Annexure No.	**45 A**
SCAA Dated	**29.02.2008**

BHARATHIAR UNIVERSITY :: COIMBATORE – 641 046

REGULATIONS FOR M. Sc. BIOINFORMATICS DEGREE COURSE WITH COMPULSORY DIPLOMA IN GENOME TECHNOLOGY
Semester System (Affiliated Colleges)

(with effect from 2007-2008)

1. Eligibility for Admission to the Course

A candidate who has passed in any one of the following the Degree Examination as main subject of study of this University or an examination of some other University accepted by the syndicate as equivalent thereto shall be eligible for admission to the Master Degree of this University.

B.Sc., Agriculture/Animal Biotechnology/Animal science/Applied science/B.Tech – Biotech/Biochemistry/Bioinformatics/Biology/Biotechnology/Botany/Chemistry/ Computer applications/Computer science/Electronics/Environmental science/ Food science/Forestry/Horticulture/Information technology/Mathematics/Medical sciences – MBBS/BDS/BVSc.,/Microbiology/Pharmacy/Physics/PlantBiotechnology/Plant science/Statistics/Zoology

2. Duration of the Course

This Course of Study shall be based on Semester System. This Course shall consist of four Semesters covering a total of two Academic Years. For this purpose, each Academic Year shall be divided into two Semesters; the first and third Semesters; July to November and the second and the fourth Semesters; December to April. The Practical Examinations shall be conducted at the end of even Semester.

3. Course of Study

The Course of the Degree of Master of Science/Arts/Commerce shall be under the Semester System according to the Syllabus to be prescribed from time to time. This Course consists of Core Subjects and Elective Subjects. There shall be one Paper on applied Skill Oriented, subject preferably in each semester as part of the adjunct Diploma Programme.

4. Requirement to appear for the Examinations

a) A candidate will be permitted to take the University Examination for any Semester, if

i) he/she secures not less than 75% of attendance out of the 90 instructional days during the Semester.

b) A candidate who has secured attendance less than 75% but 65% and above shall be permitted to take the Examination on the recommendation of the Head of the Institution to condone the lack of attendance as well as on the payment of the prescribed fees to the University.

c) A candidate who has secured attendance less than 65% but 55% and above in any Semester, has to compensate the shortage of attendance in the subsequent Semester besides, earning the required percentage of attendance in that Semester and take the Examination of both the Semester papers together at the end of the latter Semester.

d) A candidate who has secured less than 55% of attendance in any Semester will not be permitted to take the regular Examinations and to continue the study in the subsequent Semester. He/she has to re-do the Course by rejoining the Semester in which the attendance is less than 55%.

e) A candidate who has secured less than 65% of attendance in the final Semester has to compensate his / her attendance shortage in a manner to be decided by the Head of the Department concerned after rejoining the Course.

5. Restriction to take the Examinations

a) Any candidate having arrear paper(s) shall have the option to take the Examinations in any arrear paper(s) along with the subsequent regular Semester papers.

b) Candidates who fail in any of the papers shall pass the paper(s) concerned within 5 years from the date of admission to the said Course. If they fail to do so, they shall take the Examination in the revised Text / Syllabus, if any, prescribed for the immediate next batch of candidates. If there is no change in the Text / Syllabus they shall take the Examination in that paper with the Syllabus in vogue, until there is a change in the Text or Syllabus.

In the event of removal of that paper consequent to the change of Regulations and / or Curriculum after a 5 year period, the candidates shall have to take up on equivalent paper in the revised syllabus as suggested by the chairman and fulfill the requirements as per Regulations/Curriculum for the award of the Degree.

6. The Medium of Instruction and Examinations

The medium of instruction and Examinations shall be in English.

7. Submission of Record Notebooks for Practical Examinations

Candidates taking the Practical Examinations should submit bonafide Record Note Books prescribed for the Practical Examinations. Otherwise the candidates will not be permitted to take the Practical Examinations.

8. The Minimum (Pass) Marks

A candidate shall be declared to have passed in a paper if a student obtains not less than 50% of marks in that paper. A candidate shall be declared to have passed the whole Examination if the student passes in all the papers.

9. Improvement of Marks in the subjects already passed

Candidates desirous of improving the marks secured in their first attempt shall reappear once within the subsequent Semester. The improved marks shall be considered for classification but not for ranking. If there is no improvement there shall not be any change in the original marks already awarded.

10. Classification of successful candidates

A candidate who passes all the Examinations in the first attempt within a period of two years securing 75% and above marks in the aggregated shall be declared to have passed with First Class with Distinction.

Successful candidates passing the P.G. Degree Examinations, securing 60% marks and above shall be declared to have passed the examination in First Class. All other successful candidates shall be declared to have passed the Examination in Second Class.

12. Ranking

A candidate who qualifies for the PG Degree Course passing all the Examinations in the first attempt, within the minimum period prescribed for the Course of Study from the date of admission to the Course and secures 1st or 2nd Class shall be eligible for ranking and such ranking will be confined to 10% of the total number of candidates qualified in that particular subject to a maximum of 10 ranks.

The improved marks will not be taken into consideration for ranking.

13. Conferment of the Degree

No candidate shall be eligible for conferment of the Degree unless he / she has undergone the prescribed Course of Study for a period of not less than four Semesters in an Institution approved of by and affiliated to the University or has been exempted there from in the manner prescribed and has passed the Examinations as have been prescribed.

14. Evening College

The above Regulations shall be applicable for candidates undergoing the respective Courses in the Evening Colleges also.

16. Revision of Regulations and Curriculum

The above Regulation and Scheme of Examinations will be in vogue without any change for a minimum period of three years from the date of approval of the Regulations. The University may revise /amend/ change the Regulations and Scheme of Examinations, if found necessary.

17.Transitory Provision

Candidates who have undergone the Course of Study prior to the Academic Year 2007-2008 will be permitted to take the Examinations under those Regulations for a period of four years i.e. up to and inclusive of the Examination of April 2012 thereafter they will be permitted to take the Examination only under the Regulations in force at that time.

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M.Sc. BIOINFORMATICS (WITH PROJECT WORK) Affiliated Colleges

SCHEME OF EXAMINATION FOR CANDIDATES ADMITTED DURING THE ACADEMIC YEAR 2007 - 2008 AND ONWARDS

SEM	CODE	PAPER	TITLE	INSTRU-CTION/ WEEK	UNIVERSITY EXAMINATIONS	
					Duration In Hrs	Max. Marks **
I	07BICT1	Paper I	Fundamentals of biological systems	5	3	100
	07BICT2	Paper II	Structure and functions of biomolecules	5	3	100
	07BICT3	Paper III	Computer programming in C	5	3	100
	07BICT4	Paper IV	Computational methods for sequence analysis	5	3	100
	07BICP1	Practical I	Computer programming*	3	-	-
	07BICP2	Practical II	Biological databanks and sequence analysis*	3	-	-
	07BIDT1	Dip. Paper I	Biology of cloning vectors	2	3	100
	07BIDP1	Dip. Practical I	Molecular techniques*	2	-	-
II	07BICT5	Paper V	Molecular interaction	5	3	100
	07BICT6	Paper VI	Systems biology	5	3	100
	07BICT7	Paper VII	Introduction to Visual basic with RDBMS	5	3	100
	07BICT8	Paper VIII	Mathematical methods and statistical techniques	5	3	100
	07BICP1	Practical I	Computer programming	3	3	100
	07BICP2	Practical II	Biological databanks and sequence analysis	3	3	100
	07BIDT2	Dip. Paper II	Methods of gene transfer and genome sequencing	2	3	100
	07BIDP1	Dip.Practical I	Molecular techniques*	2	6	50
III	07BICT9	Paper IX	Genomics	5	3	100
	07BICT10	Paper X	Proteomics	5	3	100
	07BICT11	Paper XI	Molecular modeling and computer aided drug designing	5	3	100
	07BICT12	Paper XII	Perl Programming for Bioinformatics	5	3	100
	07BICP3	Practical III	Perl programming*	3		
	07BICP4	Practical IV	Computer aided drug design*	3	3	100
	07BIDT3	Dip. Paper III	Applications of rDNA technology	2	3	100
	07BIDP2	Dip.PracticalII	rDNA Technology *	2	6	50
IV	07BICPW		Project work, viva-voce (150+50)			200

* Practical examination to be conducted at the end of academic year.

** includes 25% internals

COMPULSORY DIPLOMA IN GENOME TECHNOLOGY

SCHEME OF EXAMINATION FOR CANDIDATES ADMITTED DURING THE ACADEMIC YEAR 2007 - 2008 AND ONWARDS

SEM.	CODE	PAPER	TITLE	INSTRUC-TION/ WEEK	UNIVERSITY EXAMINATIONS	
					Duration In Hrs	Max. Marks **
I	**07BIDT1**	Paper I	Biology of cloning vectors	2	3	100
II	**07BIDT2**	Paper II	Methods of gene transfer and genome sequencing	2	3	100
III	**07BIDT3**	Paper III	Applications of rDNA technology	2	3	100
IV	**07BIDP1**	Practical I	Molecular techniques	2	6	50
IV	**07BIDP2**	Practical II	rDNA Technology	2	6	50

Subject title : Fundamentals of Biological systems
Course number : 07BICT1 Number of lecture hours: 5
Subject description :
Some basic aspects of Molecular Biology and Genetics that are relevant to the course are included in this paper.

Goals:
To understand the basic structure of cell, mechanism and regulation of biological processes fundamental to genome structure and biochemistry.

Objectives:
Students completing this paper should be able to understand molecular biology concept that are basic to bioinformatics.

Contents:

Unit I Basic aspects of prokaryotic and eukaryotic cells: membranes and cellular compartments, cell organelles structure and function. Cell cycle and its regulations: events during mitosis and meiosis.

Unit II Prokaryotic geneme organization and structure. Prokaryotic gene expression, operons – positive and negative regulations, factors involved in gene regulation.
Eukaryotic genome organization and structure. Mechanism of gene expression in eukaryotes, promoter and regulatory sequences, basic mechanism of transcription and transcriptional activation, role of transcription factor.

Unit III Mendelian principles of inheritance, sex linked inherintance. Concepts of linkage, linkage maps and recombination. Mutation: gene/point and chromosomal.

Unit IV Enzymes: Units of activity, coenzymes and metal cofactors, temperature and pH effects, Michalis-Menten kinetics, inhibitors and activators, active site and mechanism of enzyme action, ribozyme and abzymes.

Unit V Basic immunology: Overview of immune system, innate and acquired immune system. Structure and functions of antibody molecule. Genetics basis of antibody diversity. MHC I and II polymorphism. Characteristics of B cell and T cell antigens. MHC peptide interaction. Affinity maturation. Autoimmunity and molecular mimicry.

