**BIRLA INSTITUTE OF TECHNOLOGY AND SCIENCE, PILANI**

**HYDERABAD CAMPUS**

**Second SEMESTER 2022-2023**

**COURSE HANDOUT (PART II)**

**Date: 16/01/2023**

In addition to the 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, Nisith Gupta, Ali Akbar Shoukat Safdari**

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

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 this upcoming field will be provided along with *in slilico* 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, protein structure prediction and structure analysis, and use of software packages in Bioinformatics. It will also introduce you to new areas of “omics” biologies like genomic & proteomics, human Genome, and other sequencing projects and their impact on understanding complex biology.

**2. Text Book** : “Introduction to Bioinformatics*”* ArthurM. *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.Course Plan:**

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| **Lecture**  **No.** | Learning Objectives | Topics to be covered | **Reference**  **Chap./Sec.**  **(Book)** |
| 1. | Introduction | What is Bioinformatics, Scope | Lecture Notes |
| 2-6 | 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 | Secs E/K/Q- RB1 Chap 2 RB3 |
|  | Genetic code, Codon bias | Sec P- RB1 |
| 7-13. | General overview of different techniques to generate biomolecular information and analysis | PCR, NMR, X-ray crystallography, DNA sequencing, RNA sequencing, Microarray, | Class Notes |
| 14-15 | Informatics and information Networks | WWW, TCP/IP, HTTP, URLs  Programming language for bioinformatics (R, Perl), Learning the basics programming language | Chap.2 TB |
| 16-17 | 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)  RB Chap 5  Class notes |
| 18-19 | Information Resources | Biological databases | Chap.4 TB  RB Chap 5  Class notes |
|  | Primary databases | Chap.3 TB  Class notes |
|  | Secondary databases | Chap.8 TB  Class notes |
| 20-28 | Sequence Analysis and alignment | 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 –Dynamic programming methods, the effect of scoring parameters on the alignment, Multiple sequence alignment, Searching sequence databases: Similarity searching tools | Chap. 3 and Chap. 4 RB2  Chap 8 RB6 |
| 29-33 | Phylogenetic analysis | 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, Bootstrapping | Chap. 4 TB  Chap9 RB3 |
| 34-36 | Next generation sequencing | RNAseq and its variants, Quality control experimental, Transcriptome assembly, data processing, differential expression analysis | Class Notes |
| 37- 38 | Analysis Packages | Commercial databases and software for omics | Chap. 3 & 10 TB |
| 40-42 | Bioinformatics Programming | Introduction of different scripting languages, Demo with R languages | Class notes |

**5. Evaluation scheme**:

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| --- | --- | --- | --- | --- | --- |
| EC No. | **Evaluation Component** | **Duration** | **Weightage %** | **Date, Time & Venue** | **Nature of Component** |
| 1 | Announced/surprised  Quizzes/presentation\*  (Continuous evaluation) | Variable | 35% (70M =15M+20M+  15M+20M) | To be announced | OB# (50%) and Closed book (50%) |
| 2 | Mid-Sem | 90 Min. | 30% (60M) | 13/03 11.30 - 1.00PM | OB (15%)  Closed Book (15%) |
| 3 | Comprehensive | 3 Hrs. | 35% (70M) | 08/05 AN | Closed Book |
| \*Quizzes will be conducted during lecture hours; two before the mid-semester and two after. Out of 4 quizzes 2 open books and 2 closed books.  # OB- Open Book Only prescribed textbook/Reference book(s), slides and handwritten notes are permitted | | | | | |

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

**7. Notices**: Notices will be displayed via CMS.

**8. Make up Policy:** Make up will be given on genuine grounds as determined by the IC.

**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

**Bio F242**