated sequence databases - primary sequence databases, protein sequence and structure databases; organism specific databases; Data – Access, Retrieval and Submission: Standard search engines; Data retrieval tools – Entrez DBGET and SRS; Submission of (new and revised) data; Sequence Similarity Searches: Local versus global. Distance metrics. Similarity and homology.</li> <li>• Scoring matrices. Dynamic programming algorithms, Needleman-wunsch and Smith-waterman. Heuristic Methods of sequence alignment, FASTA, BLAST and PSI BLAST. Multiple Sequence Alignment and software tools for pairwise and multiple sequence alignment; Genome Analysis: Whole genome analysis, existing software tools; Genome Annotation and Gene Prediction; ORF finding; Phylogenetic Analysis: Comparative genomics, orthologs, paralogs.</li> <li>• Methods of phylogenetic analysis: UPGMA, WPGMA, neighbour joining method, Fitch/Margoliash method, Character Based Methods</li> <li>• Protein Structure Prediction and Interaction</li> </ul>	
<p><b>Learning Resources</b></p>	<p>Text Books</p>	<ul style="list-style-type: none"> <li>• Database annotation in molecular biology, principles and practices, Arthur M. Lesk</li> <li>• Bioinformatics: Databases and Systems, by Stanley I. Letovsky</li> <li>• Bioinformatics Databases: Design, Implementation, and Usage (Chapman &amp; Hall/ CRC Mathematical Biology &amp; Medicine), by Sorin Draghici</li> </ul>

	Reference Book	<ul style="list-style-type: none"> <li>Current topics in computational molecular biology, Tao, Jiang, Ying Xu, Michael Q. Zang</li> </ul>
<b>Teaching Kits</b>	All didactic material will be shared on: <ul style="list-style-type: none"> <li>PowerPoint slides and book shared on LMS</li> <li>Recording (if any) on <a href="https://www.youtube.com/channel/UCRhcR-WWDuSrluUsRE7rd7g">https://www.youtube.com/channel/UCRhcR-WWDuSrluUsRE7rd7g</a></li> </ul>	
<b>Grading Policy</b>	<ul style="list-style-type: none"> <li>Assignments 05%</li> <li>Quizzes 10%</li> <li>Midterm 20%</li> <li>Presentation 05%</li> <li>Lab 20</li> <li>Final 40%</li> </ul>	

Date (DD-MM-YYY)	Week	Topic	Recording
02-03-2021	1	Bioinformatics and the Databases	<a href="https://www.youtube.com/watch?v=vlq8KJS_TkoQ">https://www.youtube.com/watch?v=vlq8KJS_TkoQ</a>
05-03-2021			
09-03-2021	2	Bioinformatics and the Databases	-
12-03-2021			
16-03-2021	3	Sequence Alignment	-
19-03-2021			-
23-03-2021	4	Phylogenetic Analysis	-
26-03-2021			-
30-03-2021	5	Sequence Analysis	-
02-04-2021			-
06-04-2021	6	Mutations	

09-04-2021			<a href="https://www.youtube.com/watch?v=knj4FCsOdYk">https://www.youtube.com/watch?v=knj4FCsOdYk</a>
13-04-2021	7	Mutations	
16-04-2021			
20-04-2021	8	Primer designing	-
23-04-2021			-
<b>27-04-2021</b>	<b>9</b>	<b>Midterm</b>	-
<b>30-04-2021</b>			-
04-05-2021	10	Primer designing	-
07-05-2021			-
11-05-2021	11	Protein Structure Prediction	-
14-05-2021			-
18-05-2021	12	Protein Structure Prediction	-
21-05-2021			-
25-05-2021	13	Protein Structure Prediction	-
28-05-2021			-
01-06-2021	14	Protein Ligand Interaction	-
04-06-2021			-
08-06-2021	15	Protein Ligand Interaction	-
11-06-2021			-
15-06-2021	16	Data Science R Basics	-
18-06-2021			-
22-06-2021	17	Data Science R Basics	-
25-06-2021			-
<b>Final Exam</b>		<b>June 28 to July 10, 2021</b>	-

Last date of course withdrawal: **June 18, 2021**

Eidul Fitar: **May 10-15, 2021**