Reference:

1. Lehninger A L. et al., 1993. Principles of Biochemistry. CBS publishers and Distributers, New Delhi, India.
2. Brown T A. Genomes. BIOS Scientific Publishers Ltd., 2002
3. Daniel , Molecular Cell Biology –, Sceintific American Books
4. Old & Primrose, Principles of Gene Manipulations –, Black Well Scientific Publications
5. EDP Roberties & EMF Roberties, Cell Biology & Molecular Biology , Sauder College.
6. E.J.Gardener, M.J.Simmons and D.P.Snustad, Principles of Genetics, John Wiley & Sons Publications
7. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.

Subject title **:** Structure and Functions of Biomolecules
Course number **: 07BICT2** **Number of lecture hours: 5**
Subject description :
This paper emphasizes the fundamentals of nucleic acid, carbohydrate, lipid and protein structure and high throughput techniques for structure prediction.

Goals:
A thorough understanding of biomolecular structure and function is prerequisite to study bioinformatics.

Objectives:
Students completing this paper understand biomolecular structure and function and techniques that are basic to bioinformatics applications

Contents:

Unit I Carbohydrates and lipids: their importance in cells. Proteins: amino acids and peptides, primary, secondary, tertiary and quaternary structures, conformational properties of proteins, Ramachandran plot. Nucleic acids: bases, nucleotides, RNA and DNA. Different structural forms of DNA, denaturation and renaturation of DNA.

UnitII X-ray crystallography of small molecules: x-ray generation, its application, unit cell, x-ray anomalous scattering, lattices, Bragg's law, atomic scattering factor and structure factor, phase problem, intensity data collection and reduction, direct method of solving a small molecule, refinement of crystal structure.

Unit III X-ray crystallography of macromolecules: isolation and purification of protein (chromatography, electrophoresis), crystallization (sitting and hanging drop method). Protein structure determination: molecular replacement technique, multiple isomorphous replacement methods, synchrotron radiation and its uses, multi wavelength anomalous diffraction method, calculation of electron density map, interpretation of electron density map, refinement of the structure, structure validation method.

Unit IV Protein structure modeling: homology modeling, threading, fold recognition, vector based method, neural network, model refinement and validation.

Unit V Functional classification of proteins: cell surface receptors, GPCR, kinases, channel proteins, Ubiquitin.

References:

1. Cantor and Schimmel. Biophysical chemistry, Part II, Techniques for the study of biological structure and functions, Freeman and company.
2. Thomas E Creighton. Protein structure and molecular properties, Freeman and company.
3. Ladd M F C and R A Palmer. Structure determination by X-ray crystallography, II Ed. Plenum press.
4. Cullity B D. Elements of X-ray diffraction, 2nd Ed. Addison-Wesley publishing company.
5. Duncan E. McRee. Practical protein crystallography, Academic press, INC.
6. Lehinger, A L. Principles of biochemistry, CBS publishers and distributors, New Delhi, India
7. Stryer L. Biochemistry, 4th Ed. W H Freeman and company, New york.

Subject title : **Computer Programming in C**
Course number : **07BICT3** **Number of lecture hours: 5**
Subject description :
This subject presents the fundamentals of programming techniques, namely sequence of execution, Selection of blocks to be executed, repetition of execution etc with the help of C programming language.

Goals:
To make the students to learn problem solving, execution of programs, thinking the problems in procedure manner and apply the concepts

Objectives:
On successful completion of the course the students should have:
Understood basic of approaching a problem to be computerized
Learnt the various techniques of writing codes to be executed.

Contents:

Unit I Steps in problem solving, overview of C, introduction, character set, C lopin, keyword and identifiers, constants, variables, data types, operation, expression, types of conversion and expression.

Unit II Statements: assignment of statements, decision making statements, the ?: operations, the goto statement, looping statement, the while statement, do statement, for statement.

Unit III Arrays: string handling, string manipulation, user defined function, C function, parameter passing, return values and their types, recursive function with arrays, scope and lifetime of variables and functions, structures and unions.

Unit IV Pointers: understanding pointers, accessions, the address of the variables, declaring and initializing pointers, pointer arithmetic, pointer and functions.

Unit V File management in C: defining and opening a file, closing file, I/O operations in file, error handling during I/O operation, random access files, command line arguments.

Reference:

1. Balagurusamy E, Programming in C, Tata Mc Graw Hill, 1977.
2. Byron Gottfried, - "Programming with C**"** (Schaum's Outline Series) – Tata McGrawHill Publishing Company - 1998.
3. Ramesh Bangia, Learning C, Khanna Book Publishing Co Pvt. Ltd.

Subject title : **Computational methods for sequence analysis**
Course number : **07BICT4** **Number of lecture hours: 5**
Subject description :

This paper describes how to acquire information from biological databases, use of computational approaches to analyze this data, and interpret the results as a guide to experiments in biology.

Goals:

The goal of this course is to introduce the main principles of bioinformatics. The coverage will include concepts like sequence alignments, phylogenetic trees, and structure prediction.

Objectives:

Understand Genomic data acquisition and analysis, comparative and predictive analysis of DNA and protein sequence, Phylogenetic inference etc.

Contents:

Unit I Protein and nucleic acid sequencing and sequence properties. Scoring matrices - PAM and BLOSSUM. Pairwise sequence alignment: concept, Global *versus* local. Multiple sequence alignment: concept, progressive alignment, Significance of alignments. Database searches for homologous sequences: Fasta and Blast

Unit II Evolutionary analysis: Definition and description of phylogenetic trees and various types of trees. Maximum parsimony, distance, Maximum likelihood, Bootstrapping strategies.

Unit III Sequence patterns and profiles: Basic concepts and definition of sequence patterns, motifs and profiles, various types of pattern representations viz. consensus, regular expressions and profiles, profile based database searches using PSI-BLAST, analysis and interpretation of profile based searches.

Unit IV Genome sequence assembly, Gene prediction: analysis and prediction of regulatory region.

Unit V Neural network: concepts and its applications. Hidden Markov Model: concepts and its applications

Reference:

1. **Andreas D. Baxevanis (Editor) and B. F. Francis Ouellette (Editor). Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Third Edition**
2. **David W. Mount, Bioinformatics Sequence and Genome Analysis, 2nd ed. (2004)**
3. **C. Branden and J. Tooze, Introduction to Protein Structure, 2nd ed (1999) -comprehensive information on proteins.**
4. **Arrwood A T and D J Parry-smith, Introduction to Bioinformatics, Pearson education Ltd.**
5. **K. Mani and N. Vijayaraj. Bioinformatics – A Practical Approach. Aparnaa Publication**
6. Dr.K.Mani and Mr.N.Vijayaraj, **Bioinformatics for Beginners**
7. **Rastogi et al., Bioinformatics methods and applications, Genomics, proteomics and drug discovery. Prentice-Hall of India Private Ltd.**
8. **Shanmughavel, P. 2005.** Principles of Bioinformatics, **Pointer Publishers, Jaipur, India**

Subject title : Practical I. Computer programming
Course number : 07BICP1 Number of hours: 3
Subject description :
This paper includes introduction to internet, HTML, operating systems and some of the basic programs in C, database creation
Goals:
The general aim of this course is to provide an overview of the basic concepts that appear in C programming languages, and basic computer skills to manipulate biological information.
Objectives:
Students should be able to read and write C programs, create web page, and database.

Contents:

MS OFFICE and HTML

1. Working with MS-OFFICE packages – one exercise each in word, Excel, Power point and Access
2. Working with HTML, Tags and HTML, Forms, creating HTML pages (at least five different pages to be created using all tags learnt).
3. Basic commands in MS-DOS and command line execution in LINUX.

Programming in C

I. Character array manipulations

1. Read and display a character array
2. Reverse print the array (String reverse)
3. Length of the array
4. Copying the contents of one array to another (string copy)
5. Copy the uppercase character of one array as lowercase character to another array
6. Checking whether a string is a palindrome or not
7. Copy the left 'n' character of one array to another
8. Copy last 'n' character of one array to another
9. Copy middle 'n' character of one array to another
10. Concatenate two character arrays (String concatenate)
11. Counting the numbers of words, lines and characters in a array
12. Counting the numbers of uppercase and lowercase alphabets, digits and special characters in an array
13. Check the number of occurrences of a pattern
14. Check the occurrences of a pattern and skip the same
15. Check the occurrence of a pattern and replace it with a different pattern

II. Pointers and Character array

16. Pattern counting
17. Pattern skipping
18. Pattern replacing

III. Files and command line arguments

19. Read data from the keyboard and write it in the file
20. Read data from the file and display it on the screen
21. Display the content of all the files
22. Copy data from one file to another
23. Pattern count
24. Line in which the pattern occurs with line number
25. Group all files (Pattern match all files)
26. One project to be completed in C

Visual Basic and Oracle

1. Create Tables, queries and simple PL/SQL program
2. Construct user interface with manipulation and validation
3. Provide Database connectivity and hence produce reports.
4. Mini project using Visual basic and Oracle.

Subject title : **Practical II Biological databanks and sequence analysis**
Course number : 07BICP2 Number of hours: 3
Subject description :
This paper includes data retrieval fro database and analysis
Goals:
Students will learn to use conventional software and web based applications
Objectives:
Students should be able to use available software for sequence alignment, secondary structure prediction and molecular graphics tools, understand the principles behind algorithms and the methods of cluster analysis.
Contents:

1. Biological databanks: Sequence databases, structure databases, specialized databases
2. Data retrieval tools and methods
3. Database file formats
4. Molecular visualization
5. Gene structure and function prediction (using GenScan, GeneMark)
6. Sequence similarity searching (NCBI BLAST)
7. Protein sequence analysis (ExPASy proteomics tools)
8. Multiple sequence alignment (Clustal)
9. Molecular phylogeny (PHYLIP)
10. Analysis of protein and nucleic acid sequences using EMBOSS or GCG

Subject title : Molecular Interaction
Course number : 07BICT5 Number of lecture hours: 5
Subject description :
This paper deals with some of the basic features in molecular interactions.
Goals:
To make the students familiar with chemical bonding and interaction between the molecules.
Objectives:
Students should be able to interpret the interaction between molecules.
Contents:

Unit I Fundamentals of chemical bonding and non-bonding interactions: electrovalent bond, stability of electrovalent bond, covalent bond; Shape of orbital and hybridization; Molecular geometry; partial ionic character of covalent bond; coordination bond; Vander Walls forces; metallic bond.

Unit II Fundamentals of atomic and molecular orbital: theory of atomic and molecular orbital; linear combination of atomic orbital; quantitative treatment of valency bond theory and molecular orbital theory; resonance structure; phi bond and sigma bond.

Unit III Molecular interactions: protein-protein, protein-DNA, DNA-drug, protein-lipid, protein-ligand, protein-carbohydrate, intercalation, metaloprotein.

Unit IV Folding pathways: principles of folding, role of chaperons, hydrophobic interactions, electrostatic interactions, non-bonded interactions, dispersive interactions, beta turns, gamma turns, types of helices, disulphide bridge, role of unusual amino acid dictating protein folding.

Unit V Applications of UR, IR, NMR and CD in macro molecules. Stereochemistry of protein and nucleic acid.

