#### **BACHELOR OF SCIENCE**

## 6<sup>th</sup> SEMESTER

## DISCIPLINE SPECIFIC ELECTIVES (DSEs)

**BT620D1: BIO-TECHNOLOGY: ELEMENTARY BIOSTATISTICS AND BIOINFORMATICS** 

**CREDITS: THEORY – 4, PRACTICAL – 2(4+2)** 

#### **OPTION-I**

#### THEORY (4 CREDITS: 60 HOURS)

MAXIMUM MARKS: 60, MINIMUM MARKS: 24

**Objective:**This course introduces students to basic statistical concepts involved in biology and illustrates the power of computing in modern biology.

# Unit-1 (15 HOURS)

Introduction to statistics; Understanding of data & variables (with their types and categories); Data production – experiments vs sample surveys, principles & types of experimental design, idea of randomization, detailed account of sampling designs; Graphical representation of data (bar graph, pie chart, stemplot, histogram).

## **Unit – 2 (15 Hours)**

Measures of central tendency (mean, median, mode) & dispersion (quartiles, standard deviation) with their properties and comparison; Understanding of correlation, least-squares regression & scatterplots; Overview of probability & probability rules, statistical inference with emphasis on confidence intervals and p-values.

### Unit – 3 (15 Hours)

Introduction to bioinformatics; Scope and application of bioinformatics; Introduction to biological databases (types-sequence, structure & pathway), Nucleic acid databases (NCBI, GenBank, EMBL), Protein databases (PIR, Swiss-Prot, PDB); Introduction to PubMed.

### Unit – 4 (15 Hours)

Sequence similarity and alignment – local & global alignment, pairwise & multiple sequence alignments, BLAST, FASTA & CLUSTALW; Basic idea of phylogenetic tree; Protein structure analysis - levels of protein structure, primary structure analysis (protparam), secondary structure predictions (ExPASy, JPred), tertiary structure prediction methods (homology, threading).

# PRACTICALS (2 CREDITS: 60 HOURS) MAXIMUM MARKS: 30, MINIMUM MARKS: 12

- 1. Use of excel for calculating: Mean, Mode, Median.
- 2. Use of excel for drawing, histogram, bar-chart &piechart.
- 3. Use of NCBI, GenBank, EMBL, SwissProt, PDB, TREMBL.
- 4. Pairwise and multiple sequence alignment (BLAST and ClustalW)
- 5. Use of protparam, Expasy and JPred.

# **BOOKS RECOMMENDED**

- 1. Basic Biostatistics: Bert Gurtsman
- 2. Bioinformatics: Methods and Applications: Genomics, Proteomics and Drug Discovery, -Rastogi, Prentice Hall India Learning Private Limited.
- 3. Essential Bioinformatics, Jin Xiong, Cambridge University Press.
- 4. *Bioinformatics Principles and Applications*, Ghosh, Z. and Mallick, B.,-Oxford University Press (India).

# **Expected Learning Outcomes:**

- 1. Understanding of basic statistical methods as applied to biological sciences.
- 2. Concept of Bioinformatics, types of data and databases.
- 3. Understanding of tools used for data analysis and prediction of different levels of protein structure.