

Course code	Course Title	C	H	I	E	T
17P4BMC9	BIostatistics and Bioinformatics	5	6	25	75	100

Objective:

1. To focus statistical techniques to analyze the biological data
2. To apply information technology to analyze the biological information

Learning outcome:

Equipped the students to carry out research projects in the field of biology

UNIT-I (15hr)

Introduction; definition, characteristics, scope, importance and limitations. Terms of statistics: population, sample, data, parameters, attributes and variables. Descriptive and inferential statistics. Steps in designing an experiment; sampling methods in the collection of data; frequency distribution; Tabulation, diagrammatical and graphic presentation of data.

UNIT-II (30hr)

Measures of central tendency (Arithmetic mean, mode and median) Measures of dispersion (mean deviation and standard deviation). Probability, definition, importance, explanation and application in biology. Probability distribution (Normal & Binomial). Correlation: types and scatter diagram method. Regression: Aim, equation and coefficient; Tests of significance F and χ^2 tests; A brief account on test of hypothesis.

UNIT III(5hr):

Definition and objectives of bioinformatics; Basic components of computers (CPU, RAM, ROM, Processes) –Internet, website.

UNIT IV (20hr):

Genome organization - Genome analysis ---gene sequencing methods (Maxam & Gilbert; Sanger method); proteome analysis (2D PAGE, MALDI-TOF); Biological Data bases --- types---- classification ---- Nucleic acid data bases (GenBank, EMBL, DDBJ) ----Protein data

bases (SWISS-PROT, TrEMBL, PIR, GSDB, SCOP, CATH) ---- literature data bases (PUBMED, AGRICOLA) ; Bioinformatics servers ---- NCBI, GENOMENET

UNIT V (20hr):

Sequence analysis tools (FASTA, BLAST) ---- Sequence alignment (Local & Global; Pair wise & Multiple) ---- Genetic algorithm (Needleman—Wunch ; Smith & Waterman) --- Scoring matrices (PAM & BLOSUM) ---- Phylogenetic analysis --- phylogenetic trees (Clustal W); Molecular visualization tool (RASMOL) --- prediction of protein structure. A brief account on drug designing

References:

1. Rajadurai, M. 2010. Bioinformatics- a practical manual. PBS Book Enterprises. pp.158
2. Mani, K and Vijayaraj, N. 2002. Bioinformatics for beginners. Kalaikathir Achchagam. Coimbatore. Tamil Nadu. India. pp275.
3. Attwood, T.K., Parry-Smith, D.J. and Phukan, S. 2008. Introduction to bioinformatics.. Pearson Education Pvt.Ltd., New Delhi. India. pp218
4. Attwood, T.K. and Parry-Smith, D.J. 2002. Introduction to bioinformatics.. Pearson Education Pvt.Ltd.. New Delhi. India. pp1-237
5. Malcom Campbell, A and Heyer, L.J. 2004. Discovering, Genomics, Proteomics and Bioinformatics. Pearson Education Pvt.Ltd.. New Delhi. India. pp352
6. Gomase, V.S and Chokhale, N.J. 2009. Proteomics. Himalaya Publishing House. pp360
7. Bal, H.P. 2007. Bioinformatics-Principles and Applications . Tata McGraw-Hill Publishing Company Ltd. New Delhi. India. pp217
8. Arumugam, N, Gopi, A, Meena, A, Sunderalingam, R and Kumaresan, V. 2014. Biostatistics, Computer applications and Bioinformatics. Saras Publication . Nager koil, Tamil Nadu, India. pp 458
9. Khan, I.A. and Khanum, A 1994. Fundamentals of Biostatistics , Ukaaz publications , Hyderabad , Andhrapradesh –India .
10. Pranab kumar Banerjee, 2004, Introduction to Biostatistics (A Text book of Biometry). S. Chand & Company Ltd. Ram nagar , New Delhi.
11. <https://WWW.biostat.washington.edu>
<https://WWW.omicsonline.org>.

Practicals:

1. Calculation of standard deviation for different plant sample –leaf length & pod length.
2. Chi –square test and students “t” test.
3. Problems on probability
4. Graphic representation of data. Bioinformatics:
5. Component of computer.
6. Creation of table & graph using Ms office.
7. Sequence alignment using BLAST.
8. Analysis structure of nucleic acid & protein using Rasmol.
9. Construction of phylogenetic tree.