KURUKSHETRA UNIVERSITY, KURUKSHETRA

Curriculum for B.Sc. Bioinformatics 5th & 6th Semesters

SEMESTER-V

Paper No.	Title of Paper	Max. Marks	Internal Assessment	Total Marks	Time
XXXII	Building and Interpreting Multiple Sequence Alignment	45	5	50	3 Hrs
XXXIII	Editing and publishing Alignments	45	5	50	3 Hrs
XXXIV	Applied Statistics	45	5	50	3 Hrs
XXXV	Sampling Techniques	45	5	50	3 Hrs
XXXVI	Recombinant DNA Technology	45	5	50	3 Hrs
XXXVII	Plant Biochemistry	45	5	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	45	5	50	3 Hrs
XXXIX	Programming in JAVA	45	5	50	3 Hrs
XL	Phylogenetics	45	5	50	3 Hrs
XLI	Structural Analysis: Working with RNA and Protein 3-D Structures	45	5	50	3 Hrs
XLII	Clinical Biochemistry	45	5	50	3 Hrs
XLIII	Nutritional Biochemistry	45	5	50	3 Hrs
XLIV	Software Lab – III	100	-	100	6 Hrs
XLV	Practical-V	100	-	100	6 Hrs
XLVI	Practical-VI	100	-	100	6 Hrs

PAPER-XXXII

(BUILDING AND INTERPRETING MULTIPLE SEQUENCE ALIGNMENT)

Max Marks=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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=45
Internal Assessment=5
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= 6 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= 6 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= 6 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).