

**BIRLA INSTITUTE OF TECHNOLOGY AND SCIENCE, PILANI**  
**HYDERABAD CAMPUS**  
**SECOND SEMESTER 2024-2025**  
**COURSE HANDOUT (PART II)**

**Date: 06/01/2025**

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  
**Instructor-in-Charge** : SHUVADEEP MAITY  
**Instructors** : Shuvadeep Maity, Nishith Gupta

**1. Scope and objective of the Course:**

This course 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.

The course will let you learn about biological databases and data mining using different online sources, sequence similarity search and sequence alignment, dynamic programming methods, scoring matrix, tree building, use of software package in Bioinformatics. It will also introduce you to new area of “omics” biology like genomic & proteomics, human Genome and other sequencing projects and their impact in understanding complex biology.

**2. Textbook:** “Introduction to Bioinformatics” Arthur M. Lesk; Oxford University Press (2009) (TB)

**3. Reference Books:**

1. Instant Notes in MOLECULAR BIOLOGY P.C. Turner, A.G. McLennan, A.D. Bates & M.R.H. White, viva books private ltd, New Delhi. (RB1)
2. Bioinformatics Genome and sequence Analysis by David W Mount, CSHL Press, 2003 (RB2)
3. BIOINFORMATICS AND MOLECULAR EVOLUTION Paul G. Higgs and Teresa, K. Attwood Black Well Publishing (2005) (RB3)
4. BIOINFORMATICS A practical guide to the analysis of genes and proteins by Andreas D. Baxevanis, B. F. Francis Ouellette (RB4)

**4. Course Plan:**

Lecture No.	Learning Objectives	Topics to be covered	Reference Chap./Sec. (Book)
1	Introduction	What is Bioinformatics and its scope	Lecture Notes
2-5	Overview of molecular biology & genetics	Nucleic acid; Structure & function	Sec C- RB1 Chap 2 RB3
		Protein Structure & function	Sec B- RB1 Chap 2 RB3
		Central dogma of life Replication/Transcription/Translation	Sec E/K/Q RB1 Chap 2 RB3
		Genetic code, Codon bias and its optimization (discuss bioinformatics tools to do codon optimization)	Sec P- RB1

6-7	General overview of different techniques to generate biomolecular information and analysis	PCR, NMR, X-ray crystallography, Microarray, sequencing, Human and other genome sequencing project	Class Notes
8	Informatics and information Networks	WWW, TCP/IP, HTTP, URLs	Chap.2 TB
9-10	Collection and storage of sequences	Data repositories (Genomics & proteomics), Submission of sequences to the databank, Computer storage of sequences, web resources in bioinformatics	Chap-2,3,4,5 (TB) RB2 Chap 5 Class notes
11-13	Information Resources	Biological databases, Primary databases Secondary databases, Data types, how to access and data type conversion, NCBI, EMBL, UCSC. Demonstration of the use of databases.	Chap.4 TB RB2 Chap 5 Class notes
			Chap.3 TB Class notes
14-16	Sequence Analysis and alignment	Similarity searching tools & searching sequence databases: definition of sequence alignment, method of sequence analysis, dot-matrix, dynamic programming algorithms for sequence alignment, use of scoring matrix and gap penalties, the effect of scoring parameters on the alignment, pairwise sequence alignment, Local and global alignment. BLAST and Multiple sequence alignment.	Chap. 3 and Chap. 4 RB2 Chap 8 RB2
17-20	Phylogenetic analysis	Dynamic programming methods, The PAM model of protein sequence, Evolution, PAM and BLOSSUM, distance calculation, Log-odds scoring matrices for amino acids. Tree building and evaluation methods, understanding phylogenetic trees, Choosing sequences, Distance matrices and clustering methods, Calculation of distances in the neighbor-joining method, Bootstrapping.	Chap. 4 TB Chap9 RB3
21	Bioinformatics Programming	Introduction of Linux and R basic (demo with R languages)	Class notes and tutorials
22-29	Sequencing (DNA/RNA) Next generation sequencing	Overview of nucleic acid sequencing, next generation sequencing types and its data types based on different sequencing techniques. Data generation: Quality control experimental consideration and data output types, sequence assembly, data processing, differential expression analysis of genes (RNA sequencing)	Class Notes R cookbook Tutorial hands on
29-37	Protein sequencing	Overview protein sequencing, fundamental of proteomics, proteomics method comparisons, instrument types and data generation, concept of shotgun proteomics, overview of data structure, data processing, basic data analysis in online free sources	Class Notes R cookbook Tutorial hands on
38-40	Analysis Packages	Discussion on Commercial databases and software for omics, advantages and disadvantages	Chap. 3 & 10 TB

## 5. Evaluation scheme:

EC No	Evaluation Component	Duration	Weightage %	Date, Time & Venue	Nature of Component
1	Quizzes (announced/surprised) * + Continuous evaluation	Variable	30% (60M) + 5% (10M)	To be announced	Open book (OB) <sup>#</sup> (15% of the total)
2	Mid-Sem	90 Min.	30% (60M)	To be announced	OB (5% of the total) + Closed
3	Comprehensive	180 Min.	35% (70M)	To be announced	Closed book
*Quizzes will be conducted during lecture/tutorial hours; Two before the mid-semester and two after the Midsem. Out of 4 quizzes 2 open books (OBs) and 2 closed books (CBs). <sup>#</sup> OPEN BOOK only prescribed textbook/reference book(s), slides (binding format) and handwritten notes (binding format) are permitted					

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

**7. Notices:** Notices and lecture notes will only be displayed via LMS or communicated via ERP.

**8. Make up Policy:** Make up will be given only for Midsem and Endsem with genuine grounds as determined by the IC.

**9. Grading policy:** Award of grades will be guided in general by the histogram of marks. Decision on border line cases will be taken based on individual's sincerity, attendance in classes, and the section instructor's assessment of the student. Students missing one or more component of evaluation along with Midsem and Endsem may be given NC. A student should obtain 30% of the average of the top few performers in the class, or 40% of the median marks of the class, whichever is lower to clear the course.

**10. 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  
Bio F242**