KURUKSHETRA UNIVERSITY, KURUKSHETRA

Curriculum for B.Sc. (Bioinformatics) Semester System

Scheme of Examination (w.e.f. 2011-12)

B.Sc. 1st year

SEMESTER – I

Paper No.	Title of paper	Max. Marks	Internal Assess.	Total Marks	Time
I	Introduction to Bioinformatics	40	10	50	3 Hrs
II	Computer Fundamentals	40	10	50	3 Hrs
III	Statistical Methods (I)	40	10	50	3 Hrs
IV	Introduction to Databases	40	10	50	3 Hrs
V	Cell Biology	40	10	50	3 Hrs
VI	Biochemistry- I	40	10	50	3 Hrs
	Practicals (XIII, XIV & XV will start in semester-III and the exam will be conducted at the end of Sem-II)				
SEMESTER - II					
VII	Biochemistry-II	40	10	50	3 Hrs
VIII	Genetics	40	10	50	3 Hrs
IX	Operating System & Programming in C	40	10	50	3 Hrs
X	Statistical Method-II	40	10	50	3 Hrs
XI	Introduction to Genome Projects	40	10	50	3 Hrs
XII	Information Networks	40	10	50	3 Hrs
XIII	Practical (Based on Paper I to IV)	100	-	100	4 Hrs
XIV	Practical (Based on paper V to VIII)	100	-	100	4 Hrs
XV	Practical (Based on paper IX to XII)	100	-	100	4 Hrs

Note: Practical examinations will be held at the end of even semesters.

B.Sc. 2nd year

SEMESTER – III

Paper No.	Title of paper	Max. Marks	Internal Assess.	Total Marks	Time
XVI	Hindi/Sanskrit (common with B.Sc. General Part II compulsory)	40	10	50	3 Hrs
XVII	Object-oriented analysis & design models	40	10	50	3 Hrs
XVIII	Probability	40	10	50	3 Hrs
XIX	Techniques in Biochemistry	40	10	50	3 Hrs
XX	Nucleotide Metabolism & Bioenergetics	40	10	50	3 Hrs
XXI	Working with a single DNA Sequence	40	10	50	3 Hrs
XXII	Working with a single protein Sequence	40	10	50	3 hrs
	Practicals (XXIX, XXX & XXXI will start in semester-III and the exam will be conducted at the end of Sem-IV)				
SEMESTER - IV					
XXIII	Object-Oriented Programming in C++	40	10	50	3 Hrs
XXIV	Sampling Distribution	40	10	50	3 Hrs
XXV	Molecular Biology	40	10	50	3 Hrs
XXVI	Immunology	40	10	50	3 Hrs
XXVII	Sequence Comparison	40	10	50	3 Hrs
XXVIII	Sequence Analysis	40	10	50	3 Hrs
XXIX	Software Lab-II	100	-	100	4 Hrs
XXX	Practical-3	100	-	100	4 Hrs
XXXI	Practical-4	100	-	100	4 Hrs

Note: Practical examinations will be held at the end of even semesters.

B.Sc. 3rd year

SEMESTER-V

Paper No.	Title of Paper	Max. Marks	Internal Assessment	Total Marks	Time
XXXII	Building and Interpreting Multiple Sequence Alignment	40	10	50	3 Hrs
XXXIII	Editing and publishing Alignments	40	10	50	3 Hrs
XXXIV	Applied Statistics	40	10	50	3 Hrs
XXXV	Sampling Techniques	40	10	50	3 Hrs
XXXVI	Recombinant DNA Technology	40	10	50	3 Hrs
XXXVII	Plant Biochemistry	40	10	50	3 Hrs

(Practicals for Paper No. XLIV, XLV & XLVI of semester VI will start in Semester-V and exam will be conducted at end of Semester-VI)

SEMESTER-VI

Paper No.	Title of Paper	Max. Marks	Internal Assess.	Total Marks	Time
XXXVIII	Database Management Systems	40	10	50	3 Hrs
XXXIX	Programming in JAVA	40	10	50	3 Hrs
XL	Phylogenetics	40	10	50	3 Hrs
XLI	Structural Analysis: Working with RNA and Protein 3-D Structures	40	10	50	3 Hrs
XLII	Clinical Biochemistry	40	10	50	3 Hrs
XLIII	Nutritional Biochemistry	40	10	50	3 Hrs
XLIV	Software Lab – III	100	-	100	4 Hrs
XLV	Practical-V	100	-	100	4 Hrs
XLVI	Practical-VI	100	-	100	4 Hrs

SEMESTER- I

Paper I Introduction to Bio-informatics

Marks: 40
Internal Assessment: 10
Time 3 hrs

NOTE

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2. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. Each question will carry 10 marks.
3. As far as possible the question will be of short answer type.
4. Each question should be divided into parts & the distribution of marks be indicated part wise.

UNIT-I

What is Bio-informatics- Its Definitions, Introduction, History.
Bioinformatics - Objectives, Applications, Its need, Scope, Careers.
Bioinforrnatics scenario in India & the rest of the world.
Sequences used in Bioinforrnatics- DNA, Protein, RNA.
Dawn of sequencing.
Brief understanding of the DNA, Protein, RNA
molecules. Study of Bioinforrnatics at Molecular level.

UNIT-II

Sequence analysis- a brief study.
Homology. Analogy, Similarity, Identity.
Prokaryotes- Smaller bugs with simple genes.
Eukaryotes- Bigger-bugs with complex genes.
Difference between prokaryotes &
Eukaryotes. Study of Genbank entry for
Prokaryotic gene. Study of Genbank entry for
Eukaryotic gene. Methods for retrieval of
Genbank entries.

Paper II Computer Fundamentals

UNIT-I

Marks: 40
Internal Assessment: 10
Time 3 hrs

Computer Fundamentals:

History of computers, Generations and types of computers, Classification of computers, Hardware and Software concepts, Functional components of a digital computer, Limitations and Capabilities of computers, RAM, ROM, Storage devices, I/O devices

NOTE

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UNIT-II

Problem Solving with Computers:

Problem analysis with example, Algorithms, pseudocodes, Decision tables, and Flowcharts, Structured programming concepts, Top down and bottom up Approaches, Modular programming concepts. Applications of Computers in Bio-informatics

Operating Systems & Internet: Features of commonly used operating systems e.g. DOS, Windows, UNIX,.and LINUX. Introduction to Internet.

Paper III Statistical Methods- I

NOTE

Marks: 40
Internal Assessment: 10
Time 3 hrs

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2) Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. Each question will carry 10 marks.
3) As far as possible the question will be of short answer type.
4) Each question should be divided into parts & the distribution of marks be indicated part wise.

Paper IV Introduction to Databases

UNIT-I

Marks: 40
Internal Assessment: 10
Time 3 hrs

Databases- Introduction, Functions, Types.
Data, Data mining, Data integration.
What types of data stored?
Data retrieval system.

NOTE

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4. Each question should be divided into parts & the distribution of marks be indicated part Wise.

UNIT-I

An introduction, types of data, collection, classification and tabulation of the primary data, secondary data, discrete data and continuous data, diagrammatic and graphical representation of grouped data, frequency distribution (univariate & bivariate), cumulative frequency distribution and their graphical representation, histogram, frequency polygon and ogives.