Reference:

1. Albert cotton, F. 1971, Chemical application of group theory. John Wiley and sons, Inc. New York. 386 pp.
2. Spice, J. E. 1964. Chemical bonding and structure, Pergamon Press Ltd. Headington Hill Hall, Oxford. 395 pp.
3. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.
4. Winter, M. J. 1996. Chemical bonding. Oxford University Press, Inc., New York. 91 pp.
5. Lehinger, A L. Principles of biochemistry, CBS publishers and distributors, New Delhi, India
5. Ernest Eliel, 1996. Stereochemistry of carbon compounds, Prentice hall.

Subject title : Systems Biology
Course number : 07BICT6 Number of lecture hours: 5

Subject description :
Includes the basics of analysing metabolic pathways using bioinformatics tools and also the simulation of cellular environment.

Goals:
To understand the gradual maturation of genomics and proteomics into biology insilico. Convergence of genomics, proteomics, transcriptomics and metabolomics in to phenomics.

Objectives:
Students should be able to understand the interaction within biological networks and simulation of cells.

Contents:

Unit I Functional genomics:
Developmental biology and differential expression of genes: sporulation vs. vegetative condition in Yeast and Bacillus, disease vs. normal condition (breast cancer), brain vs. gut (organ specific); method of study: microarray – types of array, tagging, documentation, stanford microarray database; microarray analysis: image analysis and normalization, hierarchial clustering, self organizing map.

Unit II Metabolic genotype:
Central metabolism: EMP, PPP, TCA, Electron transport, alternative carbon sources, amino acid metabolism, purine and pyrimidine metabolism, vitamin and cofactor metabolism, lipid metabolism, Translating biochemical network into linear algebra.

Unit III Whole cell simulation
Principle and levels of simulation: virtual erythrocytes, pathological analysis, fermentation analysis, flux balance analysis, minimal gene complement

Unit IV Relationship analysis: predicting ligand binding function, guilt by association, use of gene cluster, comparative genome analysis, binding surface comparisons, detecting protein-protein interaction.

Unit V Creative bioinformatics
Novel use of databases: use of EST database, Unigene, use of PDB database, gene discovery, primer design, restriction mapping, pharmacophore building, position specific cloning, SNP database, target identification, epitope identification, energy economy analysis.

Reference:

1. Andreas D. Baxevanis and B F Francis. Ouellete Bioinformatics. A practical Guide to the analysis of genes and proteins. A john Wiley & sons, Inc.
2. Steven R Gullans, 2000. Microarray and meandering data points. Nature genomics. 26:4-5.

3. Michael B. Eisen et al. 1998. Cluster analysis and display of genome-wide expression patterns. Proc. Natl. Acad. Sci. USA, 95: 14863-14868.
4. Chu et al. 1998. The transcriptional program of sporulation in budding yeast, Science, 282: 699-705
5. Charles M. Perou. 2000. Molecular portraits of human breast tumours. Nature, 406: 747-752.
6. Uwe Scherf et al. 2000. A gene expression database for the molecular pharmacology of cancer. Nature genetics, 24: 236-244.
7. Jeremy. S. Edwards et al. 2000. The Escherichia coli MG. 1655 in silico metabolic genotype: its definition, characteristics and capabilities, PNAS, 97:5528-33.
8. Chistoper H Schilling et al. 1998. The underlying pathway structure of biochemical reaction networks. PNAS, 95: 4193-8.
9. Masaru Tomita. 2001. Whole cell simulation: a grand challenge of the 21st century, Trends in biotechnology, 19: 205-210.
10. Stephen Schuster et al. 1999. A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks. Nature Biotechnology, 18: 326-332.
11. Christopher H Schilling et al. 1999. Towards metabolic phenomics: Analysis of Genomic data using Flux balance. Biotechnol. Prog, 15: 288-295.
12. Claire M Fraser et al., 1995. ycoplasma genitalium. Science, 270: 397-403.

Subject Title : Introduction to Visual basic with RDBMS
Course Number : 07BICT7 Number of lecture hours: 5
Subject Description :
This subject presents introduction to GUI, creation of various controls to be used in the project, connecting databases with the front end etc..
Goals:
To make the students to learn problem solving using visual basic programming language
As well as connecting front end and back end .
Objectives:
On successful completion of the course the students should have:
Understood GUI programming techniques.
Learnt the various controls used in a program.
Learnt the applications of object oriented approach.
Learnt the connectivity of databases to the controls.

Contents:

Unit I Introduction to VB, Steps in VB application, IDE Environment, Property, Method, Event, Project Explorer window, Property window, Form layout, Code window, Event driven programming, Menu bar, Tool bar, Working with forms

Unit II Variables, Constants, Literals, Datatypes, Operators, Subroutine and functions, Strings, Remark and end statements, string function, Date function, Numeric function – Program flow controls

Unit III Intrinsic controls: Pointers, label, frame, checkbox, Combobox, Scroll bar, Timer, Shape and line control, command button, list box, timer, image box, picture box, textbox, SDI and MDI form, Data Grid, Flex Grid, Menus, Dialog boxes

Unit IV RDBMS: Database, Entity, Attribute, Representing tables, SQL Commands for creating a table, updating a table, manipulation commands.

Unit V DAO, Creating a database, Creating Record set, Types of Record sets, ActiveX Data Object (ADO), RDO .

Reference:

1. Gary Cornell "Visual Basic 6 from Ground up" Tata Mc Grawhill Edition
2. Content Development Group "Visual Basic 6 programming" TMH publishers, 2002
3.introduction to database management system-Bipin Desai
4.. Paul Sheriff –"VISUAL BASIC-"- PHI Publishers-2002
5. VISUAL BASIC Programming 2005- Dreamtech press-2006.

Subject title : Mathematical methods and statistical techniques
Course number : **07BICT8** **Number of lecture hours: 5**
Subject description :

Basic mathematics pertaining to bioinformatics is included in this paper.

Goals:

To learn the basic idea that are essential for a clear understanding of various algorithms and some techniques.

Objectives:

Students should be able to understand algorithms in sequence analysis, and develops simple tools in bioinformatics.

Contents:

Unit I Matrices: types, determinants, inverse, solving a system of linear equations. Vectors: definition, types, dot product, cross product (upto three vectors) gradient, divergence, curl. Differentiation: standard results, derivatives of simple functions, partial differentiation of three variables only. Integration: standard results, integrals of simple functions.

Unit II Numerical methods and optimization: errors; solving ODE: RK method, Taylor's series, Euler's method; Minimization and maximization of function: golden section search in one dimension, Downhill simplex method in multi dimention, conjugate gradient method.

Unit III Fourier transform: definition, properties, simple problems, application of discrete Fourier transform, fast Fourier transform; randomized minimization technique: Monte-Carlo minimization, simulated annealing, Genetic algorithm

Unit IV Statistical technique: Frequency distribution, graphical representation; measures of central tendency: mean, median, mode; measures of dispersion: range, standard deviation, coefficient of variation, correlation and regression analysis; probability: addition rule, multiplication rule on probability, random variable, probability mass function, probability density function.

Unit V Theoretical distribution: Binomial, poission and normal distribution (simple applications only); test of significances: large sample test-single mean-differences of two mean. small sample (t-test): single mean-difference of two means; chi square (x^2) test for goodness of fit; Anova: one way and two way classification.

Reference:

1. Calculus – Vol1 and II T K Manickavasagam pillai and others
2. Numerical methods in science and engineering – M K Venkatraman
3. Numerical methods for engineers with personal computer applications – Chopra S C Raman and Canale P
4. Optimization techniques by S S Rao
5. Statistical methods – S P Gupta
6. Engineering mathematics – T Veerarajan

Subject title : Genomics
Course number : 07BICT9 Number of lecture hours: 5
Subject description :
This paper deals with genome map, comparative genomics, structural genomics, functional genomics and regulation.
Goals:
To make the students to familiar with genome map, comparative genomics, structural and functional genomics.
Objectives:
Understand the genome architecture and to extract information like gene function, gene regulation, protein evolution and targets for drug designing

Contents:

Unit I Genome map:
Types and their uses: high and low resolution map, map elements, polymorphic markers, Line, sine, RFLP, SNP; types: cytogenetic (linkage map, transcript map), physical map (comparative map, integrated map); map repositories: GDB-genome database, NCBI-Enterz- Human genome map viewer, OMIN, NGI/MGD-mouse genome initiative database, mouse genome expression database; Linkage map resources: CEPH reference pedigree, CHLC, radiation

hybrid map resources, STS content maps, single chromosome and regional maps; Practical uses of genome maps.

Unit II Annotation of the genome:

Structural annotation (locating coding region and other structural elements of the gene); various approaches in gene prediction: ORF prediction, gene prediction in prokaryotes, gene prediction in eukaryotes, HMM, evaluation of gene prediction method, pattern discrimination, prediction of promoter sequences; Functional annotation (prediction of gene function): employing the similarity in the sequence, gene family and metabolic pathway, employing the conserved domain, profile and motif comparison, EST comparison.

Unit III Genomic diversity:

Salient features, statistical information, size, biology, taxonomy and significance of following genomes: bacterial, cyanobacterial, plasmodium, yeast (S. cerevisiae), worm (Coenorhabditis), zebra fish, drosophila, Homo sapiens, Arabidopsis, viral, mitochondrial, chloroplast and plasmids.

General purpose comparative genomic databases: PEDANT, COG, KEGG, MBGD, WIT, organism specific database.

Unit IV Human genome and genome analysis: size, features, comparison and characteristics of human genome, sequence repeats, transposable elements, gene structure, pseudo genes.

Genome analysis: gene order, chromosome rearrangement, compositional analysis, clustering of genes, composite genes.

Unit V Comparative genomics:

Purpose and methods of comparison: comparison at nucleotide level, breakpoints level, gene cluster level, ontological comparison, phylogenetic comparison; tools for genomic comparison, applications of comparative genomics.

Reference:

1. Andreas D Baxevanis and B F Francis Ouellette. Bioinformatics, A practical guide to the analysis of genes and proteins. A John Wiley & Sons, Inc publications.
2. David Mount, 2001 Bioinformatics, Sequence and genome analysis.
3. Malcolm J Gardner et al 2002. Genome sequence of the human malarial parasite, Plasmodium falciparum. Nature, 419: 498-511.
4. Peter D Karp et al, 1996. EcoCyc: encyclopedia of E coli genes and metabolism. Nucleic acids research, 10: 86-90
5. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.
6. Shanmughavel, P. 2006. **Trends in Bioinformatics,** Pointer Publishers, Jaipur, India.
7. Ann Gibbons, 1998. Comparative genetics, Science, 281: 1432-1434.
8. Attwood & Parry-smith. Introduction to bioinformatics.
9. Rastogi et al., Bioinformatics, Methods and applications. Prentice-Hall of India Pvt. Ltd.

