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| Course title: Bioinformatics and Computational Biology | | | | | | |
| Course code: BBP 173 | | No. of credits: 3 | L-T-P: 26-16-0 | Learning hours: 42 | | |
| Pre-requisite course code and title (if any): Bioinformatics and Computational Biology- Part I | | | | | | |
| Department: Department of Biotechnology | | | | | | |
| Course coordinator(s): Dr. Pallavi Somvanshi | | | Course instructor(s): Dr. Pallavi Somvanshi | | | |
| Contact details: pallavi.somvanshi@teriuniversity.ac.in | | | | | | |
| Course type: Core | | | Course offered in: Semester III | | | |
| <p>Course description: The area of Bioinformatics is a blend of two dynamic subject areas; biology and computing. The increasingly large volumes of biological data from genome sequencing activities cannot be stored, visualized and analysed without the power of modern information technology. In this course in the student gets an exposure to various facets of bioinformatics. It aims to provide basic understanding of how biological data is stored and retrieved from various biological databases. Further, this course deals with the methodologies of sequence analysis and phylogenetic analysis. It will also focus on <i>in-silico</i> prediction of protein structure, protein-ligand docking and molecular simulations. There will be emphasis on exposing the student to wide variety of tools which they can use in their day-to-day wet lab experiments.</p> | | | | | | |
| <p>Course objectives:</p> <ol style="list-style-type: none"> To learn the core areas of Bioinformatics like sequence analysis, phylogenetic trees, genomics, proteomics To explore the students to applied areas of Bioinformatics like homology modeling and simulation methods. To provide knowledge about predicting the structure of biomolecules, structure prediction and validation. | | | | | | |
| Course contents | | | | | | |
| Module1 | Phylogenetics and structure prediction | | | L | T | P |
| 1 | <u>Sequence analysis</u> Introduction to Biological sequences, Introduction to sequence editing tools (EMBOSS, BioEdit, Ensembl) | | | 4 | 2 | 0 |
| 2 | <u>Molecular Phylogenetics</u> Molecular evolution, Overview and protocols, Nature of data use, Probabilistic models and associated algorithms, Probabilistic models of evolution, Maximum likelihood algorithm, Phylogenetic analysis algorithms, Distance based methods: UPGMA, Neighbour-joining method, Character based methods: Maximum likelihood, Maximum parsimony, Reliability methods: Bootstrap validation, Jack-knife validation | | | 6 | 3 | 0 |
| 3 | <u>Protein structure prediction</u> Introduction to protein structure, Protein stability and folding, Protein stability and denaturation, Protein folding, Application of hydrophobicity, Protein Structure Prediction and Modeling, Critical Assessment of structure prediction (CASP) ,Secondary structure prediction (Chau-Fasman method, GOR method, Nearest neighbor method, Neural network method) | | | 6 | 2 | 0 |
| 4 | <u>Profiles and Hidden markov models</u> Profiles, Hidden Markov models, Markov process, Markov models and Hidden Markov models (HMM), Components of Profile HMM, Building HMM, HMM scoring algorithms. | | | 4 | 2 | 0 |
| Module2 | Molecular Modelling and Simulation | | | | | |
| 6 | <u>Homology modelling</u> Introduction to modelling , tools and softwares , Seven steps of homology modelling, Application in drug designing | | | 2 | 3 | 0 |

www.ncbi.nlm.nih.gov/
www.ddbj.nig.ac.jp/
www.embl.org/
www.ebi.ac.uk/Tools/msa/clustalo/
www.expasy.org/

Journals

Other readings

1. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ, “*Basic local alignment search tool*” , J Mol Biol, 1990.
2. Elmar Krieger, Sander B. Nabuurs, and Gert Vriend, “*HOMOLOGY MODELING*”, Structural Bioinformatics, 2003.
3. Gregoret LM, Cohen FE ,”*Novel method for the rapid evaluation of packing in protein structures*” , J Mol Biol ,1990.
4. Hang Chen, Fei Gu,and Zhengge Huang , “*Improved Chou-Fasman method for protein secondary structure prediction*” , BMC Bioinformatics,2006.

Additional information (if any):

Student responsibilities:

1. Class attendance.
2. Study of course materials as specified by the instructor.

Reviewed by:

1. Dr. Gitanjali Yadav, Scientist IV, NIPGR, New Delhi
2. Dr. Debasis Mohanty, NII, New Delhi