

CENTRE FOR BIOINFORMATICS
M. D. UNIVERSITY, ROHTAK

PRE- PH.D. SCHEME OF EXAMINATION

S.No.	Paper Code	Paper title	Internal Evaluation	External evaluation	Total
1	BINPH1	Computational and Systems Biology	20	80	100
2	BINPH2	Structural Bioinformatics	20	80	100
3	BINPH3	Research methodology	20	80	100
4	BINPH4	Review Writing and Presentation	-	75	75
5	BINPH5	Seminar	25	-	25
				Total	400

Syllabus for Pre. Ph.D. (Bioinformatics)

Computational & Systems biology

Theory Marks:80
Internal assessment:20

Note for Examiner:Examiner should set 2 questions from each unit. Each question shall carry 16 marks. Students will have to attempt atleast one question from each unit.

Unit-1 Biological data

Types of biological data (various omics)

Biological Databases Nucleic acid and protein sequence and protein structure databases

Overview of available Bioinformatics resources on the web

Unit-2

DNA sequence analysis

Sequence annotation and sequence analysis-Phylogeny of gene (blast, fasta, HMMer) and residue conservation. Primer design and Tm Calculation, DNA Restriction pattern analysis.

Condon bias and its effect on the protein expression with reference to various expression system.

Unit-3

Bioinfo tools 2 Protein sequence and structure insights (PSSI)

X-ray, NMR, Comparative modeling, ab initio, threading methods.

Structure refining techniques Energy minimization approaches (Steepest descent, Conjugate gradient etc), Basis of Molecular dynamics simulations and its application.

Unit-4

Introduction to Systems Biology-I (SB)

Principles of Networks – Graph Theory and information theory of molecular systems Types of biological networks.

Unit-5

Basics of Systems Biology-II (SB)

Biological Network Databases Genomic networks (Gene regulation) Protein-protein interaction networks; Biochemical flux networks

Students are advised to consult relevant journal articles and reviews to gather the recent information on the above mentioned topics

Research Methodology

Theory Marks:80
Internal
assessment:20

Note for Examiner:Examiner should set 2 questions from each unit. Each question shall carry 16 marks. Students will have to attempt atleast one question from each unit.

Unit-1

Colloidal solutions of biopolymers and their electrochemical properties, Hydrodynamic properties;

Viscosity, diffusion etc of biopolymers; Molecular weight determination, osmotic pressure, reverse osmosis and Donnan effect, Structure of biomembranes and heir electrochemical properties, membrane potential, action potential and propagation of impulses; PPI

Unit-2

Electrophoresis; different methods of electrophoresis for protein, nucleic acids, small molecular weight compounds and immune precipitates (Immuno electrophoresis). Peptide mapping and combination of electrofocussing and SDS-PAGE. Blotting techniques (Northern, Southern and western blotting); RT-PCR

Unit-3

Theory of centrifugation and application to biological systems. Rotors angle/vertical/zonal/continous flow centrifuge, differential centrifugation density gradient centrifugation. Ultra centrifugation principle and application. Chromatography – adsorption, affinity, partition, Ion-exchange, gelpermeation, GLC, TLC, RPC, HPLC etc.

Unit -4

Introduction to principles and applications of (a)Spectroscopic methods (UV, Vis, IR, Fluorescence, ORD, CD, & PAS) (b)NMR, ESR & Mass spectrometry, Use of radioactive and stable isotopes and their detection in biological systems.

Unit-5

Automatic analyzer for amino acids, protein sequencer, peptide synthesizer & nucleic acid synthesizer. Cell sorters and their applications. Theory of lyophilization and its applications to biological systems. Introduction to principles and working of light and electron microscope.

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Structural Bioinformatics

Theory Marks:80

Internal assessment:20

Note for Examiner:Examiner should set 2 questions from each unit. Each question shall carry 16 marks. Students will have to attempt atleast one question from each unit.

Unit-1

Protein Structure Prediction

Introduction, Protein Stability and Folding, Application of Hydrophobicity, Superposition of Structures, DALI methods, Evolution of Protein Structures, CASP, Secondary Structure Prediction, Homology Modelling, Fold Recognition, ROSETTA, LINUS.

Unit-2

Molecular Modeling and Dynamics

Introduction, Molecular Dynamics using simple molecules, Signification of Times steps & Temperature Conformational energy calculations and molecular dynamics, Docking by Energy minimization, Ramachandran Plot.

Unit-3

Drug Discovery and Development

Drug Discovery Cycle, The Lead compound, Pharmacophore, Bioinformatics in drug discovery and development, chemical databases, ADME and Toxicity, Virtual Screening, Molecular Docking, Structure and Ligand Based Drug Designing, Case studies.

Unit-4

Structural Bioinformatics Tools

Tools for Molecular Visualization and Analysis:RASMOL, PYMOL, VMD, SWISS-PDB Viewer. Molecular Modeling and Docking: Swiss-Model, Arguslab, Hex, DOCK and Autodock. Online Tools: Biology Workbench, Marvin Sketch, Chemskech, pubchem.

Unit-5 Quantitative tools

Introduction to QSAR methodologies, Types of QSAR methods – 2D, 3D, 4D, 5D and 6D- QSAR methodologies, Descriptors classification, Application of QSAR in molecular design.

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