Subject title : Proteomics
Course number : 07BICT10 Number of lecture hours: 5
Subject description :
This paper deals with protein structure prediction and function and various tools for analysis of proteins.
Goals:
Proteomics is extensively used in drug discovery, and to learn various tools for analysis of proteins.
Objectives:
Taxonomy, structure-function relationship and functional aspects of the entire set cell.
Contents:

Unit I Protein structure comparison and classification: architecture, Blocks, Class and domains, fold, motif, PSSM, profile, principles of classification, CATH, SCOP, FSSP, MMDB, SARF.

Unit II Protein structure prediction: chou-fasman/GOR method, Neural network, nearest neighbor method, tertiary structure prediction, threading, contact potential, modeling; use of sequence pattern: leucine zipper, coiled coil, transmembrane, signal peptide, cleavage site.

Unit III Proteome analysis:
2D electrophoresis: immobilized pH gradient, sample preparation, first dimension criteria, second dimension criteria, stabilization; Detecting protein on gel: electroblot, image analysis, digital imaging, spot detection and quantification, gel matching; Data analysis: mass spectrometry based method for protein identification and analysis; database for 2D gel.

Unit IV Functional proteomics:
Integrated proteome analysis: phage antibody as tool, protein expression analysis, high throughput analysis for proteomics; Automation of proteomic analysis: organ comparison, spatio temporal comparison, cross species, intra species comparison.

Unit V Applications of Proteomics: plant breeding, clinical and biomedical.

Reference:

1. Pennigton S R. and M.J. Dunn. Proteomics, 2002.
2. Kris Gevaret et al., 2000. Protein identification methods in proteomics. Electrophoresis, 21: 1145-54.
3. Wilkins M R et al., Proteome research: New frontiers in functional genomics. Springer.
4. Andreas D Baxevanis and B F Francis Ouellette. Bioinformatics, A practical guide to the analysis of genes and proteins. A John Wiley & Sons, Inc publications.
5. David Mount, 2001 Bioinformatics, Sequence and genome analysis.
6. Attwood & Parry-smith. Introduction to bioinformatics.
7. Rastogi et al., Bioinformatics, Methods and applications. Prentice-Hall of India Pvt. Ltd
8. Shanmughavel, P. 2005. Principles of Bioinformatics**,** Pointer Publishers, Jaipur, India

Subject title : Molecular modeling and computer aided drug designing
Course number : 07BICT11 Number of lecture hours: 5
Subject description :
This paper deals with molecular modeling, quantum mechanics, molecular mechanics pertaining to drug discovery.
Goals:
Provide a broad and through background in modeling tools and docking program
Objectives:
understand the theories used to build tools and their relationship and basic concepts involved in drug design.
Contents:

Unit I Introduction to the concept of molecular modeling, molecular structure and internal energy, applications of molecular graphics, coordinate systems, potential energy surfaces, discussion of local and global energy minima

Unit II Introduction to computational quantum mechanics: one electron atom, poly electronic atoms and molecules, Hartree Fock equations; calculating molecular properties using ab initio and semi empirical methods

Unit III Molecular mechanics: general features of molecular mechanics force field, bond stretching, angle bending, torsional terms, non-bonded interactions; force field parametrisation and transferability; energy minimization: derivative and non-derivative methods, applications of energy minimization.

Unit IV Molecular dynamics simulation methods: molecular dynamics using simple models, molecular dynamics with continuous potential, setting up and running a molecular dynamic simulation, constraint dynamics; Monte carlo simulation method: Monte Carlo simulation of molecules.

Unit V Macromolecular modeling, design of ligands for known macro molecular target sites, Drug-receptor interaction, classical SAR/QSAR studies and their implications to the 3-D modeler, 2-D and 3-D database searching, pharmacophore identification and novel drug design, molecular docking, Structure-based drug design for all classes of targets.

Reference:

1. Andrew R Leach. Molecular modeling: principles and applications, Prientics Hall publications
2. Tamaer Schlick Molecular modeling and simulation, Springer publications
3. Rauter, C Horn, K 1984, X-ray crystallography and drug design
4. William B Smith Introduction to theoretical organi chemistry and molecular modeling
5. Claude N Cohen Molecular modeling in drug design
6. Principles of Bioinformatics, Shanmughavel, P. 2005 , Pointer Publishers, Jaipur, India.
7. Shanmughavel, P. 2006. Trends in Bioinformatics, Pointer Publishers, Jaipur, India.

Subject Title : PERL PROGRAMMING FOR BIOINFORMATICS
Course Number : 07BICT12 Number of lecture hours: 5
Subject Description :
This subject presents of programming techniques used with three languages like PERL,BIOPERL AND PYTHON namely data types used, lists and hash sequence of execution,

Goals:
To make the students to learn problem solving skills using pattern recognition techniques, using scripting language.

Objectives:
On successful completion of the course the students should have:
Understood basic of pattern recognition.
Learnt the various techniques of writing codes for pattern recognition.
Apply the coding in bioinformatics

Contents:

Unit I Introduction to PERL-history of PERL-application of PERL-availability-Basic concepts-Scalar data type-Arrays and list-Statements-blocks-decision and looping statements-Hashes

Unit II Basic input/output-Regular expressions-concepts-simple uses of patterns-more on matching operator-substitution-functions-file handles

Unit III Object oriented programming in PERL-sequences-format and inheritance-a class for restricting enzymes.

Unit IV PERL and bio informatics-Introduction to BIOPERL-

Unit V PYTHON-what is python-installation-python basics – applications in Bioinformatics

References:
1.Genomic PERL-from bio informatics basic to working code-Rex A Dwyer
2.PERL cook book
3.Mastering PERL for bioinformatics-James D Tisdall-O'rilley press-2000.
4.UNIX Power tools –Mike loukides,Tim O'reilly,Jerry peek,Shelly pwers-O'rielly press
5.Learning PERL-III Edition-Randal L schwartz,Tom Phoneix
6.PERL 5complete-Ed Peschko &michele Dewolfe-McHill publications

Subject title : Practical III – Perl programming.
Course number : 07BICP3 Number of hours: 3
Subject description :
Some of the basic programs in perl
Goals:
The use of Perl and available modules for routinely performed bioinformatics tasks.
Objectives:
Ability to write simple Perl scripts.
Contents:

1. Program to store a DNA sequence
2. Programme to concatenate DNA fragments
3. Program to convert DNA to RNA
4. Program to calculate reverse complement of DNA sequence
5. Program to read protein sequence data from a file
6. Program to print the elements of a array
7. Program to take an element off the end of an array
8. Program to take an element off the beginning of an array
9. Program to put an element at the beginning of an array
10. Program to put an element at the end of an array
11. Program to reverse an array
12. Program to get the length of an array
13. Program to insert an element at a random position in an array
14. Program to find motif in a protein sequence
15. Program to count nucleotide in a sequence
16. Program to find the percentage of G and C in a DNA sequence
17. Program to find the percentage of type of amino acid in a sequence
18. Program to append ATGC to a DNA sequence using subroutines
19. Program to concatenate two strings using subroutines
20. Program to count the number of given motifs
21. Program to convert DNA to RNA using subroutines
22. Program to find is a DNA is stable or not.
23. One Project to be completed in Perl

Subject title : Practical IV – Computer Aided Drug Design
Course number : 07BICP4 Number of hours: 5
Subject description :
This paper includes small molecule generation, protein modeling and docking
Goals:
To provide an understanding of molecular modeling and hands-on experience of chemical databases and modeling software.
Objectives:
Understand molecule generation, target identification, modeling and docking software
Contents:

1. Small molecule building using ISIS DRAW and Chemsketch
2. Homology modeling using SPDBV
3. Modeled structure refinement using SPDBV
4. Model validation using What Check and Pro Check
5. Docking using DOCK or AUTODOCK or AMBER

PRACTICALS – MODEL QUESTION PAPER
Bharathiar University, Coimbatore – 46.
Practical I
07BIP01- Protein, Nucleic Acid, Immunology and Pharmacology

Time 6Hrs **Total Marks 60**

1. Experiment on Protein wet lab	10 marks
2. Experiment on Nucleic acid Wet lab	10 marks
3. Experiment in Immunology	10 marks
4. Experiment on Pharmacology Wet lab	10 marks
5. Record work	10 marks
6. ViVa	10 marks
Total	**60 marks**

(Subject to MODIFICATION by the EXAMINERS)

Practical II
07BIP02 - Computer Programming

Time 3Hrs **Total Marks 60**

1.	Programming in C (2 programs in C)	10 marks
2.	Programming in Perl (2 programs in PERL)	10 marks
3.	Mini project	20 marks
4.	Record	10 marks
5.	Viva	10 marks
	Total	**60 marks**

(Subject to MODIFICATION by the EXAMINERS)

PRACTICALS – MODEL QUESTION PAPER
Bharathiar University, Coimbatore – 46.

Practical III
07BIP03 - Biological Databanks & Sequence Analysis

Time 3Hrs **Marks 60**

1.	Exercise in EMBOSS	10 marks
2.	Exercise on Multiple Sequence Alignment	10 marks
3.	Exercise on protein sequence analysis using Proteomic Tools	10 marks
4.	Exercise on Gene structure and function prediction (using GenScan, GeneMark)	10 marks
5.	Record	10 marks
6.	Viva	10 marks
Total		**60 marks**

(Subject to MODIFICATION by the EXAMINERS)

Practical IV
07BIP04 – Computer Aided Drug Design

Time 3Hrs **Marks 60**

1.	Small molecule building, using ISIS DRAW and CHEM SKETCH	10 marks
2.	Homology Modeling using SPDBV	10 marks
3.	Find out Ramachandran plot deviant	10 marks
4.	Calculate RMSD	10 marks
5.	Record	10 marks
6.	Viva	10 marks
Total		**60 marks**

(Subject to MODIFICATION by the EXAMINERS)

07BIDT1 Diploma Paper – I: Biology of Cloning Vectors

SEM I

Plasmids (pUC 18 and Ti plasmids), Bacteriophages (λ phage), Plasmids, Cosmids (pJB8), SV40, retrovirus and Artificial Chromosomes (BAC, YAC).

Strategies in gene cloning: restriction, ligase, insertion into vector, cloning, transformation into host cell, Enzymology of Recombinant DNA.

Screening for recombinant (Insertional inactivation, Colony/in situ hybridization, radioactive antibody test, Xgal, complementation and physical methods)

07BIDT2 Diploma Paper – II: Methods of gene transfer and genome sequencing

SEM II

$CaPO_4$ mediated gene transfer, liposomes, electroporation, electro fusion, micro-injection, particle bombardment.

DNA sequencing (Sanger and Coulson method; Maxam and Gilbert method and Automated method) - Chromosomal walking, transposons, construction of genomic and cDNA libraries; molecular markers- RAPD, RFLP.

07BIDT3 Diploma Paper –III : Applications of rDNA technology

SEM III

Transgenic plants – high yielding, salt, draught, herbicide, disease resistant.

