

COLLEGE OF FISHERIES, KISHANGANJ
BIHAR ANIMAL SCIENCES UNIVERSITY, PATNA

Lecture Plan
FBT 505 (1+1) Bioinformatics Tools for Fisheries
Theory

S. No.	Topic	No. of Classes
1	Basics of Bioinformatics: Resources, applications, and operating platforms (Linux/Windows), Primary Databases: Nucleotide (GenBank, ENA) and Protein sequence databases (UniProt)	1
2	Secondary and Structure Databases (PDB); Overview of analysis packages	1
3	Sequence Alignment Principles: Dot Matrix and scoring matrices (PAM, BLOSUM)	1
4	Database Searching: Sequence retrieval and Pairwise alignment using BLAST, Multiple Sequence Alignment (MSA): Tools and significance	1
5	Sequence retrieval, quality assessment, and assembly of Sanger sequencing reads, Identification of ORF (Open Reading Frames)	1
6	Identification of cis-acting regulatory elements and signal sequences	1
7	Data analysis tools for SNP (Single Nucleotide Polymorphism) and ESTs	1
8	Evolution of Genome: Basic forces of evolution (mutation, selection, drift)	1
9	Genetic variation and divergence of populations, Phylogenetic Species Concept: Principles and importance	1
10	Estimation of divergence time and molecular clocks	1
11	Phylogenetic Analysis: Building and interpreting trees, Phylogenetic trees, Cladistics, and the concepts of Monophyly, Paraphyly, and Polyphyly.	2
12	Principles and methodology of UPGMA and Neighbour-Joining (NJ) for tree reconstruction, Fundamental principles of Maximum Parsimony and its application in evolutionary studies.	2
13	Concepts of Maximum Likelihood and Bayesian Inferences for complex data sets, Methodology of Tree comparisons, Statistical tests, and Parametric Bootstrapping.	2
14	Interpretation of phylogenetic results, identifying limitations, and case studies in Fisheries.	1
	Total	17

Practical

S. No.	Topic	No. of Classes
1	Sequence retrieval from database	1
2	Refining search criteria using different parameters	1
3	Pairwise Sequence Alignment (BLAST)	1
4	Multiple Sequence Alignment (MSA) by Clustal W	1
5	Identification of ORF (Open Reading Frames)	1
6	Primer designing	1
7	Restriction Site Identification	1
8	Protein Structure prediction using software	1
9	Construction of Phylogenetic tree	1
	Total	09

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