

BTOE 001: COMPUTATIONAL BIOLOGY

Course Objective:

- To understand the basics of computational science and apply it to solve biological problems.
- To learn about developing algorithms for solving complex biological problems as theoretical level.

Credits: 03

L-T-P-J: 3-

0-0-0

| Module No. | Course Content | Teaching Hours/ Percentage |
|------------|---|----------------------------|
| I | Problem solving Technique: Algorithm, Flowchart, Compiling, Testing and Debugging, Documentation – Data structures – Array, Stack, Queue, Linked, List concepts. BioPerl language, programming using BioPerl | 10//25% |
| II | Complexity of algorithms –NP complete problem- polynomial-Reducibility-sorting problem and Fibonacci Problem; Algorithm types: Linear, Exhaustive search, Branch and Bound, divide and conquer, Expectation and Maximation (EM) with forward and backward algorithms, discriminative learning, Knuth-Morris- Pratt and Boyer-Moore algorithm for exact match and maximum likelihood algorithm | 10//25% |
| III | Dynamic programming methods of sequence analysis: Principles and its uses. Hidden Markov models in sequence analysis. Introduction of Markov Chain and Hidden Markov models. Forwardbackward algorithm, Viterbi and Baum-Welch algorithms, Heuristics second generation alignment tool (Blast, FASTA, ClustalW), Monte Carlo method, Molecular dynamics | 10//25% |
| IV | Molecular computational biology: Gene prediction, sequencing genomes, similarity search, restriction mapping, DNA binding motif finding by sequence alignment, Gibbs sampling approaches Laboratory Work: BioPerl programming, Multiple sequence | 10//25% |

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| | alignment, DNA binding motif finding by sequence alignment | |
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Text Books/ Reference Books:

- Pevzner, P. A., Computational Molecular Biology, PHI Learning Pvt. Ltd, ISBN-978-81-203-2550-0.
- Ghosh, Z. and Mallick, B., Bioinformatics Principles and Applications(2008) Oxford University Press
ISBN 9780195692303
- Mount, D. W., Bioinformatics – sequence and genome analysis

Course Outcome:

CO1: To perform programming in BioPerl programming language

CO2: To explain underlying algorithms for sequence analysis

CO3: To explain various types of algorithms with their possible application in solving biological problems.

CO4: To use HMM and other algorithms

CO5: To explain the computational aspects of complex biotechnological analyses.

MAPPING COURSE OUTCOMES LEADING TO THE ACHIEVEMENT OF PROGRAM OUTCOMES

| | Program Outcomes | | | | | | | | | | | |
|-----|------------------|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|
| | PO1 | PO2 | PO3 | PO4 | PO5 | PO6 | PO7 | PO8 | PO9 | PO10 | PO11 | PO12 |
| CO1 | H | H | H | | H | | L | M | H | M | H | L |
| CO2 | L | L | L | L | | M | | | M | | H | L |
| CO3 | H | H | | | L | | L | L | | L | | M |
| CO4 | H | H | L | M | L | | | | M | L | M | L |
| CO5 | L | H | | L | | L | L | L | | M | L | M |

H = Highly Related; M = Medium; L = Low