Transgenic animals - for improved livestock production.

rDNA in medicine: Vaccines, enzymes, blood factors, interferon, gene therapy,

DNA fingerprinting and its applications in forensic sciences.

REFERENCES:

1. Principles of genetic manipulation; Ed. Old and Primrose, 6th Edition. Blackwell Science publication
2. Gene Cloning, a introduction – T. A. Brown, Chapman and Hall publications, 3rd Edition, 1995

07BIDP1 **Diploma Practical I – Molecular techniques**

SEM IV

1. Pure culture techniques
2. Preparing competent culture
3. Agarose gel electrophoresis
4. SDS-PAGE
5. Blotting techniques
6. PCR

07BIDP2 **Diploma Practical II - rDNA Technology**

SEMIV

1. Microbial genomic DNA isolation
2. Microbial plasmid isolation
3. Plant genomic DNA isolation
4. Animal genomic DNA isolation
5. Restriction mapping with Lamda DNA
6. Ligation

MODEL QUESTION PAPERS

FUNDAMENTALS OF BIOLOGICAL SYSTEMS

Time: 3Hrs **Max.Marks: 100**

SECTION-A (10 X 2= 10)

Choose the Best Answer

1. A thick cell wall composed primarily of the fibers of the
   a) Starch b) Polysaccharide cellulose
   c) Chromatin fibers d) both b and c
2. In mitochondria the matrix contains
   a) Several ATP b) Several circular
   c) Several enzymes d) Both a and c
3. The length of the prokaryotic cells ranging from
   a) 1 to 3 microns b) 3 to 4 microns
   c) 2 to 3 microns d) 6 microns
4. DNA polymerase was found in the year of
   a) 1969 b) 1959
   c) 1979 d) None of the above
5. Mutation causing changes in the metabolites is called
   a) Metabolic mutation b) Biochemical mutation
   c) Meto mutation d) both a and b
6. What is the ratio of dihybrid back cross
   a) 1:1:1:1:1 b) 1:3
   c) 9:3:3:1 d)12:1
7. Enzyme used for joining two molecules coupled to the hydrolysis of ATP is
   a) Lyases b) Ligases
   c) Isomerase d) Oxidoreductase
8. Michaelis Menten equation is
   a) V=Vmax[s]/Km+[s] b) V=Vmax+[s]/Km[s]
   c) V=Km+[s]/Vmax d) V=Vmax+[s]/Km+[s]
9. The immunity that is inherited by the organisms from their parent known as
   a) Innate b) acquired
   c) Passive d) Active
10. The molecular weight of IgH is
   a) 160,000 b)150,000
   c)170,000 d)180,000

SECTION-B (5 X 6 = 30)
Answer all the Questions
Each question carry equal Marks

11a) Elucidate the structure of an Eukaryotic cell with a neatly labeled sketch(Or)
   b) Describe about the various components of cell membrane

12 a) Explain the concept of attenuation in gene regulation(Or)
   b) Discuss about the basic mechanism of initiation of transcription

13 a) Discuss about the different types of point mutations(Or)

b) What do you know about Linkage Maps?

14 a) Discuss the role of co-enzymes in enzyme catalysis(Or)

b) Write about abzymes

15 a) Explain the structure of an antibody with a neatly labelled diagram(Or)

b) Give the characteristics of B cell antigens

SECTION-C (5 X10=50)
Answer all the Questions
Each question carry equal Marks

16a) Differentiate prokaryotic and eukaryotic cell(Or)

b). Define membrane. Discuss about the different membrane models

17 a) How lac operon is regulated(Or)

b) Detail the events of transcription

18 a) Discuss about the Mendelian principles of inheritance(Or)

b) Explain sex-linked inheritance with a suitable example

19 a) Describe M.M equation and explain its significance(Or)

b) Briefly explain the different types of enzyme inhibitors.

20a) Give an overview of the immune system(Or)

b) Explain antigen processing and presenting by MHC

STRUCTURE AND FUNCTION OF BIOIMOLECULES

Time : Three hours Maximum : 100 Marks

SECTION A – (10X 2 = 20 marks)

Answer **ALL** Questions

Choose the correct answer

1. SOM is

a. Self organising map b. Support organised map

c. Support membrane d. None of the above

2. The change due to transport of a metabolite from one compartment of a cell to another in a biochemical pathway is called

a. Internal flux b. External flux

c. Total flux d. All of the above

3. Inhibition by the product of the pathway is called

a. competitive b. Non-competitive

c. feedback d. Allosteric

4. The study of the interconnection of biological pathways is called

a. systems biology b. insilico biology

c. both of the above d. none of the above

5. Which of the following is the key enzyme in glycolysis

a. phosphofructokinase b. hexokinase

c. pyruvate kinase d. All of the above

6. The minimum number of gene required for the cell to function
   a. 127 b. 133
   c. 237 d. none of the above
7. Protein-protein interaction
   a. Microarray b. Yeast Two-hybrid
   c. X ray crystallography d. None of the above
8. Biochemical pathway is well organized in
   a. KEGG b. EMP
   c. WIT d. All the above
9. Stanford
   a. Microarray database b. Genomic database
   c. Proteomic database d. all the above
10. EST
   a.Exon specific sequence b.From cDNA
   c.Represent a gene d. All the above

SECTION B (5 X 6 = 30)

Answer **ALL** questions

11.a. Explain different types of microarray or
   b. Explain hierarchial clustering
12.a. Explain glycolytic pathway or
b. Explain electron transport chain
13.a. Explain different levels of simulation or
   b. What is flux balance? How does it operate?
14. a. Define the conformational flexibilities in the prediction of protein structures or
b. Discuss the types of clusters and their benefits derived for system's understanding
15.a. Comments on restriction mapping or
   b. Describe the method of EST production and explain EST database

SECTION C (5 x 10 = 50)

16.a. Highlight the techniques used to study the expression and regulation of genes in the prokaryotic systems
   or
   b. Explain microarray data analysis in detail
17.a. Explain the central metabolism via a EMP system or
   b. What is genotype? Explain with TCA cycle
18.a. Minimal gene complement are necessarily studied for a whole cell simulation approach – Give your views in support of this or
   b. How will you identify the various pathological status of diseases through a simulation approach
19.a. Explain in detail the detection of protein-protein interaction or
   b. Highlight on a comparative scale the role of binding surfaces and its relativity to relationship analysis between organisms
20.a. Write a note on (i) primer design (ii) Epitope identification or
   b. Write a note on (i) Target identification (ii) pharmacophore building

PROGRAMMING IN C

Max.Time:3.00 hrs **Max.marks:100**

Section A Answer all 10*2 =20 marks

1.A set of symbolic instructions used to solve a problem is called
a)algorithm b)flow chart c) program d)none of the above.
2.unsigned long int data type in C utilizes ------ bytes
a)1 b)2 c) 8 d) 16.
3.? : is a. conditional
a) expression b)expression c) variable d)none.
4. while statement executes only when the specified condition becomes --------
a) true b)false b) either a or b d) none.
5. An array can be declared using the format ----------.
a)data type array[] b) data type : array[] c)data type array d)data type : array
6.recursive functions call
a)other functions b)themselves c) both a and b d) neither a nor b
7.* operator in C can be used as ------- operator.
a)multiplication b)dereferencing c) both a and b d)none.
8. int *p has points to a ----------.
a)int data b)integer address c) address of integer data d)none
9.w+ mode is used for ----------.
a)writing b)writing and reading a new file c)writing and reading existing file d)append
10.fseek(fp,0L,1) has the position as -------- of the file.
a)beginning b)end c)current position d)none.

Section B Answer all 5*6 =30 marks

11a) Explain the properties of an algorithm. (OR)
b) Explain about float, double data types .
12a)Explain in brief else **if** ladder with an example. OR
b)Explain while statement with syntax.
13a) how does a strcpy() function work?give an example. (OR)
b)write a function to compare two strings and display the status.
14a)What is the difference between a pointer to an array and array of pointers?
Explain.
b)Write a program to swap two integers using pointers.
15)a) write a program to enter a record into a file. OR
b)Explain about fseek()function in detail.

Section C Answer all 5*10 =50 marks

16a)Explain about arithmetic and relational operators with examples. OR
b) Explain about arithmetic assignment operators in detail.
17a)Explain about switch…case statement in detail with an example. OR
b) Write a program to display the type of element given the element code as follows
code type

1 acid
2 base
3 alcohol.

Use switch statement.

18a)Explain in detail about unions in detail. OR

b)Write a program to create a union called gene with two members name, count. Create an array of structures called a with 10 members and manipulate them, and display them one by one .

19a) How is pointer arithmetic handled. Explain in detail .OR

b)Write a program which copies an array of integers to another array using pointers.

20a)Explain error handling in file I/O . OR

b) Write a program to store records and display them randomly.

COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS

Time: 3 hrs **Total: 100 marks**

SECTION A: (10 x 2=20)
Multiple Choice Questions

1. The numerical representation of a multiple sequence alignment is
a .Patterns b .Blocks c .Profiles c.Pfam
2. Protein sequenced with protein sequence.
a .Blast p b .Blast n c .Blast x c.T blast n
3. PSI blast is
a. Protein specific implementation b. Protein specific iterative
c. Paired specific iterative d. Paired specific implementation
4. The database stores 3d atomic coordinates of proteins and nuclic acid and the data is obtained by experimental methods like…….
a. Chromatography b. Colorimetry
c. X-ray crystallography d. Electrophorosis
5. The chou-fasman algorithm is used for the prediction of
a. Protein primary structure b. Secondary structure
c. Tertiary structure d. Quarternary structure
6. The human genetic material consists of ……
a. 3 Thousands nucleotides b. 300
c. 3 Billion d. None of these
7. Protein allows one to input protein sequences and compares the sequences against other protein sequences
a. Nucleotide blast b. Mega blast c. Protein blast d. Phi-blast
8. Blast was found out by
a. Thompson et al b. Alstuch *et. al* c. Both a and b d. None
9. The most popular methods conducting multiple sequence alignment are summarized in the
a. Venn diagram b. Tree diagram c) Dot plot d) Root
10. The phenetic method is applied for comparing organisms at genetic level and is suitable for smaller evolutionary divergence. This method is also called
a) Parsimony b) Maximum likelihood c) cladistic d) distance

SECTION B: (5 x 6=30)

11. (a) Write about the data retrieval systems.(Or)
    (b) Write about the major protein sequence databases.
12. (a) What is a scoring matrix? Write about PAM in detail.(Or)
    (b) Write the dynamic programming method used for local alignment.
13. (a) Briefly explain about the clustering method used for evolutionary analysis.(Or)
    (b) Explain about the rooted and unrooted tree representation used for evolutionary analysis.
14. (a) Write about the various gene-finding methods used.(Or)
    (b) Write about the significance of repeats.Expalin how repeats are identified in a sequence
15. (a) Write about the concept of secondary structure prediction of RNA.(Or)
    (b) Write about the concept of secondary structure prediction of protein.