UNIT-II

Concept of central tendency or location and their measures, partition values: quartiles, deciles and percentiles, dispersion and their measures, relative dispersion.

Moments (single & double variables) and their relationships, Karl pearson's, Beta & gamma coefficients, Charlier's checks and Sheppard's correction for moments for grouped data (without derivation), skewness & kurtosis and their measures

Biological Databases - Nucleotide & Protein databases.
Nucleotide databases- DDB], EMBL, GenBank.
Protein databases- SWISS-PROT.
Study of Gene centric databases.
NCBI- The National Centre for Biotechnology Information.

UNIT-II

EMB-net The European Molecular Biology Network.
Virtual tourism.
Formats in Bioinformatics. Searching
through Pubmed/Medline. EXPASY.
Biological sequence & structure deficiet.

Paper V Cell Biology

NOTE

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3. As far as possible the question will be of short answer type.
4. Each question should be divided into parts & the distribution of marks be indicated part Wise.

Marks: 40
Internal Assessment: 10
Time 3 hrs

UNIT-I

Cells: Cellular Dimensions, Structure of Prokaryotic and Eukaryotic Cells. Differences between plants animal cells.

Viruses - Parasites of Cells

a) Cell Wall- Structure and function of bacterial and plant cell wall.
b) Plasma Membrane - Fluid Mosaic Model, Various Models of transport across the membrane, mechanism of active and passive transport, endocytosis and exocytosis.

UNIT-II

Paper VI Biochemistry I

NOTE

Marks: 40
Internal Assessment: 10
Time 3 hrs

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ULTRASTRUCTURE & FUNCTIONS OF THE FOLLOWING CELL ORGANELLES

A brief account of the subcellular organelles (Endoplasmic Reticulum, Mitochondria, Golgi complex. Ribosome, Lysosomes, Plastids, Nucleus & Microbodies).Cytoskeleton (Microtubules, Microfilaments. intermediate filaments) Cilia & Flagella.

Cell division- Mitosis, Meiosis, An introduction to cell cycle.

Proteins: Classification based on structure and function. Structural organization of proteins: Primary structure;
Secondary structure- alpha- Helix, beta- pleats and beta- turn

Tertiary structure- myoglobin and lysozyme etc.

Quaternary structure- hemoglobin.

Forces stabilizing different structural levels.

Amino acid analysislN-terminal amino acid analysis- Sanger's method, Edmann's degradation, dansyl chloride and dabsyl chloride
Lipids: Introduction and Classification - simple and complex lipids.
Fatty acids - structure and nomenclature, soap value, acid value, iodine number, rancidity.
Essential fatty acids. A general account of structure and function of triacylglycerols, phospholipids, glycolipids, sphingolipids, steroids, bile acids, bile salts and terpenes
Nucleotides and Nucleic acids:
Building blocks: bases, sugars and phosphates.
Structure and nomenclature of nucleosides and nucleotides; polynucleotides, DNA (A, B, Z-

UNIT -I

Biomolecules: Introduction, important features, covalent and non-covalent interactions

Carbohydrates: Introduction and Biological Significance.

Definition and classification: Monosaccharides; families of monosaccharides; simple aldoses and ketoses, Configuration and Conformation, Stereoisomerism/ Asymmetric centres, Fischer and Haworth projection formula, pyranose and furanose ring forms, reducing and non-reducing sugars, sugar derivatives viz. sugar alcohols, amino sugars. deoxy sugars, acidic sugars, Glycosidic bond

Disaccharides and Oligosaccharides: Definition, structure and function of important di and oligosaccharides viz. lactose, sucrose, maltose, raffinose, stachyose, verbascose etc.

Polysaccharides: Homo and Hetero polysaccharides, storage polysaccharides: Starch and Glycogen. Structural polysaccharides: Cellulose and Chitin .. A brief account of structure and function of Mucopolysaccharides/ Glycosaminoglycans (Hyaluronic acid, Chondroitin sulphate), Glycoproteins and Proteoglycans.

Amino acids, Peptides and Proteins: Classification and structure of amino acids, essential amino acids, rare and non-protein amino acids, optical and chemical properties of amino acids; acid-base behaviour/zwitterions; pKa value and titration curve.

Peptide bond - nature and characteristics. Definition; structure and function of some biologically important peptides.

DNA) and RNA (rRNA, mRNA, tRNA).
Properties of DNA - absorption, denaturation, renaturation, hybridization, Tm/Cot values.
Biologically important nucleotides and their functions - ATP, GTP, Coenzyme A, NAD, F AD and cAMP.

Semester II

NOTE

I. Seven Questions will be set in all.

Paper VII Biochemistry II

Marks: 40
Internal Assessment: 10
Time 3 hrs

2. 2. Q. No. I which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be

UNIT II

set section wise with 3 questions from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. Each question will carry 10 marks.

3. As far as possible the question will be of short answer type.
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UNIT-I

Enzymes: Introduction, active site, energy of activation, transition state hypothesis, lock and key hypothesis, induced fit hypothesis.

Enzyme classification (Major classes only)

Enzyme Kinetics - substrate concentration, Km, Vmax, MM equation, Lineweaver Burk plot/ Double reciprocal plot. Effect of pH, temperature on enzyme activity.

Allosteric enzymes (A brief account)

Enzyme Inhibition - Competitive, non-competitive and uncompetitive inhibition

Vitamins and Hormones: Introduction. Types of vitamins - structure of water soluble vitamins and their coenzyme, derivatives, Fat soluble vitamins
Deficiency symptoms and dietary sources.

Steroid Hormones: structure and importance

Peptide Hormones: structure and function of important peptide hormones.

UNIT -II

Metabolism: General introduction, catabolism and anabolism

Carbohydrates metabolism: Glycolysis, Tricarboxylic acid cycle, Gluconeogenesis

Glycogenolysis, glycogen synthesis and their regulation,

Lipid Metabolism: ~- oxidation of fatty acids. Degradation of Triacylglycerols.

Synthesis of Fatty acids.

Amino acid Metabolism: Transamination, oxidative deamination, decarboxylation. Urea cycle.

Different classes of oxidation and synthesis of amino acids.

Glycogenic and ketogenic amino acids.

Paper VIII Genetics

UNIT-I

Marks: 40
Internal Assessment: 10
Time: 3 hrs

Genetics, Elements of heredity and variations, The Varieties of gene interactions Linkage and recombination, coupling and repulsion hypothesis,crossing over and chiasma formation, gene mapping

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3) As far as possible the question will be of short answer type.
4) Each question should be divided into parts & the distribution of marks be indicated part Wise.

Sex determination and its mechanisms, male and female heterozygous system. Genetic balance system. Role of Y chromosomes, male haploidy, cytoplasmic and environmental factors, role of hormones in sex determination

Sex linked in heritance, haemophilia and color blindness in man, eye color in *Drosophila.* Sex limited and sex influenced inheritance.

