

W.e.f 20AH Batch

OBJECTIVES: To enable the students to –

- Opt the appropriate research and hypothesis in a project
- Know the various statistical methods to evaluate the data\
- Acquire the basic concepts in bio-informatics
- Comprehend the knowledge about the sequence alignment and analysis

I. Learning outcomes:

1. Will be opt the appropriate research design and develop appropriate research hypothesis for a research project
2. Described the appropriate statistical methods required for a particular research design
3. Can be introduced to the basic concepts of Bioinformatics and its significance in biological data analysis
4. Would be provided knowledge about the basics of sequence alignment and analysis

UNIT-I: Data

1. Data types, collection of data, classification and tabulation.
2. Measures of central tendencies: Mean, median and mode.
3. Measures of variation: Range, quartile deviation, mean deviation and standard deviation. Coefficient of variation.
4. Probability, Addition and Multiplication theories, conditional probability and probability distributors. Binomial, poisson and normal distribution.
5. Correlation and linear regression. Regression: Regression coefficients and properties.
6. Small sample tests- t, F and chi square tests.
7. ANOVA: one way and two-way classifications.

UNIT – II: Origin of bioinformatics

1. Disciplines of bioinformatics, transcriptomics, functional genomics, structural genomics.
2. Metabolomics, pharmaco-genomics.
3. Structure prediction, drug design and Microarrays.

UNIT – III: Genome projects

1. General introduction to genome projects (Rice and Mycobacterium tuberculosis genome project).
2. Special emphasis on Human Genome Project (HGP).
3. Science behind HGP, benefits of HGP, ELSI of HGP in use of genetic information.
4. Genetic testing standard, quality and commercialization.

UNIT – IV: Biological Databases

1. Introduction of database (DB), need, organization, search of DB.
2. An over view of biological databases - NCBI, EMBL, DDBJ, SWISS-PROT, PDB, KEGG.
3. Decoding of the genome (Nathan blow study).
4. Ribosomal bar codes.
5. Molecular signatures.

UNIT V: Database querying

1. Database querying with NCBI using key words, sequences (proteins and genes), finding similarities, identifying genes and proteins from different organisms.
2. Sequence alignment: Introduction, significance of sequence alignments and use of dot matrices.
3. Pair wise and multiple sequence alignment (MSA) using Clustal programs.
4. Sequence analysis: concepts of sequence analysis and their importance.
5. BLAST. Blastn, blastp, blastx, tblastx,
6. Output analysis matrix BLOSSUM, PAM, e-value.
7. Proteomics - Introduction, principle, technique, 2-D data base.
8. Gel analysis, post gel analysis, MALDI-TOF.
9. Significance and applications of proteomics in modern biology.

REFERENCES

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4. Primrose SB. Principles of Genome Analysis: a guide to mapping and sequencing DNA from different organisms. 2nd Ed. 1998. Blackwell Science: Oxford. ISBN 0-632-04983-9.
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6. Developing Bioinformatics Skills. Alfonso Valencia and Blaschke. L (2005) Oreille.s Publication.
7. Bioinformatics sequence, structure and data banks ed. By Des Higgins Willie Taylor. (2006).
8. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins" (Andreas D. Baxevanis, B. F. Ouellette), Paperback, 2nd ed., 470 pp., ISBN: 0471383910, Publisher: Wiley, John & Sons, Inc., Pub.

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