

BIRLA INSTITUTE OF TECHNOLOGY AND SCIENCE, PILANI
HYDERABAD CAMPUS
Second SEMESTER 2023-2024
COURSE HANDOUT (PART II)

Date: 09/01/24

In addition to part I (General Handout for all courses appended to the timetable) this portion gives further specific details regarding the course.

Course NO. : Bio F242
Course Title : Introduction to Bioinformatics mm
Instructor-in-Charge : SHUVADEEP MAITY
Instructors : Shuvadeep Maity, Nishith Gupta

1. Scope and objective of the Course:

Introduction to computational aspects to understand biological questions. Overview of Biological databases and data mining, sequence similarity search and sequence alignment will be introduced along with new "omics" based (transcriptomics & proteomics) data handling. It includes use of software packages required for different high throughput study. This course is designed to impart the beginner with the fundamentals, which would enable understanding of the intricacies and vast scope of Bioinformatics. A sampling of the different areas required for understanding of this upcoming field will be provided along with *in silico* exercises to familiarize individuals with different program packages like R.

2. Text Book : "Introduction to Bioinformatics" Arthur M. Lesk; Oxford University Press (2009) (TB)

3. Reference Books: 1. "BIOINFORMATICS: A practical GUIDE to Analysis of Genes and proteins, 3rd edition by ANDREAS D BAXEVANIS B.F. FRANCIS OUELLETTE (2005), Willy Student edition
2. Introduction to Bioinformatics with R - A practical Guides for biologists EDWARD CURRY, CRC press (2020)
3. Essential Bioinformatics JIN XIONG Cambridge press (2006)

4. Course Plan:

Lecture No.	Learning Objectives	Topics to be covered	Reference Chap./Sec. (Book)
1.	Introduction	What is Bioinformatics, Scope	Lecture Notes
2-8	Molecular biology from the perspective of bioinformatics	Central dogma, Nucleic acid, protein structure-function relation, Genetic code, Mutations, PTM etc	Lecture Notes Chap 1 - TB
9-10	General overview of different techniques to generate biomolecular information and analysis	PCR, NMR, X-ray crystallography, DNA sequencing, Microarray, RNA sequencing, protein sequencing, system biology, MS	Chap1/2 - TB
10	Informatics and information Networks	WWW, TCP/IP, HTTP, URLs, Public library of science, Programming language for bioinformatics (R, Perl) and tools (JAVA, markup languages)	Chap3 - TB Lecture notes
12-13	Information Resources	Biological databases (Primary databases, Secondary databases), Sequence Databases, Mapping Databases, Genomic Databases, information retrieval from biological databases, Data repositories (Genomics & proteomics), Submission of sequences to the databank.	Chap 3,4 – TB Chap 1- RB1

14-18.	Sequence Analysis and alignment	<p>Definition of sequence alignment, Method of sequence analysis, Dot-matrix, dynamic programming algorithms for sequence alignment, use of scoring matrix and gap penalties, Pairwise sequence alignment –The problem, pairwise sequence alignment – the effect of scoring parameters on the alignment, Multiple sequence alignment, searching sequence databases: Similarity searching tools</p> <p>Database Similarity Searching: Unique Requirements of Database Searching Heuristic Database Searching Basic Local Alignment Search Tool (BLAST) FASTA Comparison of FASTA and BLAST Database Searching with the Smith–Waterman Method</p>	<p>Chap 5 - TB Chap 4 - RB3 Chap 4 - RB1</p>
19-21	Phylogenetic analysis	<p>Tree building and evaluation methods, The PAM model of protein sequence, Evolution, PAM distances, Log-odds scoring matrices for amino acids Understanding phylogenetic trees, Choosing sequences, Distance matrices and clustering methods, Calculation of distances in the neighbor-joining method.</p>	<p>Chap 5 - TB Chap 4 - RB1</p>
21-24	Bioinformatics Programming	Introduction with R language, overview statistical analysis	Chapter - 1, 2, 4 RB2, class notes
25-30	Next generation sequencing/ "Omics" informatics	Human genome project, introduction to genomics, transcriptomics, proteomics	Chap 17, 18 - RB3
31-36		RNAseq and its variants, Quality control experimental, Transcriptome assembly, data processing, differential expression, functional enrichment	Chap 18 - RB3 Class notes
36-38		Proteomics informatics, data acquisition overview, file types, online tools to basic proteomics data handling	Chap 19 - RB3
39- 42	Analysis Packages	Commercial databases and software, plotting	Chap 2 - RB2 Class Notes

5. Evaluation scheme:

EC No.	Evaluation Component	Duration	Weightage %	Date, Time & Venue	Nature of Component
1	Announced/ Quizzes/assignments/ presentation* (Continuous evaluation)	Variable	35% = 70M 15M(CB)+ 20M(OB) + 15M(CB) + 20M(OB)	To be announced	OB [#] (20%) and Closed book (15%)
2	Mid-Sem	90 Min.	30% = 60M	14/03 - 4.00 - 5.30PM	Closed Book
3	Comprehensive	180 Min.	35% = 70M	14/05 AN	Closed Book
*Quizzes will be conducted during tutorial hours; Two evaluations before the mid-semester and two after. # OB- assignments/ presentations : submission criteria, parameters are subject to individual instructor's choice					

6. Consultation Hour: To be announced in the class.

7. Notices: Notices will be displayed via CMS.

8. Make up Policy: Make up (Midsem and Endsem) will be given on genuine grounds as determined by the IC.
No Make up for Quiz/presentations/ continuous evaluation.

9. Academic Honesty and Integrity Policy: Academic honesty and integrity are to be maintained by all the students throughout the semester and no type of academic dishonesty is acceptable.

**Instructor-in-charge
BIOF242**