Extrachromosomal and Cytoplasmic inheritance

1. Kappa particles in paramecium
2. Shell coiling in snails
3. Milk factor in mice

Paper IX Operating System Internet & Programming in C

NOTE

Marks: 40
Internal Assessment: 10
Time 3 hrs

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3) As far as possible the question will be of short answer type.
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UNIT-I

Character Set, Identifiers & keywords, Constants & variables, data types, expressions & statements. Arithmetic, Logical, Relational and bitwise operators and their hierarchy,

UNIT-II

Assignment and conditional operators. Input / Output statements, control statements-if-else, switch, break, continue & loops. Arrays, functions, pointers, structure & unions. File handling, Implementation of data structures e.g. Array, Stack, Queue, Linked list and tree

Multiple alielism: Eye colour in *Drosophila,* A,B,O blood Groups in man

UNIT-II

Human Genetics - Human karyotype, chromosomal abnormalities involving autosomes and sex chromosomes, monozygotic and dizygotic twins.

Inborn Errors of Metabolism in man (Alcaptonuria, phenylketonuria, albinism, and sickle cell anemia.Principles of population genetics, Hardy Weinberg Principle

Mutations - Molecular basis of Mutations, type of mutations: transition, transversion. frameshift, insertion, deletion, suppressor sensitive, germinal and somatic, backward and forward mutations, true reversion and suppression, dominant and recessive mutations, spontaneous and induced mutations

Mutagenecity Testing - Ames test, natural and artificial mutants

Genetic recombination and transposition.

Paper X Statistical Methods- II

Marks: 40
Internal Assessment: 10
Time 3 hrs

NOTE

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3) As far as possible the question will be of short answer type.
4) Each question should be divided into parts & the distribution of marks be indicated part wise.

UNIT-I

Mathematical expectation (single & bivariate), expectation of sum of random variables, expectation of independent random variables. Variance and covariance, moment generating and commulent generating function.

UNIT-II

Binomial distribution, poisson distribution as a limiting form of binomial distribution and properties of these distributions, moments, moment generating function, cumulant generating function. Geometric distribution and exponential distribution and properties of these distributions

Paper XI Introduction to Genome Projects

UNIT-I

Human genome project- Status & Size.
Genome browsing tools.
TIGR

Marks: 40
Internal Assessment: 10
Time 3 hrs

NOTE

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3. As far as possible the question will be of short answer type.
4. Each question should be divided into parts & the distribution of marks be indicated part wise.

Mapping & sequencing.
Physical & Genetic Maps.
Finding out more about biochemical pathways.

UNIT-II

Brief study of BLAST as data mining tool.
UCSC- Brief introduction.
Ensembl project.
Finding out more about protein structure. Finding out more about major protein families. Dawn of sequencing.

Paper XII

Information Networks

Marks: 40
Internal Assessment:10
Time 3 hrs

NOTE

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3. As far as possible the question will be of short answer type.
4. Each question should be divided into parts & the distribution of marks be indicated part-wise.

UNIT-I

Complete study of SWISS-PROT entry
EGF-R. Protein folding problem.
Role of Chaperons.
Final destination for each
protein. Diversity of folds &
function.
Genes, Chromosomes,Genetic codon, ORF.
Metaphor for biology or Rube Goldberg
invention.

UNIT-II

Computer Network.
Internet- Definition, History,
Applications. How do computers find
Each other? HTTP, HTML, URL's.
Web browsers.
Role of internet in Bioinformatics.
Post Translational Modification Databases PIR-RESID.

B.Sc. – II (Bioinformatics)

SEMESTER- III

Paper- XVII (OBJECT-ORIENTED ANALYSIS & DESIGN MODELS)

Max Marks= 40
Internal Assessment=10

NOTE: Seven Questions will be set in all. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

Time allowed = 3 Hrs

UNIT - I

Domain, analysis, Static models, Dynamic models, Concurrency models, Functional models, Overview of Booch's OOA and OOD approach.

UNIT – II

Introduction to UML classes and objects, encapsulation and information hiding, Data abstraction, message passing, links and associations, generalization and inheritance, and meta classes.

Suggested reading:

1. Object- oriented modeling and design, by Rambaugh, PHI.
2. Object- oriented analysis and design, by Booch, Grady, Addison Wesley.

Paper- XVIII (PROBABILITY)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven Questions will be set in all. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Definition of probability, classical and relative frequency and axiomatic approach to probability, Addition law of probabilities, Random experiment, discrete sample space, Events, operation of events, mutually exclusive and exhaustive of events.
Conditional probability, Multiplication law of probability, Independence of events, boole's inequality, Bay's theorem and it's application.

UNIT-II

Random variables, Definition of discrete random variable, Probability mass function, definition of continuous random variables, probability density function joint, Marginal and Conditional distribution and density functions, Independent Random variables.

Suggested reading:

1. Fundamentals of Mathematical Statistics: S.C.Gupta and V.K.Kapoor
2. Basic concepts of probability and statistics: J.L Hodges, E.L.Lehman.
3. An introduction to probability theory and mathematical statistics: V.K Rohtagi.

Paper XIX (TECHNIQUES IN BIOCHEMISTRY)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/ short answer type covering the entire syllabus will be compulsory. Remaining 6 questions will be set taking 3 questions from each section. Candidates will be required to attempt Q. No. 1 & four others selecting 2 questions from each section. All questions carry equal marks.

UNIT-1

HYDRODYNAMIC METHODS: Sedimentation: Sedimentation velocity including factors affecting it, Preparative & analytical centrifugation techniques.

pH & BUFFERS: Ionization of water. Weak acids & bases. pH, Buffers. Handerson-Hasselbalch equation & physiological buffers. Principles of glass & reference electrode; types of electrodes. Complications of pH measurement (dependence of pH on ionic strength, electrode contamination & sodium error). Use of pH paper & pH indicators.

RADIO ISOTOPIC TECHNIQUES: Types of radiations. Radio active decay. Units of radio- activity. Detection & measurement of radioactivity (methods based on gas ionization & liquid scintillation counting & quenching). Autoradiography: overview; nuclear emulsions used in biological studies. Isotopes commonly used in biochemical studies (^{32}P, ^{35}S, ^{14}C, ^{3}H). Track length of emitted particles and physical arrangements between emitting sources & emulsions. Biological hazards of radiation & safety measures in handling radioisotopes. Biological applications of radioisotopes.

UNIT-2

CHROMATOGRAPHY: General principles & applications of absorption; ion-exchange; thin layer; molecular sieve; hydrophobic; affinity; paper; gas- liquid & high performance liquid chromatography.

SPECTROSCOPIC TECHNIQUES: Beer- Lambert's law. Light absorption & its transmission. Determination & application of extinction coefficient. Applications of visible & UV spectroscopic techniques (structure elucidation excluded). Principle & applications of fluorescence spectroscopy.

ELECTROPHORES: Basic principle of electrophoresis. PAGE. SDS-PAGE & ioselectrofocusing.

Suggested reading:

1. Physical biochemistry, 2nd edition, by D. Friefelder (1983), W.H. Freeman and company, USA.
2. Outlines of biochemistry by Eric E Conn, PK Stumph, G. Bruening and Roy H Doi (1987) John Wiley and Sons, NY.
3. Biophysical chemistry: principles and techniques,2nd edition by A Upadhyay, K. Upadhyay and N.Nath (1998), Himalaya publishing house, Delhi.
4. Principles and techniques of practical biochemistry 5th edition by Keith Wilson and Walker(2000), Cambridge university press.
5. Introductory Practical Biochemistry by S.K.Sawhney and Randhir Singh (2000), Narosa Publishing House, New Delhi.