SECTION C: (5 x 10=50)

16. (a) What are the various secondary structure databases? Write its uses.(Or)
    (b) What is Bioinformatics? Write about the applications of bioinformatics in various fields.
17. (a)Write about sequence similarity search using BLAST and FASTA.(Or)
    (b) What is multiple sequence alignment? Write its applications.
18. (a) Write the uses of Clustal and PHYLIP?(Or)
    (b) What are the methods used for evolutionary analysis.
19. (a) Explain the various aspects of genome sequence assembly.(Or)
    (b) Write in detail about restriction mapping.
20. (a) Describe Markov model and Hidden Markov model.(Or)
    (b) What are the applications of probabilistic models used for secondary structure prediction.

PRACTICALS – MODEL QUESTION PAPER
Bharathiar University, Coimbatore – 46.
Practical II
Computer Programming

Time 3Hrs **Total Marks 60**

1.	Programming in C (2 programs in C)	10 marks
2.	Programming in Perl (2 programs in PERL)	10 marks
3.	Mini project	20 marks
4.	Record	10 marks
5.	Viva	10 marks
	Total	**60 marks**

PRACTICALS – MODEL QUESTION PAPER
Bharathiar University, Coimbatore – 46.
Practical III
Biological Databanks & Sequence Analysis

Time 3Hrs **Marks 60**

1. Exercise in EMBOSS 10 marks
2. Exercise on Multiple Sequence Alignment 10 marks
3. Exercise on protein sequence analysis using Proteomic Tools 10 marks
4. Exercise on Gene structure and function prediction (using GenScan, GeneMark) 10 marks
5. Record 10 marks
6. Viva 10 marks

Total **60 marks**

(Subject to MODIFICATION by the EXAMINERS)

BIOLOGY OF CLONING VECTORS

Paper Code – 07BTDT2

Time : Three hours Maximum : 100 Marks

SECTION A – (10X 2 = 20 marks)

Answer **ALL** Questions

1) **W**hat are PUC3 Plasmids
2) Example for cosmids plasmids
3) M13 Phage vector are used in----------
4) EcoRI restrictes the site----------
5) Phage DNA are Double stranded - True/False
6) What are Centromere Plasmid
7) Cloning means
8) Give are example of Ligase enzyme
9) A Vector which multiplies in two different species are called----------
10) Episomal Plasmid are driven from----------

SECTION B – (5 x 6 = 30 marks)

Answer **ALL** Questions

1. (a) Explain the General Structure of Plasmid Or
   (b) Illustrate Non-Conjugative Plasmid
12. (a) Describe Bacteria Phage Or
   (b) Explain single circular DNA Vector with example
13. (a) Describe artificial chromosomes Or
   (b) Give few examples for Animal vectors
14. (a) Characterstitic features of host cell Or
   (b) What are all the sites are must in Plasmid before selecting as vector
15. (a) Narrate PVC Plasmid constriction and explain Or
   (b) What are Hybrid Vectors?

SECTION C – (5 X 10 = 50 MARKS)

Answer **ALL** Questions

16. (a) Illustrate with Diagramatic sketch, the Structure of Plasmid Or
    (b) Explain in detail about COSMID – Hybrid vectors
17. (a) Give a detail account of shuttle – vector and its application Or
    (b) Explain Baculovirus and its usages
18. (a) Describe how a desirable gene was inserted in a Vector Or
    (b) How the transformation of gene from vector to host cell happens
19. (a) Explain artificial constricted Plasmids with an examples Or
    (b) Give detail account of T-DNA Plasmid
20. (a) Give a note of rDNA technology application Or
(b) How will you screen properties for a vector Plasmid for recombinant work

PRACTICAL-I MOLECULAR TECHNIQUES

Paper Code – 07BTDT1

Time : six hours Maximum : 100 Marks

SECTION A – (20X 2 = 40 marks)

Answer **ALL** Questions

Minor –I

Separate plasmid from the given bacterial culture.

Minor –II

Isolate the genomic DNA from the given blood sample.

SECTION B – (40X 1 = 40 marks)

Answer **ALL** Questions

Major

Give a detail procedure and perform the suitable experiments to study the protein profile of the given animal or plant samples.

SECTION C – (5X 4= 20 marks)

Answer **ALL** Questions

Spotters:-

1)
2)
3)
4)

MOLECULAR INTERACTION

Time : Three hours Maximum : 100 Marks

SECTION A – (10X 2 = 20 marks)

Answer **ALL** Questions

Choose the correct answer

1. The partial ionic character can be calculated by using
   a. ionic radius b. atomic radius
   c. dipole moment d. ionization energy
2. The geometry of a molecule whose central atom enjoys sp3d3 hybridization
   a. Td b. Oh
   c. TBP d. PBP
3. When two atomic orbitals combine together, the energy
   a. remains the same b. decreases
   c. increases d. all the above
4. The bond between the two ‘s’ orbitals is known as
   a. sigma b. Phi
   c. delta d. Hydrogen bond
5. Pick out the non-bonded interaction among the following
   a. Ion-Ion interaction b. Ion-dipole interaction
   c. Atom-atom interaction d. Atom-ion interaction
6. The anticancer drug cis-platin interactis with
   a. Protein b. DNA
   c. Lipid d. Ligand
7. The number of disulphide bridge in insulin is
   a. Two b. One
   c. Three d. Four
8. Folding and super folding of the helical chain in proteins are seen in _____ structure
   a. Primary b. Secondary
   c. Tertiary d. All
9. The hydroxyl group in any organic compound can be identified by IR spectroscopy if there is a peak at
   a. 1500 cm^{-1} b. 3300cm^{-1}
   c. 765 cm^{-1} d. 675 cm^{-1}
10. NMR method is used in the determination of the structure of
    a. Cellulose and hemicellulose
    b. Carbohydrates and lipids
    c. Proteins and nucleic acids
    d. All the above

SECTION B – (5 x 6 = 30 marks)

Answer **ALL** Questions

11 (a) What is meant by hybridization? Give examples

Or

(b) Write a note on Co-ordination bond in biomolecules

12. (a) Compare atomic and molecular orbitals

Or

(b) Write a brief note on resonance

13. (a) Explain the significance of DNA-drug interaction

Or

(b) What is intercalation? Give examples

14. (a) What is the role of unusual aminoacids dictating protein folding

Or

(b) Describe the role of chaperons in the stability of biomolecules

15. (a) Justify the utility of UV spectroscopy to macromolecule structure elucidation

Or

(b) Draw the stereochemical structure of proteins

SECTION C – (5 X 10 = 50 MARKS)

Answer **ALL** Questions

16. (a) Discuss the advantages of non-bonding interactions over chemical bonding

Or

(b) Write a note on (i) Metallic bond (ii) Hydrogen bond

17. (a) Illustrate with a suitable example, explain the valence bond theory

Or

(b) Compare sigma bond and phi bond with examples

18. (a) Narrate the significance of protein-DNA and protein-protein interactions

Or

(b) Write a note on (i) Metalloprotein (ii) Protein-lipid interactions

19. (a) Bring out the significance of non-bonded interactions in biomolecular structure

Or

(b) Outline the structure of secondary and tertiary structure of protein

20. (a) Discuss the utility of NMR in structure elucidation

Or

(b) Explain the stereochemical structure of nucleic acid

SYSTEMS BIOLOGY

Time : Three hours Maximum : 100 Marks

SECTION A – (10X 2 = 20 marks)

Answer **ALL** Questions

Choose the correct answer

1. SOM is

a. Self organising map b. Support organised map

c. Support membrane d. None of the above

2. The change due to transport of a metabolite from one compartment of a cell to another in a biochemical pathway is called

a. Internal flux b. External flux
c. Total flux d. All of the above

3. Inhibition by the product of the pathway is called
   a. competitive b. Non-competitive
   c. feedback d. Allosteric
4. The study of the interconnection of biological pathways is called
   a. systems biology b. insilico biology
   c. both of the above d. none of the above
5. Which of the following is the key enzyme in glycolysis
   a. phosphofructokinase b. hexokinase
   c. pyruvate kinase d. All of the above
6. The minimum number of gene required for the cell to function
   a. 127 b. 133
   c. 237 d. none of the above
7. Protein-protein interaction
   a. Microarray b. Yeast Two-hybrid
   c. X ray crystallography d. None of the above
8. Biochemical pathway is well organized in
   a. KEGG b. EMP
   c. WIT d. All the above
9. Stanford

a. Microarray database b. Genomic database
c. Proteomic database d. all the above

10. EST
   a.Exon specific sequence b.From cDNA
   c.Represent a gene d. All the above

SECTION B (5 X 6 = 30)

Answer **ALL** questions

11.a. Explain different types of microarray or
   b. Explain hierarchial clustering
12.a. Explain glycolytic pathway or
b. Explain electron transport chain
13.a. Explain different levels of simulation or
   b. What is flux balance? How does it operate?
14. a. Define the conformational flexibilities in the prediction of protein structures or
b. Discuss the types of clusters and their benefits derived for system's understanding
15.a. Comments on restriction mapping or
   b. Describe the method of EST production and explain EST database

SECTION C (5 x 10 = 50)

16.a. Highlight the techniques used to study the expression and regulation of genes in the prokaryotic systems or
   b. Explain microarray data analysis in detail
17.a. Explain the central metabolism via a EMP system or

b. What is genotype? Explain with TCA cycle

18.a. Minimal gene complement are necessarily studied for a whole cell simulation approach – Give your views in support of this or

b. How will you identify the various pathological status of diseases through a simulation approach

19.a. Explain in detail the detection of protein-protein interaction or

b. Highlight on a comparative scale the role of binding surfaces and its relativity to relationship analysis between organisms

20.a. Write a note on (i) primer design (ii) Epitope identification or

b. Write a note on (i) Target identification (ii) pharmacophore building

INTRODUCTION TO VISUAL BASIC WITH RDBMS

Max.Time:3.00 hrs Max.marks:100

Section A Answer all 10*2 =20 marks

1.VISUAL BASIC is a ---------- oriented programming language
a)function b)procedure c) object d)none of the above.

2.IDE stands for
a).Integrated Design Environment ------
b)Integrated Development Environment.
c)Integrated Data Environment
d) Integrated Document Environment.

3. ---------- represent memory locations
a) variables b) constants c) operators d) files.

4. data types can be used with ----- statement.
a) declare b)dim b) dimensional d) data.

5. text box is a ----------.
a)control b) data type c) menu d) value

6.find the odd man out
a)text box b) list box c) combo box d) command button

7. RDBMS stands for ---------- .
a)Rational Data Management System
b)Rational Database Management System
a)Relational Data Management System
b)Relational Database Management System

8. Entity is an ----------.
a) operator b) object c) operation d)none

9.Add in manager is related to ----------.
a)databases b) programs c)values d)all the above

10.ADO stands for -------.
a)Active Data Operation b)Active Data Object.
c)ActiveX Data Operation b)ActiveX Data Object.

