17CS32E2 - BIOINFORMATICS

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| **Course Category:** | Professional Elective | **Credits:** | 3 |
| **Course Type:** | Theory | **Lecture – Tutorial – Practical:** | 3-0-0 |
| **Prerequisite:** | Need to have basic knowledge on genetic algorithms | **Sessional Evaluation:****Univ.Exam Evaluation:****Total Marks:** | 4060100 |
| **Objectives** | * To explore the applicability of various techniques in different applications
* To select good visualization tools for Analysis
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| **Course Outcomes** | Upon successful completion of the course, the students will be able to: |
| CO1 | Understand the basics of Bioinformatics and patterns |
| CO2 | Get idea on different Protein Information |
| CO3 | Design DNA Sequences |
| CO4 | Study of Pairwise Alignment Technique |
| CO5 | Explore Multiple Sequence alignment techniques |
| CO6 | Develop Sequence Search Protocol for real time applications |
| **Course Content** | UNIT – IIntroduction: The dawn of sequencing, What is bioinformatics?, The Biological sequence/structure deficit, Genome projects, Status of genome project, Why Bioinformatics is important?, Pattern recognition and prediction, The folding problem, The role of chaperones, Sequence analysis, Homology and analogyUNIT – II**Protein Information Resources:** Introduction, Biological Databases, Primary sequence databases, Composite Protein Sequence databases, Secondary databases, Composite Protein pattern databases, Structure Classification databases.UNIT – IIIDNA Sequence Analysis: Introduction, Why analyse DNA, Gene Structure and DNA sequences, Features of DNA sequence analysis, Issues in the interpretation of EST searches, Two approaches to gene hunting, The expression profile of cell, cDNA and EST’s, Different approaches to EST analysis, Effects of EST data on DNA databasesUNIT – IVPairwise alignment techniques: Introduction, Database searching, Alphabets and complexity, Algorithms and programs, Comparing two sequences – a simple case, Sub – sequence, identity and similarity, The dotplot, Local and global similarity, Global alignment, local alignment, pairwise database searching.UNIT – VMultiple Sequence alignment : Introduction, The goal of multiple sequence alignment,Multiple sequence alignment: a definition, Computational complexity, Manual methods. Simultaneous methods, Progressive methods, Databases of multiple alignments, Searching databases in multiple alignments.UNIT – VISecondary database searching: Introduction, why bother with secondary database searches? What’s in secondary databaseBuilding a Sequence search protocol: Introduction, A practical approach, when to believe a result, Structural and Functional interpretation. |
| **Text Books****and References:** | **Text Book:**1. Introduction to Bioinformatics. Terese K.Attwood and David J. Parry - Smith.

**Reference Books:**1. Andreas D.Baxevanis, B.F. Francis Ouellette, "Bioinformatics - A Practical Guide to the Analysis of Genes and Proteins", Third Edition, 2005-2006, ISBN: 978-81-265-2192-0, published by John Wiley & Sons INC., U.K.2. Jean-Michel Claverie, Cedric Notredame, “Bioinformatics For Dummies”, 2nd Edition,2006, ISBN: 978-0-470-08985-9. |
| **E-Resources** | 1. <https://nptel.ac.in/courses>
2. <https://freevideolectures.com/university/iitm>
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