Paper XX (NUCLEOTIDE METABOLISM & BIOENERGETICS)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/ short answer type covering the entire syllabus will be compulsory. Remaining 6 questions will be set taking 3 questions from each section. Candidates will be required to attempt Q. No. 1 & four others selecting 2 questions from each section. All questions carry equal marks.

UNIT-1

NUCLEOTIDE METABOLISM: Sources of atoms in purine & pyrimidine molecules. Denovo biosynthesis & degradation of purines & pyrimidines. Salvage pathways of purines & pyrimidines. Regulation of purine & pyrimidine biosynthesis.

TRANSPORT ACROSS MEMBRANES: Fluid mosaic model for structure of biological membranes. Passive, facilitated & active transport across biological membranes. Primary & secondary active transport. Na^+- K^+ ATPase system.

BIOLOGIC OXIDATION: Free energy and standard free energy, relationship between free energy and equilibrium constant, enzymes involved in oxidation-reduction (oxidases, oxygenases, hydroxylases etc.).

UNIT-2

HIGH ENERGY COMPOUNDS: Phosphate group transfer potential. Free energy of hydrolysis of ATP. PEP & other sugar phosphates along with reasons for high free energy change.

ELECTRON TRANSPORT CHAIN & OXIDATIVE PHOSPHIORYLATION: Organization & sequence of electron carriers in mitochondria. Electron transport from NADH & $FADH_2$ to oxygen, Sites of ATP production & inhibitors of electron transport chain. Oxidative phosphorylation: chemiosmotic theory; inhibitors & uncouplers of oxidative phosphorylation. Transport of reducing equivalents from cytosol to mitochondria.

Suggested reading:

1. Bio-chemistry,4th edition by L. Stryer(1995) W.H Freeman & co., New York.
2. Bio-chemistry , 4th edition by G. Zubay(1998), W.C.B. Publishers.
3. Bio-chemistry, 2nd edition by Laurence A. Moran, K.G. Scrimgeour, H.R. Horton, R.S. Ochs& J.David Rawn(1994), Neil Patterson. Publishers, prentice Hall.
4. Lehniger: Principles of Bio-chemistry, 3rd Edition by David L. Nelson and M.M Cox(2000) Macmillan/worth publisher.

Paper- XXI (WORKING WITH A SINGLE DNA SEQUENCE)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

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UNIT-I

Catching Errors- Removing vector sequences, Cases when you shouldn't discard your sequence.
Computing / Verifying a Restriction Map.
Designing PCR Primers.
Analyzing DNA Composition- Establishing the G+C content of your sequence, Counting words in DNA sequences, Counting long words in DNA sequences, Experimenting with other DNA composition analyses, Finding internal repeats in your sequence, Identifying genome-specific repeats in your sequence, Identifying genome specific repeats in your sequence.

UNIT-II

Finding Protein coding Regions – ORFing your DNA sequence, Analysing your DNA sequence with Gene Mark, Finding internal exons in vertebrate genomic sequences, Complete gene parsing for eukaryotic genomes. Analyzing your sequence with Genome Scan.
Assembling Sequence Fragment- Managing large sequencing project with public software, Using the IFOM assemblers.

Suggested reading:

1. Teresa K. Attwood and David J. Parry-Smith 2001, Introduction to BioinformaticS, Pearson education Asia.
2. Lean- Michel Claverie and Cedric Notredame. 2003, Bioinformatics: a beginner's guide, Wiley- dream Tech India Pvt. Ltd.
3. S.C. Rastogi, Namita Mendiratta and Parag Rastogi. 2002. Bioinformatics: concepts, skills and applications, CBS publishers & distributors.

Paper- XXII (WORKING WITH A SINGLE PROTEIN SEQUENCE)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven Questions will be set in all. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Doing Biochemistry on a Computer- Predicting the main physicochemical properties of a protein, Interpreting Prot Param results, Digesting a protein in a computer.
Doing primary structure analysis –looking for transmembrane segments, Looking for coiled-coil regions.
Predicting Post-translational modifications in your protein- Looking for PROSITE patterns, Interpreting Scan Prosite result.

UNIT-II

Finding domains in your Protein- Choosing the right collection of domains, finding domains with InterProScan , Interpreting InterProScan results, Finding domains with the CD server, Interpreting and understanding CD server results, Finding domains with Pfscan.

Suggested reading:

1. Baxevanis a., Ouellette F.B.S (Eds.) 1998.Bioinformatics: a practical guide to the analysis of genes and proteins, sequence analysis , a practical approach. IRL Press, Oxford.

2. Bishop M.J, Rawlings C.J., (Eds.) 1997 Nucleic acid and Protein sequence analysis, A practical approach. IRL Press, oxford.

3. Doolittle, R.F. 1986, of UFRs and ORFs :A Primer on how to analyze derived amino acid sequences, university science books. Mill valley California.

4. Doolittle,R. F (ed.) 1996, Computer methods for macromolecular sequence analysis (Methods in Enzymology, vol 266), Academic press, San Diego.

SEMESTER- IV

Paper- XXIII (OBJECT-ORIENTED PROGRAMMING IN C++)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven Questions will be set in all. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT – I

Data types, classes and objects, Abstract data types, encapsulation and information hiding, data abstraction, generalization, inheritance.

UNIT-II

Aggregation, constructors, destructors, polymorphism, exception handling, templates.

Suggested reading:

1. Object- oriented programming in c++, by Balaguruswani E, Tata Mcgraw-Hill.
2. C++ the complete reference, by Schildt, Herbet; Tata Mcgraw-Hill.

Paper- XXIV (SAMPLING DISTRIBUTION)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven Questions will be set in all. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Normal distribution as a limiting case of the Binomial distribution area under normal curve with its applications.
Concepts of correlation and Regression, Properties of regression Fitting of a straight line and curves by the method of Least square, Multiple and Partial (for three variables only) correlation, coefficient of multiple and partial correlation with their properties.
Concept of Population, Sample, Parametes and Statistic and its sampling distributions.
Estimation of mean and variance, Criteria for a good estimator, unbiasedness, efficiency consistency and sufficiency (definition only)

UNIT-II

Confidence interval, Null and Altemative hypothesis, two types of errors, level of significance.
Sample properties of Chi-square, Student's t and Snedecor's F- distribution with their applications in test of significance.

Suggested reading:

1. Fundamentals of mathematical statistics: S.C.Gupta, V.K Kapoor.
2. Fundamentals of statistics : A.M Goon, M.K Gupta, B.Dass Gupta

Paper XXV (MOLECULAR BIOLOGY)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

Unit - I

BASIC CONCEPTS OF GENETIC INFORMATION: Nucleic acids as genetic information carriers: experimental evidences e.g. bacterial genetic transformation, Hershey- Chase experiment, TNV reconstitution experiment. Central dogma of molecular genetics: current version. Highly repetitive, moderately repetitive & unique DNA sequences. Telomeres. SINES & LINES. C- Value paradox. Satellite DNA. DNA supercoiling. Brief account of topoisomerases.

DNA REPLICATION: DNA replication on prokaryotes: conservative, semi conservative & dispersive types; experimental evidence for semiconservative replication. Enzymes & protein factors involves in replication. Mechanism of replication & inhibitors of replication. Differences in replications of prokaryotes & eukaryotes. Mutations: types of mutations; physical & chemical mutagens; molecular basis of mutation & Ames test of carcinogenicity. DNA repair. Significance of thymine in DNA.