Section B Answer all 5*6 =30 marks

11a) Explain in brief about IDE environment (OR)
b) Explain the form lay out of a VB application.

12a)Explain about literals and constants in VB. OR
b) Explain any two date functions with examples.

13a) Explain about the properties of a label control(OR)
b) Write code to set any three properties related to 2 labels.

14a)Explain any two DML commands in detail. OR
b)How is a table updated using DML statement ?Explain.

15)a) write code to connect a table to the current form . OR
Explain about any two types of record sets.

Section C Answer all 5*10 =50 marks

16a)Explain about Project explorer window of VB with an example (OR)
b) What is event driven programming? Explain in detail.
17a)Explain various data types of VB in detail. OR
b) Write VB code to implement various string functions.

18a)Explain in detail about combo box control.. OR
b)Write a VB program which simulates a calculator

19a) Explain about SELECT, SELECT …WHERE SQL commands with example. OR
b)Write SQL Commands to update a table in various possible ways.

20a)Explain DAO in detail. How is a database created in VB? OR
b) Explain how database connectivity is achieved in VB .Give an example

MATHEMATICAL METHODS AND STATISTICAL TECHNIQUES

Time : Three hours Maximum : 100 Marks

SECTION A – (10X 2 = 20 marks)

Answer **ALL** Questions

Choose the correct answer

1. If r = x i + y j + z k then div r= _____
(a) 0 (b) 1 (c) 2 (d) 3
2. If A=2 5
6 7 then 2A=_____
(a) 4 10 (b) 4 5 (c) 4 5 (d) 4 10
6 7 12 7 6 14 12 14
3. The general formula for the euler's method is _____
(a) $y_{n+1} = y_n + h\, f(x_0,y_0)$ (b) $y_{n+1} = y_0 + h\, f(x_0,y_0)$
(c) $y_{n+1} = y_n + h\, f(x_n,y_n)$ (d) None
4. Golden section search is used to evaluate in case of _____
(a) One dimension (b) multi dimension (c) both a and b (d) none
5. In spectral analysis which of the following is used?
(a) Newton's method (b) Fourier Integers (c) both a and b (d) none
6. In monte carlo simulation method ---------- are created
(a) Random numbers (b) probability distribution (c) both a and b (d) none
7. Correlation Coefficient lies between-------
(a) 0 and 1 (b) $-\propto$ and $\propto$ (c) 0 and –1 (d) –1 and +1
8. Bar diagram is ----------
(a) One dimensional (b) two dimensional (c) three dimensional (d) none
9. Mean and variance of ----------distribution are equal
(a) Binomial (b) Poisson (c) normal (d) none
10. The sample is large if sample size is----------
(a) <30 (b) >30 (c) <25 (d) >25

SECTION B – (5 x 6 = 30 marks)

11. (a) Differentiate (x-1)(3x-1)
(OR)
(b) Integrate $\int x^2 e^{3x} dx$
12. (a) Explain the errors (i) Absolute error (ii) Relative error (iii) Percentage error
(OR)
(b) Given $dy/dx = x-y^2$; y(0) =1, Find y(0.1) using Taylor's series
13. (a) write the properties of Fourier transform
(OR)
(b) Discuss in detail about the simulated annealing
14. (a) A random variable x has the following distribution

X=x:	-2	-1	0	1	2	3
P (x):	0.1	k	0.2	2k	0.3	3k

Find (i) k (ii) P ($x \geq 2$)
(OR)
(b) Calculate standard deviation

X: 10 20 30 40 50
F: 8 12 20 10 7

15. (a) 12 coins are tossed . What is the probability of getting 9 or more heads?

(OR)

(b)A random sample of 900 members is found to have a mean of 4.45cms.Can it be reasonably regarded as a sample from the large population whose mean is 5 cms and variance is 4 cms.

SECTION C – (5 x 10 = 50 marks)

16 (a) Solve by matrix method

$2x + 4y + z = 5$
$x + y + z = 6$
$2x + 3y + z = 6$

(OR)

(b)If $u = (x^2 + y^2 + z^2)^{-1/2}$ P.T $\partial^2u/\partial x^2 + \partial^2u/\partial y^2 + \partial^2u/\partial z^2 = 0$

17. (a) Given $dy/dx = y - x, y_0 = 2$ & $x_0 = 0$ Find y(0.1) using the Runge-Kutta method of 4^{th} order

(OR)

(b) Explain how downhill simplex method is used to get the solution in multidimension

18. (a) Explain in detail about Fast Fourier transform and give the application of it.

(OR)

(b) Explain in detail about genetic algorithm

19. (a) Calculate correlation coefficient

X: 9 8 7 6 5 4 3 2 1
Y: 15 16 14 13 11 12 10 8 9

(OR)

(b)From the following data obtain two-regression equation

X: 6 2 10 4 8
Y: 9 11 5 8 7

20 (a) A random sample of size 10 had a mean $\bar{}_X$ =14.3 and variance $s^2 = 2.1$.Test at 5% level that the mean of the population is $\mu = 15$

(OR)

(b) 4 Coins were tossed 160 times and the following results were obtained

No. Of heads:	0	1	2	3	4
Observed frequency:	17	52	54	31	6

Under the assumption that coins are balanced, find the expected frequencies of getting 0,1,2,3 or 4 heads and test the goodness of fit.

METHODS OF GENE TRANSFER & GENOME SEQUENCING

Paper Code – 07BIDT2

Time : Three hours Maximum : 100 Marks

SECTION A – (10X 2 = 20 marks)

Answer **ALL** Questions

1) Gene Pooling means
2) A study of structure and function of genes are called
3) Expand RELP & RAPD
4) What is Gene Mapping
5) Name few Library which store the Data Bank of sequenced microbial genome
6) What are Lipsomes
7) Molecular Markers are used in----------
8) Tagging means
9) "ORF" & Motif strands for
10) Synteny means

SECTION B – (5 x 6 = 30 marks)

Answer **ALL** Questions

11 a) Method adapted to find out the functional genes

Or

(b) Add a note about sequencing of an 'X' chromosome DNA.

12. (a) why phosphate is important for gene transfer during transformation.

Or

(b) Explain electro fusion techniques.

13. (a) Maxam & Glibert method for DNA sequencing.

Or

(b) Explain chromosomal working concepts.

14. (a) Describe low molecular markers and its applications.

Or

(b) What are mediated gene transfer mechanism.

15. (a) Give an detailed account of account of RAPD application.

Or

(b) How will you predict the transfer gene is expressed or not.

SECTION C – (5 X 10 = 50 MARKS)

Answer **ALL** Questions

16. (a) Describe DNA sequencing by automated method.

Or

(b) Method adopted to transfer the desirable gene by practical bombardment method.

17. (a) Explain in detail about the genome constriction.

Or

(b) Give an elaborate procedure for RFLP and its application in the field of diagnostic & forensic areas.

18. (a) Add a note on Electrophoretic method of gene transfer system.

Or

(b) Briefly describe the micro injection procedure.

19. (a) What are the molecular ruller's, how it is made or prepared.

Or

(b) Application of molecular markers in different fields.

20. (a) Describe in detail about the mechanism to identify the functionality of the expressed genes.

Or

(b) Application of co-cultivation method of gene transfer.

PRACTICAL-I MOLECULAR TECHNIQUES

Paper Code – 07BTDT1

Time : six hours Maximum : 100 Marks

SECTION A – (20X 2 = 40 marks)

Answer **ALL** Questions

Minor –I

Separate plasmid from the given bacterial culture.

Minor –II

Isolate the genomic DNA from the given blood sample.

SECTION B – (40X 1 = 40 marks)

Answer **ALL** Questions

Major

Give a detail procedure and perform the suitable experiments to study the protein profile of the given animal or plant samples.

SECTION C – (5X 4= 20 marks)

Answer **ALL** Questions

Spotters:-

1)
2)
3)
4)

GENOMICS

Time: 3Hrs **Max.Marks: 100**

SECTION-A (10 X2 =20)

Choose the Best Answer

1.Polymorphic maps are used to construct _____ maps.

a) Genetic linkage maps b) cytogenetic maps

b) Low resolution markers d) high resolution markers

2. CEPH stands for.

a)Centre d'etude du polymorphism humain

b)centre du etude d' polymorphism human

c)centre du etude d' polymorphism humanin

d) Centre d'etude du polymorphism human

3. Hidden markov model is a

a). Stastical model b). Computational method

c). Homology model d).Sequence analysis

4. Such cDNA were sequenced and deposited in what is called ……

a) Expressed sequence tag b). Reverse transcribed

c). Sequence database d). None of the above

5.The size of Drosophila Melanogaster genome _____.

a) 130 million bases. b) 155 million base.

c) 165 million bases. d) None of the above

6. Arabidopsis Thaliana is a member of._____ Family

a) Brassicaceae b) Rubiaceae

c) Drosophilidae d) none of the above

7 . The DOE Human Genome Program and the NIH National Human Genome Research Institute (NHGRI) together sponsored the U.S_____.

a) Short gun sequence b) NCBI

c) Human Genome Project d) Mouse genome project

8. The process of determining the nucleotide order of a given DNA fragment, called the _____

a) DNA sequence b) Genome assembly

c) DNA amplification d) Chain termination

9.Rearrangements are starts at

a) Break points b) GO

c) TFs d) None of the above

10. Gene that have arisen from a common ancestors is called

a)homologous b) orthologous

c) pralogous d) xenologous

SECTION-B (5 X 6 = 30)

Answer all the Questions

Each question carry equal Marks

11a) Give an account of mouse genome database and snapshot the data content in MGD

(Or)

b) Explain about STS content map

12. a)How will you predict gene function employing the similarity in sequence

(Or)

b) Explain about EST comparison

13 a) Explain genomic organization of Arabidosis thaliana

(Or)

b) Give an account of genome organization of S.Cerevisiae

14 a) Discuss about sequence repeats and its importance

(Or)

b) Explain about transposable elements

15 a) Explain about breakpoint level

(Or)

b) Discuss ontological comparison

SECTION-C (5 X10=50)

Answer all the Questions

Each question carry equal Marks

16 .a) Explain about high and low resolution map

(Or)

b) Discuss about cytogenetic and physical map

17a) How will you predict gene function? Explain details with tools (GRAIL; GENSCAN; NNPREDICT)

(Or)

b) Explain the methods of gene prediction in eukaryotes

18 a). Explains the comparative genomic database pedant, COG

(Or)

b). How will you analyze metabolic pathway. Explain in detail using KEGG database

19 a) Explain human genome, size, features and comparison

(Or)

b) What is pseudogene? Explain in detail?

