ADVANCE COMPUTATIONAL BIOLOGY   (IBT-826) Credit Hrs 3 (3-0)

1. **Educational objectives:**

   a.   Introduce the aims and uses of computational biology.

   b.   Describe how biological information is stored and accurately retrieved.

   c.   Describe the sources of data, in particular from the characterization of genomes and proteomes.

   d.   Introduce computational algorithms that can be used for querying and manipulating biological data.

   e.   Study some of the practical uses of these algorithms.

   f.   Understand some of the issues and challenges in contemporary Bioinformatics and Computational Biology (BCB)

Course Outcomes:

2. By the end of the course the student should be familiar with,

   a.   Principles used in modelling dynamic phenomena in cells and methods that are used to analyse computational models.

   b.   Understand basic research methods in bioinformatics.

   c.   Understand the inner working of some of the most widely-used bioinformatics methods, such as, sequence comparison and structure prediction, protein structure and function analysis.

   d.   Implement alignment algorithms on protein sequences, modify and implement gene and motif finding algorithms, gather and present statistics on protein structures.

   e.   Understand the data structure (databases) used in bioinformatics and interpret the information (especially: find genes; determine their functions), understand and aware of current research and problems relating to the area of their research project.

   f.   Aware of the range of technologies available to computer scientists in bioinformatics.

g.　　Able to carry out data mining gene and protein expression patterns and modelling cellular interactions and processes.

3.　　**Course Contents:**

a.　　Introduction to Bioinformatics

　　(1)　　Definitions of bioinformatics and related fields

　　(2)　　Objective and scope of bioinformatics

　　(3)　　Kind of data used in bioinformatics

　　(4)　　Data integration and data analysis

　　(5)　　Major biological databases

b.　　Sequence Alignment

　　(1)　　Pairwise Sequence Alignment

　　(2)　　Methods and tools of sequence alignment

　　(3)　　Multiple Sequence Alignment

c.　　Phylogenetic Analysis

　　(1)　　Phylogenetic trees

　　(2)　　Methods of Phylogenetic analysis

　　(3)　　Methods of evaluating phylogenies

　　(4)　　Gene Prediction

d.　　Introduction

　　(1)　　Methods of gene prediction

　　(2)　　Gene prediction tools

e.　　Protein Folding/Structure

　　(1)　　Protein structure and its classification

　　(2)　　Protein classification methodology and tools

　　(3)　　Protein structure databases and visualization tools

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        (4)   Protein structure prediction

        (5)   Protein function prediction

f.   Genomics and Proteomics

        (1)   Introduction to genomics

        (2)   Tools for genome analysis

        (3)   Approaches for Genome-wide scan

        (4)   Introduction to proteomics

        (5)   Tools for proteome analysis

        (6)   Familiarization with Linux OS

        (7)   Introduction to perl scripting

        (8)   Creating a simple bioinformatics database

        (9)   Accessing the publicly available databases

        (10)   Pair wise and multiple sequence alignment

        (11)   BLAST database and genome annotation

        (12)   An Introduction to the vector/primer design Program

        (13)   Protein structure prediction for known folds

        (14)   Protein structure prediction for unknown folds

        (15)   Visualization of biomolecular structures

Books Recommended:

1.   **Fundamentals of Biostatistics** by Bernard Rosner, Duxbury 2000.
2.   **An Introduction to Biostatistics** by Glover & Mitchell, McGrawHill 2002.
3.   **Beginning of Perl for Bioinformatics** by J Tisdall, O'Reilly 2002.
4.   **Bioinformatics: Sequence and Genome Analysis** by DW. Mount, Clod Spring Harbor 2002.
5.   **Bioinformatics: Genes, Proteins & Computers** by C.A. Orengo, Advanced Text 2003.
6.   **Bioinformatics: A practical guide to the analysis of genes and proteins** by Baxevanis & Ouellette, Wiley 2005.