Unit - II

TRANSCRIPTION: Transcription in prokaryotes. RNA polymerases. Promoters. Initiation, elongation & termination of RNA synthesis, Inhibitors of transcription. Reverse transcripltase. Post transcriptional processing of RNA.

TRANLATION: Genetic code: major features; biological significance of degeneracy; ribosome binding technique; wobble hypothesis; overlapping genes. Protein synthesis: structure & role of RNA & ribosomes in protein synthesis; activation of amino acids; initiation, elongation & termination of protein synthesis; folding & processing of polypeptides; inhibitors of protein synthesis.

PRINCIPLES OF GENE REGULATION: Regulation of gene expression in prokaryotes. Induction & repression. Lac operon.

Suggested Reading:

1. Biochemistry, 6th edition, by L.Stryer (2006). W.H.Freeman & Co.,NY.
2. Principles of Biochemistry by Voet, Voet & Prat 3rd ed. , (2008) , John Wiley & Sons, NY
3. Lehninger: Principles of Biochemistry, 5th edition, by David L. Nelson and M.M. Cox (2008). Worth Publishers

Paper XXVI (IMMUNOLOGY)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven Questions will be set in all. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-1

INTRODUCTIOTORY IMMUNOLOGY: Components of immunity. Introduction to adaptive (cells & organs of immune system) & non- adaptive/ innate (anatomic, physiological, phagocytic & imflammatory barriers); humoral & cell- mediated immunity. Primary & secondary immune response.

ANTIGENS & ANTIBODIES: Antigens (nature of antigens; immunogens; haptens). Immunogenicity versus antigenicity. Factors influencing immunogenicity. Adjuvants. Epitopes (properties of B-cell & T-Cell epitopes). Antibody structure; physicochemical properties of different classes of immunoglobulins. T & B lymphocytes.

UNIT-2

OTHER COMPONENTS OF IMMUNE SYSTEM: Major histocompatibility complex (MHC): location & function of MHC regions; structure of class I & II MHC molecules; role of MHCs. Compliment system: components, activation & functions. Antigen processing & presentation: a brief account of antigen processing & presentation pathways.

IMMUNOLOGICAL TECHNIQUES: Monoclonal antibodies: introduction; formation f hybrid cells, their production & applications. Antigen- antibody interactions: antibody affinity; antibody avidity ; agglutination & precipitation reactions; immonodiffusion; RIA; ELISA.

Suggested Reading:

1. Immunology, 4th ed. by Roitt et al., Mosby Publications
2. Cellular and Molecular Immunology, 5th ed. by Abbas and Litchman (2003), Saunders Publication.
3. Kuby Immunology, 4rd ed. by R.A. Goldsby et al, W.H. Freeman & Co.
4. Immunology: an introduction, 4th Edition by Ian R Tizard, (1995), Saunders College Publishing

Paper- XXVII (SEQUENCE COMPARISON)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven Questions will be set in all. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Making Sure you Have the Right Sequence and the Right Methods- Choosing the right sequences, Choosing the right method.
Making a Dot Plot- Choosing the right dot –plot flavor, using Dotlet over the Internet, Doing biological analysis with a dot plot.

UNIT-II

Making local Alignments over the internet- Choosing the right local alignment flavor, Using Lalign to find the ten best local alignments, Internet the lalign output, making Global Alignments over the Internet, Using Lalign to make a Global Alignment free Pairwise Sequence Comparison over the Internet.

Suggested Reading:

1. Teresa K. Attwood and David J. Parry-Smith, 2001.Introduction to Bioinformatics. Pearson Education Asia.
2. Lea- Micheal Claverie and Cedric Notredame, 2003, Bioinformatice: A Beginner's Guide. Wiley- Dream Tech India Pvt. Ltd.
3. S.C.Rastogi, Namita Mendiratta and Parag Rastogi, 2002, Bioinformatics: Concepts, skills, and Applications.CBS Publishers & Distributiors.
4. Baxevanis A., Ouelete F.B.F. (Eds), 1998, Bioinformatics : A Practical Gudie to the Analysis of Genes and Proteins, John Wiley and Sons, New York.
5. Bishop, M.J, Rawlings, C.J (Eds.), 1997, Nucleic Acid and Protein Sequence Analysis: A Practical Approach. IRL Press, Oxford.

Paper- XXVIII (SEQUENCE ANALYSIS)

Max Marks= 40
Internal Assessment=10
Time allowed = 3 Hrs

NOTE: Seven Questions will be set in all. Q. No 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with questions 3 from each section. The candidates will be required to attempt Q. No 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

The Importance of similarity, The Most Popular Data- Mining Tool- BLAST, blasting protein sequences, Understanding Blast output, Blasting DNA sequences.

UNIT-II

Controlling BLAST: Choosing the right parameters, controlling the sequence making, changing the blast alignment parameters, controlling the blast output, Making Iterative BLAST with PSI-BLAST. PSI-Blasting protein sequences, avoiding mistakes when running PSI-BLAST.
Similarity Searches for free over the internet.

Suggested Reading:

1. Teresa K. Attwood and David J. Parry-Smith, 2001.Introduction to Bioinformatics. Pearson Education Asia.
2. Lea- Micheal Claverie and Cedric Notredame, 2003, Bioinformatice: A Beginner’s Guide. Wiley- Dream Tech India Pvt. Ltd.
3. S.C.Rastogi, Namita Mendiratta and Parag Rastogi, 2002, Bioinformatics: Concepts, skills, and Applications.CBS Publishers & Distributiors.
4. Baxevanis A., Ouelete F.B.F. (Eds), 1998, Bioinformatics : A Practical Gudie to the Analysis of Genes and Proteins, John Wiley and Sons, New York.
5. Bishop, M.J, Rawlings, C.J (Eds.), 1997, Nucleic Acid and Protein Sequence Analysis: A Practical Approach. IRL Press, Oxford.

Paper- XXIX
(Software Lab-II)

Max Marks: 100
Time: 4 Hours

Programming in C++:

1. To find simple and compound interest.
2. To generate Fibo nicci series.
3. To generate Sine and Cosine Series.
4. Demonstrate function and operator overloading with suitable example.
5. Demonstrate Inheritance with suitable example.
6. Demonstrate Polymorphism using virtual functions with suitable example.
7. Demonstrate inheriting abstract classes with suitable example.
8. Demonstrate Aggregation with suitable sxample.
9. Demonstrate Exception handling with suitable example.
10. Demonstrate use of Templates with suitable example.
11. Demonstrate Inheritance with suitable example.

Statistical:

The following Topics are prescribed for computer based practicals.

1. Fitting of normal distribution.
2. Fitting of Curve by the principle of least square.
3. Karl Pearson's Coefficient of Correlation, Rank Correlation Coefficient Test of significance based on t, Chi-Square and F.

