COURSE TITLE	**ANALYTICAL BIOINFORMATICS**
COURSE CODE	**01CB1102**
COURSE CREDITS	**4**

Objective:

1. This subject aims to provide an introduction to the bioinformatics and its application, with a focus on analytics using web resources in the different field of life sciences.
2. To build computational skills for sequence analysis, molecular evolution, and predictive modeling in bioinformatics.

Course Outcomes: After completion of this course, student will be able to:

1. Apply bioinformatics concepts for interpretingand managing biological data.
2. Analyze sequence alignment methods for biological data analysis.
3. Evaluate sequence alignment and scoring matrices for similarity search and phylogenetic analysis.
4. Design bioinformatics workflows using appropriate tools.

Pre-requisite of course:NA

Teaching and Examination Scheme

Theory Hours	Tutorial Hours	Practical Hours	ESE	IA	CSE	Viva	Term Work
3	0	2	50	30	20	25	25

Contents : Unit	Topics	Contact Hours
1	**Introduction to bioinformatics** Vocabulary of Bioinformatics, Challenges, Scope, and Applications of Bioinformatics in Sequence, Structure, and Function Analysis and Other Fields, Introduction and Definition of Sequence Alignment, Types of Sequence Alignment-Pairwise and Multiple Sequence Alignment, Difference Between Pairwise and Multiple Sequence Alignment, Methods of Pairwise Sequence Alignment-Dot Matrix, Dynamic Programming and Heuristic Approach	8
2	**Pairwise sequence alignment** Concept of Substitution, Insertion, and Deletion, Global Alignment, Local Alignment, Dynamic Programming Algorithms for Sequence Alignment, Types of Dynamic Programming and their Steps-Needleman-Wunsch Algorithm, Smith-Waterman Algorithm, Gap penalty, BLAST, FASTA	8

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Contents : Unit	Topics	Contact Hours
3	**Multiple sequence alignment** Purpose and Applications of Multiple Sequence Alignment, Scoring Functions, Dynamic programming Method for Multiple Sequence Alignment, Heuristic Methods-Progressive and Iterative Alignment Methods and their Tools, MSA using CLUSTALW, PILEUP and CLUSTALX, Phylogenetic Tree Terminology, Phylogenetic Tree Analysis	7
4	**Scoring matrices** Types of Scoring Matrices, Dayhoff Mutation Matrix,Construction of PAM and BLOSUM matrix, Similarity Searches Using PAM and BLOSUM Matrices, Differences between PAM & BLOSUM	7
5	**Artificial Intelligence** Introduction-Priors and Likelihoods, Basics of Learning Algorithms, Applications of Artificial Intelligence in Crop Improvement and Healthcare	6
6	**Hidden Markov Models** Basic Concepts-States, Observations, Initial, Transition, and Emission Probabilities and its calculation, Likelihood and Basic Algorithms, Learning Algorithms, Applications of HMMs- General Aspects, Genomics, and Proteomics	6
Total Hours		**42**

Suggested List of Experiments:

Contents : Unit	Topics	Contact Hours
1	**Experiment 1** To identify and retrieve the nucleotide sequences of five genes from different species using the NCBI database	2
2	**Experiment 2** To identify and retrieve the protein sequences of five different proteins using the NCBI database.	2
3	**Experiment 3** To identify and retrieve the protein sequences of five different proteins using the UniProt.	2
4	**Experiment 4** To identify nucleotide sequence and convert it into protein sequence using EBI tool.	2
5	**Experiment 5** To compare the nucleotide sequences using EMBOSS Water.	2
6	**Experiment 6** To compare the protein sequences using EMBOSS Water.	2
7	**Experiment 7** To compare the nucleotide sequences using EMBOSS Needle.	2
8	**Experiment 8** To compare the protein sequences using EMBOSS Needle.	2

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Suggested List of Experiments:

Contents : Unit	Topics	Contact Hours
9	**Experiment 9** To perform database similarity search against non-redundant database and identify the homologous sequences using BLAStn.	2
10	**Experiment 10** To perform database similarity search against non-redundant database and identify the homologous sequences using BLAStp.	2
11	**Experiment 11** To perform multiple sequence alignment among closely related nucleotide sequences using Clustal Omega.	2
12	**Experiment 12** To perform multiple sequence alignment among closely related protein sequences using Clustal Omega.	2
13	**Experiment 13** To identify the functional domain in a protein sequence using InterProscan.	2
14	**Experiment 14** To perform pairwise sequence alignment using dottup.	2
Total Hours		**28**

Textbook :

1 Bioinformatics: Sequence and Genome Analysis, David W. Mount, Cold Spring Harbor Laboratory Press, 2004

References:

1 Bioinformatics: The Machine Learning Approach, Bioinformatics: The Machine Learning Approach, Baldi, P., & Brunak, S., MIT Press, 2001

2 Bioinformatics Basics, Bioinformatics Basics, Rashidi, H. H., & Buehler, L. K., CRC Press, 2000

3 Developing Bioinformatics Computer Skills, Developing Bioinformatics Computer Skills, Gibas, C., & Jambeck, P., O'Reilly Media, 2001

4 Bioinformatics Methods and Protocols, Bioinformatics Methods and Protocols, Misener, S., & Krawetz S. A., Humana Press, 1999

Suggested Theory Distribution:

The suggested theory distribution as per Bloom's taxonomy is as follows. This distribution serves as guidelines for teachers and students to achieve effective teaching-learning process

Distribution of Theory for course delivery

Remember / Knowledge	Understand	Apply	Analyze	Evaluate	Higher order Thinking / Creative
0.00	0.00	35.00	35.00	30.00	0.00

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Instructional Method:

1. The course delivery method will depend upon the requirement of content and need of students. The teacher in addition to conventional teaching method by black board, may also use any of tools such as demonstration, role play, Quiz, brainstorming, MOOCs etc.
2. The internal evaluation will be done on the basis of continuous evaluation of students in the laboratory and class-room.
3. Practical examination will be conducted at the end of semester for evaluation of performance of students in laboratory.

Supplementary Resources:

1. https://visualgo.net/en
2. https://www.cs.usfca.edu/~galles/visualization/Algorithms.html
3. https://quizlet.com
4. Students will use supplementary resources such as online videos, NPTEL videos, e-courses, Virtual Laboratory

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