DEPARTMENT OF BIOINFORMATICS

Syllabus for Pre-Registration Qualifying Entrance Examination for Ph.D. Programme

PART B - BIOINFORMATICS

UNIT-I: INTRODUCTION TO COMPUTERS AND OPERATING SYSTEMS

Computer System: Storage devices, Hardware, Software, Input devices, Output devices; Processing Unit: Types of processing, Modern Computers; Operating system: Windows, Linux, UNIX commands; Internet: Web browsers, Internet protocols; Data Security; Antivirus & Firewall.

UNIT-II: MOLECULES OF LIFE

Principles of Genetics, Cell cycle and Cell division, Molecular control of cell cycle; Structure and functions of cell organelles, Nucleus organization and nuclear transport; Structure and dynamics of Biological Membrane; Chemical basis of heredity; Informational molecules and Central Dogma: Structure of DNA, RNA and Protein, Multiple forms of DNA (A, B, Z); DNA Repair mechanisms, DNA Replication in Prokaryotes and Eukaryotes; Mitochondrial DNA Replication; Mutations and Mutagenesis.

UNIT-III: GENOMICS AND PROTEOMICS

Genome Organization, Transcription and Translation in Prokaryotes and Eukaryotes, Genetic code & Wobble Hypothesis, Regulation of gene expression; Post-Transcriptional Modification, Protein synthesis; Recombinant DNA Technology, Protein Biology: Protein structure and function, folding, modification and processing; Protein-Protein & Protein DNA Interactions. Genome sequencing methods, Strategies for genome sequencing; RFLP, RAPD and AFLP techniques.

UNIT-IV: BIOINFORMATICS DATABASES AND RESOURCES

Sequence Analysis: MSA, ClustalW, Phylip, BLAST, FASTA, ExPASY Tools; Databases: Structure databases – PDB, MMDB, CATH, SCOP, PDBsum; Sequence databases – NCBI, DDBJ, EMBL, Uniprot, Prodom, NEBcutter - Primer3 - Visualization tools - Modeller -Ramachandran Plot.

UNIT-V: DRUG DESIGN AND STRUCTURE ACTIVITY RELATIONSHIP

Homology modeling, Molecular Docking, Structure based drug design, Protein-ligand Interactions, Protein-Protein Interactions, Force fields, inter and intra-molecular interactions, Molecular Dynamics Simulations, QSAR, QSPR, Active site analysis, Combinatorial Library Design and Atomic constant, Pharmacophore, Virtual Screening and Hit lead optimization.

References:

- 1. Arthur M. Les-k (2014) Introduction to Bioinformatics; Oxford University Press.
- 2. Baxevanis, A.D. and Francis Ouellellette, B.F., (2009) Bioinformatics- a Practical Guide to the Analysis of Genes and Proteins; Wiley India Pvt Ltd.
- 3. David C. Young (2009) Computational Drug Design: A Guide for Computational and Medicinal Chemists; Wiley
- 4. Engelbert Buxbaum, & Springerlink Online Service (2015). Fundamentals of Protein Structure and Function. Cham: Springer International Publishing
- 5. James D. Watson, A. Baker Tania, P. Bell Stephen, Gann Alexander, Levine Michael, Losick Richard (2016) Molecular Biology of the gene; Pearson Publishers 7th edition
- 6. P.B. Kaufman, W. Wu, D. Kim and L. J. Cseke (2011) Molecular and Cellular methods in Biology and Medicine; CRC Press, Florida.
- Shortliffe EH and Ciminio JJ (2014) Biomedical Informatics: computer applications in Health care and Biomedicine (Health Informatics); Springer-Verlag London 4th edition.
- 8. Yashavant P. kanetkar (2009) Unix shell programming -- BPB Publication, Delhi.