Paper- XXX

(PRACTICAL - 3)

Max Marks: 100

Time: 4 Hours

1. Estimation of ascorbic acid by titrimetric method
2. Separation of amino acids by TLC
3. Estimation of protein by biuret/ Lowry method
4. Assay of acid phosphatase activity from germinating mungbean seeds and calculation of specific activity
5. Assay of serum alkaline phosphatase activity
6. Effect of enzyme concentration on enzyme activity
7. Effect of Temperature on Enzyme activity
8. Determination of achromatic point for salivary amylase
9. Estimation of nitrogen by Nessler/ micro-Kjeldahl method
10. Estimation of chlorophyll content of leave by using acetone

Suggested readings:

1. Introductory Practical Biochemistry by S.K Sawhney & R. Singh (2000), Narosa Publishers.
2. Practical Biochemistry by David Plummer(1990). Tata McGraw Hill.
3. Bio-chemistry Methods by Sadasivem & Manicham (1996) New Age Internalional (P) Ltd.
4. Modern Experimental Biochemistry, 3rd edition, by R.Boyer(2002), Addison- Wesley Longman.
5. A Lab. Manual in Biochemistry by J.Jayaraman (1996) New Age Inernational (P) Ltd.

Paper- XXXI

(PRACTICAL – 4)

Max Marks: 100
Time: 4 Hours

1. Internet resources and Pubic Databases for Bioinformatics Protein Classification Databases.
2. Use of bioinformatics mining.
3. The basis methodological tools for comparative and phylogenetic analyses of molecular data from an evolutionary perspective.
4. Basic clustering methods that are used analysis of DNA array image data, classification of proteins, computing multiple alignments and phylogenetic tree construction.
5. The roles of computer programming to model real life biological systems.
6. The different analysis and models, such as Monte-carlo Methods and the use of Markov chains & Hidden Markov Models in Bioinformatics.
7. Basic genome analysis, Genome structures, Basic methodology and principles.
8. Algorithms for primary sequences analysis: Based on string/ word searches(patterns, PROSITE, restriction sites): Based on sliding windows (hydrophobicity, transmembrane regions, coiled coil domains etc.), Based on weight matrices (profiles), Based on classical statistic methods such as determinant analysis and other multivariate techniques (codon usage, functional classification by amino acid composition, etc.) Based on graphical representations (sequences ‘logo’, chaos game representations, vector representation of sequences etc.)
9. Optimal two-way alignments using dynamic programming: Amino acid substitution matrices, Gap penalization, Optimization of the method : FASTA, Blast, Parrallelization of WS: multiple processor approaches and specialized, hardware, Dot matrices.
10. Multiple alignments: Clustering methods (UPGME, etc.), Rigorous dynamic programming, simulated annealing.

PAPER-XXXII

(BUILDING AND INTERPRETING MULTIPLE SEQUENCE ALIGNMENT)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

BUILDING A MULTIPLE SEQUENCE ALIGNMENT**:** Introduction and goal of Multiple Sequence Alignment (MSA), Finding out if a multiple sequence alignment can help you-Identifying situations where multiple alignments do not help, Helping your research with multiple sequence alignments.

CHOOSING THE RIGHT SEQUENCES**:** The kinds of sequences you are looking for and Gathering your sequences with online BLAST servers.

CHOOSING THE RIGHT MULTIPLE SEQUENCE ALIGNMENT METHOD**:** Using ClustalW, making and evaluating alignments with T-coffee

UNIT-II

INTERPRETING YOUR MULTIPLE SEQUENCE ALIGNMENTS**:** Recognizing the good parts in a protein alignment, taking your multiple alignment further.

COMPARING SEQUENCES THAT YOU CANT ALIGN**:** Making multiple local alignments with Gibbs sampler, searching conserved patterns.

INTERNET RESOURCES FOR DOING MULTIPLE SEQUENCE COMPARISONS**:** Making simple alignments with ClustalW around the clock, finding your favourite alignment method, searching for motifs or patterns.

Suggested Readings:

1. Introduction to Bioinformatics, Teresa K. Attwood and David J. Parry-Smith
2. Bioinformatics- A Beginners guide, Lean-Micheal Claverie and Cedric Notredame
3. Bioinformatics: Concepts skills and Applications, S. C. Rastogi

PAPER-XXXIII

(EDITING AND PUBLISHING ALIGNMENTS)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No.1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

EDITING AND PUBLISHING ALIGNMENTS**:** Getting your Multiple Alignments in the right format- Recognizing the main formats, Working with the right format, Converting formats and Watching out for lost data.

USING JALVIEW TO EDIT YOUR MULTIPLE ALIGNMENT ONLINE**:** Starting Jalview, Working offline with Jalview, Changing the color scheme in Jalview, Editing a group of sequences, Useful features of Jalview and Saving your alignment in Jalview.

UNIT-II

PREPARING YOUR MULTIPLE ALIGNMENT FOR PUBLICATION**:** Using Boxshade, Logos.

EDITING AND ANALYSING MULTIPLE SEQUENCE ALIGNMENTS FOR FREE OVER THE INTERNET**:** Finding multiple sequence alignment editors, Finding tools to interpret your MSA, Finding tools for publishing multiple alignments.

Suggested Readings:

1. Introduction to Bioinformatics, Teresa K. Attwood and David J. Parry-Smith
2. Bioinformatics- A Beginners guide, Lean-Micheal Claverie and Cedric Notredame
3. Bioinformatics: Concepts skills and Applications, S. C. Rastogi
4. A Practical Guide to the Analysis of Genes and Proteins**,** Baxevanis A., Ouellette.
5. Nucleic Acid and Protein Sequence Analysis. A Practical Approach**.** Bishop, M.J., Rawlings C. J.

PAPER-XXXIV

(APPLIED STATISTICS)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

INDEX NUMBER**:** Uses of Index number, Problem in construction of Index numbers, Methods of Constructing Index Numbers, Unweighted, Weighted, Quantity, Volume and Chain Index Numbers, Consumer Price Index Numbers, Calculation of Index numbers, tests of index numbers, Chain index numbers, limitations of index numbers.

UNIT-II

TIME SERIES**:** Definitions, different components of time series, determination of trend, analysis of seasonal variations. Concept of population and sample, advantages of sampling, principle steps involved in sample survey. Simple random sampling (with and without replacement), merits and demerits, Estimation of population mean and variance.

Suggested Readings:

1. Experimental design by W.G.Cochran & J.M.Cox.
2. Applied Statistic by S.C.Gupta & V.K.Kapoor.
3. Sampling Theory and Methods by M.N.Murthy.
4. Sample Survey Methods and its Applications by B.V.Sukhatme.
5. Sample Survey Theory by Des Raj.

PAPER-XXXV

(SAMPLING TECHNIQUES)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Types of Sampling-Purposive Sampling, Random Sampling, Simple Sampling, Stratified Sampling, Estimation of sample size, Sampling Distribution for Static's, advantages, estimation of population mean, variance of estimates of the population mean, proportional and optimum allocations. Standard Error.

Tests of Significance: Null and Alternative hypothesis, Errors in Sampling, Critical Region and Level of Significance. One-Tailed, and Two-Tailed Test. Test of Significance for Single Proportion and Differences of Proportion

UNIT-II

Block Design:Concept of experiments, treatments, experiments, units, blocks, experimental error, replication, precision, fundamental principle of design: replication, randomization and local control.

Basic design CRD, RBD and their analysis.

Suggested Readings:

1. Experimental design by W.G.Cochran & J.M.Cox.
2. Applied Statistic by S.C.Gupta & V.K.Kapoor.
3. Sampling Theory and methods by M.N.Murthy.
4. Sample survey methods and its applications by B.V.Sukhatme.
5. Sample survey Theory by Des Raj.

