LABORATORY CURRICULUM & PRACTICAL OBJECTIVES
BTD08: Computational Biology- Semester VI

PRACTICAL 01
Objective: To write a simple sequence assembly program
Methodology: Understanding the logic, translating it into an algorithm and further into a program using languages such as C, C++.
Outcome: Learning the statistical significance of sequence matching and challenges involved in Whole Genome Assembly post sequencing

PRACTICAL 02
Objective: To implement a selected sequence alignment algorithm
Methodology: Character comparison using the naïve and pre-processing approaches for sequence alignment using programming languages such as C, C++.
Outcome: Learning the methodology and time complexity of exact string matching of biological sequences.

PRACTICAL 03
Objective: Introduction to NCBI – basic structure and organization of the portal.
Methodology: Demonstration on the NCBI website www.ncbi.nlm.nih.gov using laptop, tab or mobiles. Retrieval of different types of sequences and information about NCBI constituent databases, as well as their integration.
Outcome: An introduction to the basic database resources available for sequence, structure and literature for computational analysis, and methods for obtaining related biological information from various sources using NCBI website.

PRACTICAL 04
Objective: Introduction to the Literature resources provided by NCBI
Methodology: Learning about the different types of information available in NCBI Bookshelf, PubMed, PubMed Central, OMIM, and OMIA. Use of simple and advance search tools for retrieval of relevant results.
Outcomes: Learning about the information availability, salient features and search techniques for each literature repository.

PRACTICAL 05
Objective: Introduction to NCBI – Sequence and Structure resources
Methodology: Learning how to retrieve sequences using NCBI Genbank and protein sequence databases. Refinement of results using different parameters e.g. organism, date, molecule type etc. Integration of gene and protein information. Database identifiers and formats. Structure and comparison resources in the MMDB database
Outcome: Knowledge of accessing sequence and structure of different biological molecules.

PRACTICAL 06
Objective: Pair-wise sequence comparisons – effect of sequence similarity, type of algorithm and scoring parameters on the alignment
Methodology: To understand the essential differences between local and global alignments for similar and divergent sequences using Emboss Needle and Waterman programs. Varying the default parameters for local and global sequence alignments.
Outcome: To understand the effect of differential gap scoring for change of global alignments into local and vice versa in divergent sequences.

PRACTICAL 07
Objective: To carry out a similarity search for a specific query protein. Evaluating the statistical significance of the match when using a short string versus full sequence. Effect of presence of low complexity regions in the sequence and filtering
Methodology: Demonstration of effective database (e.g. nr sequence, pdb, patent etc.) searching techniques using filters (e.g. organism name, keyword etc.) and available parameters (e.g. sequence range, pairwise alignment, etc.) using the Blast interface.
Outcome: Comprehensive understanding of meaning and use of an effective combination of filters and adjustment of parameters for Blast search.

PRACTICAL 08
Objective: Anatomy of a blast output
Methodology: Understanding the graphical output, including conserved domain search. Integration of graphical output with hit table and pairwise alignments. Alignment scores and statistical significance.
Outcome: To become familiar with the various parts of a Blast output. To understand scoring of alignments and be able to download or construct multiple sequence alignments, distance trees, organism reports using Blast.

PRACTICAL 09
Objective: Multiple Sequence Alignment editing - tools and resources
Methodology: Generating a graphical summary and hit table using BLAST for a query sequence, using BioEdit to annotate, edit and obtain significant information from the MSA.
Outcome: Ability to visualize, evaluate and correct a multiple sequence alignment

PRACTICAL 10
Objective: Phylogenetic Analysis-Tools and Resources
Methodology: Generation and Annotation of phylogenetic Trees using BioEdit and FigTree softwares.
Outcome: Working Knowledge of the tools and features of important softwares, comprehensive understanding of evolutionary relationships deduction, significance of clades, nodes, leaves and distances from the generated tree.