**BASICS OF BIOINFORMATICS**

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| **Course code** | **Course name** | **Course Category** | **L-T-P** | **Credits** |
| 22BEXY06 | Basics of Bioinformatics | Open free elective | 3-1-0 | 4 |

**Course Learning Objectives:**

1. To understand the importance of Bioinformatics
2. To understand the types of database and their applications
3. To convey the concepts of sequence similarity, identity and homology.
4. To understand the molecular evolution
5. Determine the function of genes and the elements that regulate genes throughout the genome
6. To understand the sequencing technologies of protein and their annotation

**Course Content:**

**UNIT-1:** **Introduction and Historical Background (9 hours)**

Introduction to Bioinformatics, History of Bioinformatics, concept of central dogma of molecular biology, Bioinformatics applications.

**Unit-2 : Bioinformatics Databases (7 hours)**

Introduction to Biological databases, Formats Biological databases, Types of data bases: Primary and Secondary Databases, Nucleic acid databases.

**UNIT-3: Sequence Similarity and Alignment (8 hours)**

Concepts of sequence similarity, identity and homology. Sequence alignment, Simple sequences alignment, Extra sequence alignment, Scoring matrix, Dynamic programming algorithm, Extra- Scoring matrix, Multiple sequence Alignment using Clustal W, BLAST Programs: Types of BLAST, BLASTn search.

**Unit-4: Molecular Phylogenetics (6 hours)**

Molecular Evolution, Understanding Evolution, study of a Phylogenetics Tree, Methods of Phylogenetic analysis, Building a phylogenetic tree methods.

**Unit 5: Genomics (8 hours)**

Introduction to Genomics, Sequencing technologies- Sanger sequencing, Next-generation sequencing (NGS) , Genome Assembly, Genome Annotation, Comparing Genomes project of bacteria (*Mycobacteria*), plants (*Arabidopsis thaliana*) and humans and its significances.

**Unit 6: Proteomics (7 hours)**

Introduction to proteomics, Sequencing Technologies of Protein (Edman degradation), Role of mass spectroscopy in proteomics methods, Protein Assembly, Protein Annotation, Study of proteome database.

**Learning Resources**

**Text Book:**

1. A. K. Lesk,‘ *Introduction to Bioinformatics*’ Oxford University Press. 2019.

2. R. Durbin, S. Eddy, A. Krogh and G.Mitchison, ‘*Biological Sequence Analysis Probabilistic Models of proteins and nucleic* acids’ Cambridge University Press, 1998.

3. J. Tindall, ‘*Beginning Perl for Bioinformatics: An introduction to Perl for Biologists’*,

O’reilley Media, 2001.

**Reference Books:**

1. D.W. Mount ‘*Bioinformatics: Sequence and Genome Analysis’* Cold Spring Harbor Laboratory Press,U.S, 2004.

2. T. K. Attwood, D. J. Perry-Smith and S. Phukan ‘*Introduction to Bioinformatics’* , Pearson Education 1(Singapore) Pvt. Ltd, 2002.

3. D. Gusfield ‘*Algorithms on Strings, Trees and Sequences’* Cambridge University Press, 2010.

4. D. W. Mount ‘*Bioinformatics Sequence and Genome Analysis’* Cold Spring Harbor Laboratory Press, 2004.

5. P. Baldi and S. Brunak ‘*Bioinformatics The Machine Learning Approach’* Bradford Books, 2001.

**Web Resources:**

1. NPTEL:

[https://nptel.ac.in/courses/102/106/102106065/]( https://nptel.ac.in/courses/121106008/)

**Course Outcomes:** At the end of the course, the student will be able to

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| CO 1 | Students should be able to apply basic bioinformatics tools for various needs in biotechnology and microbiology programs, such as finding gene/protein homologs, designing primers, identifying mutations, etc. |
| CO 2 | Explore different database like Primary and Secondary Databases, Nucleic acid databases |
| CO 3 | Study the sequence similarity and alignment of different sequences (genes, proteins) |
| CO 4 | Study and analysis of a Phylogenetics Tree |
| CO 5 | Study the variations in the DNA sequence among organisms and determine their significance. |
| CO 6 | Analyze the proteome. |

**Evaluation pattern for Theory Course Only:**

**Assessment Method**

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| Assessment Tool | Monthly tests | End Semester Test | Total |
| Weightage (%) | 40% | 60% | 100% |