PAPER-XXXVI

(RECOMBINANT DNA TECHNOLOGY)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Restriction endonucleases, Ligases and other enzymes involved in Recombinant DNA Technology. Introduction to the steps of Gene cloning: Plasmid and phage cloning vectors for *E.coli*, Cloning vectors for yeast, plant cells and mammalian cells. Methods for direct DNA transfer into plant and mammalian cells. Ligation of inert DNA with the vector, Introducing recombinant DNA into the host cells, Selection and Screening of the recombinants, Construction of gene library and cDNA library.

UNIT-II

Expression vector, General problems with the production of recombinant proteins in *E.coli*; Applications of Recombinant DNA Technology; Nucleic acid Blotting Techniques: Southern Blotting, Northern Blotting, and Dot Blotting; Polymerase Chain Reaction (PCR): Principle, Techniques of PCR, Sources of DNA polymerase and applications of PCR.

Suggested Readings:

1. Gene Cloning and DNA analysis- An Introduction by T. A. Brown, Blackwell Science
2. Molecular Biotechnology-Principles & applications of recombinant DNA by Glick and Pasternak, ASM press (Indian print available)
3. Principles of Gene Manipulation by Old & Primose, Blackwell Scientific Publication
4. Analysis of Genes and Genomes, 2004 by Richard Reese, John Wiley & Sons
5. Biochemistry by B.D. Singh

PAPER- XXXVII

(PLANT BIOCHEMISTRY)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

PHOTOSYNTHESIS**:** Photosynthetic pigments; light phase: absorption of light energy and transfer of excitation energy to the reaction centers, Photosystem I and II, Non-cyclic and cyclic electron flow; Photophosphorylation: Structure of Chloroplast ATP Synthase and mechanism of ATP synthesis; Calvin Cycle, C4 pathway, Photorespiratory pathway and its role, CAM pathway.

Biosynthesis of sucrose and starch (in chloroplast).

UNIT-II

Nitrate Assimilation**:** Nitrate uptake, structure and function of nitrate reductase and nitrite reductase.

Sulphate assimilation: Sulphate uptake; assimilation of sulphate into cysteine.

Biological N_2-fixation: N_2 - fixing organisms, structure and mechanism of action of nitrogenase, strategies for protection of nitrogenase from inhibition by oxygen; role of leghaemoglobin; Ammonia assimilation.
Plant Hormones**:** Physiological functions of Auxins, Gibberellins, Cytokinins, Ethylene and Abscisic acid.

Suggested Readings:

1. Biochemistry and Molecular Biology of Plants by Bob, B. Buchanan, W. Gruissen and R.L.Jones (2000). Published by American Society of Plant Physiologists and distributed by Panima Educational Book Agency, New Delhi.
2. Plant Biochemistry and Molecular Biology, 2nd edition, by Peter J. Lea and Richard C. Leegood (1999). John Wiley and Sons.
3. Plant Biochemistry & Molecular Biology, 3rd ed., by Hans–Walter Heldt (2005), Academic Press
4. Plant physiology, 2nd edition, by L. Taiz and E-Zeigler (1998), Sinauer Associates, Inc., Publishers

SEMESTER-VI

PAPER-XXXVIII

(DATABASE MANAGEMENT SYSTEMS)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

OVERVIEW OF DBMS**:** Basic DBMS terminology, DBA and his responsibility, physical and logical data independence, architecture of DBMS: distributed database (structure design), client/server architecture.

MODELS OF DATABASE: Entity relationship model, relational model, hierarchical model, network model.

UNIT-II

RELATIONAL QUERY LANGUAGE**:** Users of DBMS, DDL, DML, DCL, data integrity, domain integrity, entity integrity, referential integrity.

SECURITY**:** Authorization, access matrix, concurrency, locks, serializability, recovery.

Suggested Readings:

1. An introduction to database systems by C.J.Date, Addison Wesley.
2. Database processing fundamentals, Design and implementation by Kroenke David and M., Galgotia publication.
3. Database system concepts by Korth & Silberschatz, tata McGraw-Hill.
4. Fundamentals of database systems by Elmarsi & Navathe, Benjamin Cummings.
5. Advance Database systems by Vipin Desai.

PAPER- XXXIX

(PROGRAMMING IN JAVA)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

JAVA LANGUEGE: The java programming language and its characteristics, java runtime environment, java compiler, java development kit, running java applications and java applets.

JAVA PROGRAMMING: Elements of java: data types, scalar data types, first class object, control structures. Control structures. Classes and objects, Exception handling array and strings.

UNIT-II

INPUT / OUTPUT**:** Basics, streams, byte and character streams, the class Printstream, data streams, string Tokenizer class, stream Tokenizer.

APPLETS: Introduction, essential applet methods. Drawing and handlings events, inserting applets in a web page. Introduction to Servlets.

Suggested Readings:

1. Programming with java A Primer by E.Balaguruswami, Tata McGraw-Hill.
2. Java The Complete Reference by Schildt. Herbert: Tata McGraw-Hill.
3. The java programming languages by Arnold, Gosling Addison Wesley.

PAPER- XL

(PHYLOGENETICS)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Phylogenetics**:** What is Phylogenetics? Finding out what Phylogenetic Trees can do, Preparing Phylogenetic Data – Choosing the right sequences for the right tree, Preparing Multiple sequence alignments.

UNIT-II

Building the kind of tree you need: Computing your tree, Knowing what's what in your tree, Displaying your phylogenetic tree.

Doing phylogeny for free over the internet: Finding online resources, Finding generic resources, Collections of orthologus genes.

Suggested Readings:

1. Teresa K. Attwood and David J.Parry-Smith, 2001, Introduction to bioinformatics. Pearson Education Asia.
2. Lean-Micheal Clavereie and Cedric Notredame, 2003, Bioinformatics: A Beginner's Guide. Wiley-Dream Tech India Pvt.Ltd.
3. S.C.Rastogi, Namita Mendiratta and Parag Rastogi, 2002, Bioinformatics: Concepts skills and applications.
4. Baxevenis A and Ouellette F.B.F., 1998, Bioinformatics: a practical Guide to the analysis of genes and proteins.

PAPER- XLI

(STRUCTURAL ANALYSIS: WORKING WITH RNA AND PROTEIN 3D STRUCTURES)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answer type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

WORKING WITH RNA**:** Predicting, Modelling and Drawing RNA Seondary structures, Using Mfold.

Searching Databases and Genomes for RNA Sequences- Finding tRNAS in a genome, Using PatScan to look for RNA patterns.

Doing RNA analysis for free over the Internet-Studying evolution with ribosomal RNA, Finding the small non-coding RNA you need, Generic RNA resources.

UNIT-II

WORKING WITH PROTEIN 3-D STRUCTURES: From Primary to Secondary Structures-Predicting the secondary structure of a protein sequence- Predicting additional structural features.

From the Primary structure to the 3-D Structure- Retrieving and displaying a 3-D structure from a PDB site, Guessing the 3-D structure of your protein, Looking at sequences features of 3-D.

Finding other PDB viewers, Classifying your PDB structure, Doing homology modeling, Folding proteins in a computer, Threading sequences onto PDB structures, Looking at structures in movements, Predicting interactions.