20 a) Explain the importance of comparative genomics using phylogenetic comparison

(Or)

b) Give a detail account of applications of comparative geno

PROTEOMICS

Time:3 Hrs **Max.Marks 100**

SECTION-A (10 X 2= 10)

Choose the Best Answer

1.The conserved regions of protein known as

a) Domains b)Motifs c)patterns d)Blocks

2.The numerical representation of a multiple sequence alignment is

a) Patterns b) Blocks c)Profiles d)pFam

3.The secondary structure of protein is predicted by using
a) GOR b)Chou-Fasman c)nn predict d)a and b
4.The input layers in the sliding windows has the residues of
a)12 b)13 c)15 d)20
5. IPGIEF is the current method of choice for the first dimension of 2DE called
a)IPG DALT b)NEPHGE c)IEF d)IPG technology
6.morphologoy of spots depend upon the
a)gel preparation b) log c) gaussion d) image
7.A_____ level of variability for organ specific polypeptides was found in maize
a) Low b) High c) Stable d) Linear
8.The technique used for genetic and physiological studies of protein
a) 1-DE b) Isoelectric point c) 2-DE d) a & c
9.In intra specific variability Bahrmal etal(1994) used 2DE to study the relationship of
a) Pinus pinaster b) Populus nigra
c) Picea abies d) Eucalyptus gunii
10.In plants elevated temperatures induce the synthesis of
a) Low molecular weight b) Heat shock protein
b) a & b d) None of the above

SECTION-B (5 X 6 = 30)
Answer all the Questions
Each question carry equal Marks

11. a)Explain about protein structure classification (Or)
b) Where we identify the stability of protein? Explain
12. a)Discuss contact potential method(Or)
b) Why the secondary structure prediction is important, discuss with one example
13. a) Explain MALDI with diagram(Or)
b) How will you detect protein on gel using image analysis
14 a). The techniques were peptide and protein libraries are created on viral surfaces and Screened for activity enmass? Discuss(Or)
b) Explain ABC model that describes the specification of floral organ by Devieena in the year 1988
15 a) Distinguish lines, varieties and cultivars(Or)
b) Explain proteome database

SECTION-C (5 X10=50)
Answer all the Questions
Each question carry equal Marks

16 a). Explain the principles of classification of protein - CATH, FSSP(Or)
b) Explain about MMDB in detail
17.a) How will you predict the secondary structure of protein using Chou-Fasman method(Or)
b). Explain neural network in detail
18 a). Explain the methods for detection of protein spots in proteomics(Or)

b) Discuss principle, sample Intro, analysis, and detector of Mass spectrometer

19.a) Explain high throughput analysis technologies(Or)

b) Explain variation between organ and development stages

20. a) Explain proteomics in plant breeding in detail(Or)

b) Discuss application of proteomics in clinical

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN

Time: 3 hrs **Total: 100 marks**

SECTION A: (10 x 2=20)

1. Which one is a ab initio computer programs
a.ATMOL b.GAUSSIAN c.IBMOL d. All the above

2. General-purpose molecular dynamics computer simulation package stands for
a.GROMOS b. GMDCS c. GMDSP d.None of the above

3. Energy minimization techniques used for minimizing potential energy surface are
a. steepest descent b. conjugate gradient), c. Newton-Raphson d. All the above

4. The parameter not contributing for force field is
a. bond length b. hydrogen bond c. bond angles d. partial charge values

5. A molecular dynamics simulation involves law
a. $F = ma$ b. $F = m/a$ c. $K.E=1/2\ mv^2$ d. All the above

6. The software used for molecular modeling is
a GAUSSIAN b. GROMOS c. MOE d. None of the above

7. The Lennard-Jones potential is commonly used to describe
a van der Waals force b. Electrostatic bond c. Covalent bond d. None of the above

8. Which one is not an application of Monte-Carlo algorithm in computer science
a. Las Vegas algorithm b. LURCH c. Computer Go d. PENELOPE

9. CADD stands for
a. Computer Aided Drug Design b. Computer Assisted Drug Design
c. Chemical Approach for Drug Deign d. Computer Assisted Data Design

10. The software packages that carry out semi-empirical methods are
a. AMPAC b. MOLCAS c. VASP d. All the above

SECTION B: (5 x 6=30)

11.(a) What is molecular modeling? Write the applications of molecular graphics.

(Or)

(b) Briefly discuss the terminologies- local and global energy minima.

12.(a) What is density functional theory? How it can be applied to find the energy of molecular system?(Or)
(b) What are the techniques used for molecular dynamics?
13.(a) Write about different drug-receptor interaction.(Or)
(b) What are QSAR studies? How it plays a significant role in molecular modeling?
14.(a) What are the different types of docking?(Or)
(b) How are new targets for anti-cancer drugs identified?
15.(a) Write short notes on enzyme-inhibitor strategies.(Or)
(b) How do you find new drug targets for treating diseases? Write about drugs that rescue mutant P53's.

SECTION C: (5 x 10=50)

16.(a) Write about molecular mechanics.(Or)
(b) What are the main methods used to minimize energy of small molecules?
17.(a) What is Monte- Carlo simulation?(Or)
(b) Explain about the various methods used for conformational analysis.
18.(a) How is 2D-3D database searching applied for pharmacophore identification?(Or)
(b) What are the methods used for energy minimization? Write its applications.
19.(a) Write about SAR/QSAR studies in modeling.(Or)
(b) Write about *ab initio* and semi-empirical methods.
20.(a) Explain structure based drug design? (Or)
(b) Write about novel drug design

PERL PROGRAMMING FOR BIOINFORMATICS

Max.Time:3.00 hrs **Max.marks:100**
Section A **Answer all** **10*2 =20 marks**

1.PERL is a ---------- based language
a)regular expression
b)arithmetic expression
c)data
d)none.
2.Vector data type represents----------.
a)value
b)direction
c)both
d)none.

3.output statements used to ------ values
a)write
b)read
c)both a and b
d)none

4.pattern is a ---------
a)variable b) data item c) either a or b d)none

5.BIOPERL is a------- oriented language
a)procedure

6.sequences is a set of--------
a)values b)variables c) both d) none.

7.PERL can be used for ----------
a)pattern recognition
b)sequence analysis
c) both a and b
d)none

8.PERL can be used with ---------- plat form
a) DOS
b)WINDOWS
c)LINUX
d)none

9.PYTHON is a ----------
a)language
b)database application
c) file programming
d)none
10.PYTHON supports ---------- types of data
a) 4 b)5 c)6 d)none

SECTION-B ANSWER ALL (5* 6=30)

11a)Explain the history of PERL. OR
b) Explain the applications of PERL?

12a)What is the format of input statement in PERL?Explain OR
b)Explain in brief about regular expressions.

13a)Explain about two OOPS features of PERL. OR
b) Explain inheritance in PERL.

14a)Explain PERL applications in sequence and data analysis. OR
b)Explain any two features of BIOPERL.

15a)Explain briefly PYTHON. OR
What are the tag types in PYTHON?Explain
SECTION-C ANSWER ALL 5* 10=50

16a) Explain the blocks of PERL in detail. OR
b)Explain about arrays and lists in PERL.

17a)Explain regular expresseion concepts in PERL.OR
b)Explain in detail about pattern matching in PERL .

18a)Explain formats and inheritance in PERL.OR
b)Explain a class for restricting enzymes using PERL.

19a)Explain in detail applications of BIOPERL in Bioinformatics.OR
b)Explain about class structures in BIOPERL.

20.a) Explain the various tags of PYTHON.OR
b)Explain the applications of PYTHON in BIOINFORMATICS in detail

PRACTICALS – MODEL QUESTION PAPER
Practical III
07BIP02 - Perl Programming

Time 3Hrs **Total Marks 60**

1.	Programming in Perl (2 programs in Perl)	10 marks
2.	Programming in Perl (2 programs in Perl)	10 marks
3.	Mini project	20 marks
4.	Record	10 marks
5.	Viva	10 marks
Total		**60 marks**

(Subject to MODIFICATION by the EXAMINERS)

PRACTICALS – MODEL QUESTION PAPER
Practical IV
07BIP04 – Computer Aided Drug Design

Time 3Hrs **Marks 60**

7.	Small molecule building, using ISIS DRAW and CHEM SKETCH	10 marks
8.	Homology Modeling using SPDBV	10 marks
9.	Find out Ramachandran plot deviant	10 marks
10.	Calculate RMSD	10 marks
11.	Record	10 marks
12.	Viva	10 marks
Total		**60 marks**

APPLICATIONS OF rDNA TECHNOLOGY

Paper Code – 07BTDT3

Time : Three hours Maximum : 100 Marks

SECTION A – (10X 2 = 20 marks)

Answer **ALL** Questions

1) Origin of BT - Cotton
2) Var – Genes are used in
3) Dolly is a----------
4) Edible vaccines are----------
5) Blue print of DNA is called
6) What are Interferon's
7) Golden rice
8) Steam cell therapy means
9) Gene masking
10) Primary cell culture is related to Animal tissue culture means

SECTION B – (5 x 6 = 30 marks)

Answer **ALL** Questions

11 (a) Explain in detail about the transgenic plants development against pest Or
(b) Explain method adapted to develop high yield plants

12. (a) What are Biopesticides? Explain with examples. Or
(b) Brief out the cloning techniques in Animals and its ethical issues.

13. (a) What are DNA – Vaccines, where it applicable. Or
(b) Explain about IPR.

14. (a) How ELISA and MAT test were important to recognize Antigen & Antibody reactions. Or
(b) Which is responsible Hydrocarbons degradation, give an example organism (Genetically modified one).

15. (a) Milk production in cow's were increased by genetical engineered clones, comments on it.

Or

(b) Brief out of the properties of blood and factors affecting it.

SECTION C – (5 X 10 = 50 MARKS)

Answer **ALL** Questions

16. (a) Narrate by using rDNA technology, how you will develop crop plant which will resist to salt and drought condition.

Or

(b) Explain the toxic gene, protein structure and function of *Bacillus thuringiensis.*

17. (a) Illustrate the methodology to improve the livestock in animals related to meat and milk production using rDNA technology.

Or

(b) Explain in detail about recombinant vaccines with examples

18. (a) Add a note on interferon and its applications in medical revolution.

Or

(b) Give a comparative study of chemotherapy and gene therapy.

19. (a) Illustrate the application of DNA fingerprinting in forensic science.

Or

(b)Role of rDNA technology in commercial enzyme production.

20. (a) Explain in detail about the gene mapping and how it is applicable in diagnostic Purpose.

Or

(b) Recent development in RDNA technology in the field of medicine.

PRACTICAL-II rDNA TECHNOLOGY

Paper Code – 07BTDT2

Time : six hours Maximum : 100 Marks

SECTION A – (20X 2 = 40 marks)

Answer **ALL** Questions

Minor –I

Isolation of microbial plasmid and find out whether it is circular, coiled or linear by using standard markers.

Minor –II

Isolation of plant genomic DNA from given sample. Or

Isolation of animal genomicDNA from given sample. Or

Isolation of microbial genomic DNA from microbial culture.

SECTION B – (40X 1 = 40 marks)

Answer **ALL** Questions

Major

Restrict the given genome with given enzyme and profile with Phage-DNA marker.

SECTION C – (5X 4= 20 marks)

Answer **ALL** Questions

Spotters:-

1)
2)
3)
4)