Suggested Readings:

1. Nucleic acid and protein sequence analysis by Bishop M.J. Rawlings C.J. 1997.
2. A primer on how to analyze derived amino acid sequence by Doolittle R.F. 1986.
3. Computer methods for macromolecular sequence analysis (methods in Enzymology, vol.266) by Doolittle R.F.1996.

PAPER- XLII

(CLINICAL BIOCHEMISTRY)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No. 1 which will be objective/short answers type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & 4 others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Hormones: General characteristics, classes with examples, major endocrine systems and their target tissues, physiological roles of hormones, Role of cyclic nucleotides and calcium in hormones action; Mechanism of action of epinephrine and steroid hormones. Biochemical aspects of diabetes mellitus.

Collection and preservation of biological fluids (blood, serum, plasma, urine and CSF). Normal and abnormal constituents of blood and urine; Plasma proteins; Mechanism of blood coagulation.

UNIT-II

Metabolic Disorders: Metabolic disorders of carbohydrate (Hypo- and hyper-glycemia, galactosemia, lactose intolerance, glycogen storage diseases), lipid (Sphingolipidosis, atherosclerosis, lipoproteinemia), protein (Phenylketonuria, alkaptonuria, tyrosenimea, maple syrup urine disease, Hartnup's disease, homocysteinuria etc.) and nucleic acids (Gout, Lesch-Nyhan syndrome).
Clinical enzymology: Definition of functional and non-functional plasma enzymes. Enzyme and isoenzyme pattern in health and disease with special mention of plasma lipase, amylase, SGOT, SGPT, LDH, CPK, alkaline phosphatase and acid phosphatase.

Detoxification mechanism of the body**:** Phase I and phase II pathways.
Evaluation of organ function tests: Assessment of liver, kidney, pancreas and G.I. tract functions

Suggested readings:

1. Harper's Biochemistry, 25th edition, by R.K.Murray, P.A.Hayes, D.K.Granner, P.A. Mayes and V.W.Rodwell
2. Biochemistry by U. Satyanarayana (1999). Books and Allied (P) Ltd.
3. Lehninger: Principles of Biochemistry, 3rd edition, by David L. Nelson and M.M. Cox (2000) Maxmillan/ Worth publishers.
4. Text Book of Biochemistry & Human Biology by G.P. Talwar (1989) Prentice Hall, New Delhi

PAPER- XLIII

(NUTRITIONAL BIOCHEMISTRY)

Max Marks=40

Internal Assessment=10

Time allowed=3 Hrs

NOTE: Seven questions will be set in all. Q. No1 which will be objective/short answers type covering the entire syllabus, will be compulsory. The remaining questions will be set section wise with 3 questions from each section. The candidates will be required to attempt Q. No. 1 & four others selecting 2 questions from each section. All questions will carry equal marks.

UNIT-I

Composition of human body; Energy content of foods; Measurement of energy expenditure (Direct & indirect calorimetry); Respiratory Quotient of foods, BMR; SDA; Biological value of proteins, Determination of protein quality, Diseases associated with protein malnutrition and protein-calorie malnutrition (Kwashiorkor and Maramus), Nutritional value of carbohydrates and lipids, Dietary fiber and Nitrogen balance.

Vitamins**:** Dietary sources, structure, functions, and deficiency diseases associated with fat and water soluble vitamins; Hypervitaminosis symptoms of fat soluble vitamins

UNIT-II

Minerals: Nutritional significance and deficiency manifestations of mineral elements

Naturally occurring toxicants Antinutrients: Naturally occurring food born toxicants: Protease inhibitors, Hemagglutin, hepatotoxins, allergens, oxalates, toxin from mushrooms, animal food stuffs and sea foods

Obesity: Definition and classification; Genetic and environmental factors leading to obesity; Biochemical basis of obesity

Starvation**:** Protein, carbohydrate and lipid metabolism in prolonged fasting; Role of ketone bodies during starvation. Inter-organ relationship during starvation

Lipoproteins**:** Structure, classification, metabolism and disorders

Suggested Readings:

1. Food Chemistry, 3rd edition, by Owen R Fennema (1996), Indian Reprint
2. Biochemistry by U. Satyanarayana (2002). Books and allied (P) Ltd.
3. Harper's Biochemistry, 26th edition, by R.K.Murray, P.A.Hayes, D.K.Granner, P.A. Mayes and V.W.Rodwell (2003) Prentice Hall International.
4. Modern Nutrition in Health & Disease, 9th edition, by Maurice E. Shils, James A. Oslon, M. Shihe and A. Catherine Ross (1999) Lippincott Williams & Wilkins, New York

PAPER- XLIV

(SOFTWARE LAB-3)

Max Marks=100

Time allowed= 4 Hrs

Programming in JAVA

1. A simple program explaining basic structure of JAVA program.
2. To generate pyramid of digits.
3. To generate graphical shapes using character like *.
4. To find largest and average of the given n values.
5. To sort array elements in ascending and descending order.
6. To search an element in array.
7. To manage employee status using class employee.
8. Demonstrate inheritance by extending a class with suitable example.
9. To create your own packages.
10. Demonstrate exception handling.
11. Demonstrate method overloading with suitable example.
12. Demonstrate various string methods with suitable example.

Statistics

The following topics are prescribed for the computer based practicals:

1. Calculation of Index Numbers of wholesale prices using different formulae.
2. Determination of trend in a time series and seasonal variations.
3. Analysis of variance for problems based on one way and two way classification.
4. Estimation of mean variance and its standard error (i) Simple random samples (ii) Stratified Samples.

PAPER- XLV

(PRACTICL-V)

Max Marks= 100

Time allowed= 4 Hrs

1. Estimation of DNA by diphenylamine method.
2. Estimation of RNA by orcinol method.
3. Separation of Proteins by PAGE.
4. Collection and preservation of urine sample.
5. Qualitative detection of sugars, proteins, ketone bodies and bile pigments in urine.
6. Separation of blood plasma and serum.
7. Estimation of blood haemoglobin.
8. Identification of blood group and Rh-factor.
9. Determination of erythrocyte sedimentation in blood.
10. Determination of clotting time of blood.
11. Estimation of blood urea and creatinine.
12. Estimation of serum cholesterol.
13. Estimation of calcium and phosphorus in serum and urine.
14. Estimation of lactose in milk.
15. Estimation of serum proteins and determination of albumin/globulin ratio.
16. Determination of enzyme assay of any one enzyme

PAPER- XLVI

(PRACTICL-VI)

Max Marks= 100

Time allowed= 4 Hrs

1. Introduction to Perl. Representing sequence data. Command interpretation. Statements. Variables. Strings. Assignment output. Concatenating DNA fragments.

2. Transcription: DNA to RNA perl documentation. Producing the reverse complements of a strand of DNA. Arrays. Reading protein sequences from files Scalar and list contexts.

3. Perl exercises.

4. Motifs and loops. Flow control. Conditional Statements. Conditional tests and matching braces. Loops.

5. Open and unless. Finding motifs. Keyboard input. Turning arrays into scalars with join. Do-Until loops.

6. Regular expressions character classes. Pattern matching. Counting nucleotides. Exploding strings into arrays. Operating on strings. Writing to files.

7. Perl exercises.

8. Programming project clinics (java).