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

BHARATHIAR UNIVERSITY : COIMBATORE-641 046
M. Sc., BIOINFORMATICS

School of Distance Education

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

SCHEME OF EXAMINATION

Year	Subject and Paper	Exam Duration	Total Marks
I	Paper-I : Fundamentals of Biological Systems	3	100
	Paper-II : Computational methods for Sequence analysis.	3	100
	Paper-III : Programming in C and PERL	3	100
	Paper-IV : Molecular interactions.	3	100
	Practical-I : C & Perl programming	3	50
	Practical II : Databanks and Sequence analysis	3	50
II	Paper-V : Genomics & Proteomics	3	100
	Paper-VI : Systems biology	3	100
	Paper-VII : Programming in visual basic with RDBMS	3	100
	Paper-VIII : Molecular modeling & Computer aided drug design	3	100
	Practical-III : Programming in VB with RDBMS	3	50
	Practical –IV : Computer aided Drug design	3	50

Paper-I **FUNDEMENTALS OF BIOLOGICAL SYSTEMS**

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 concepts of molecular biology that are basic to bioinformatics.

UNIT-I

Introduction to cells. Structure of prokaryotic and eukaryotic cells. Cell organelles and their functions. Differences and similarities between plant and animal cells. Cell transport across plasma membrane. Mechanisms of transport.

UNIT-II

Molecules of life: Introduction to carbohydrates, proteins, lipids and nucleic acids – Different structural forms and functional organizations.

UNIT-III

Cell Energetics: Glycolysis, Aerobic oxidation and photosynthesis, Utilization of glucose, fat and protein.

UNIT-IV

Enzymes: Unit of activity, coenzymes and metal cofactors, temperature and pH effects, Michaelis – Menten kinetics, inhibitors and activators, active site and mechanism of enzyme action, Isoenzymes, allosteric enzymes.

UNIT-V

Cell Cycle and regulation – Mitosis, Meiosis. DNA as genetic material, DNA replication, Transcription and Translation. Gene regulation.

REFERENCES:

1. Lehninger, A. L. 1984. **Principles of Biochemistry.** CBS publishers and distributors, New Delhi, India.
2. Horton, Moran, Ochs, Rawn, Scrimgeour **Principles of Biochemistry** Prentice Hall Publishers.
3. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.
4. David. E. Sadava **Cell Biology: Organelle Structure and Function** Jones & Bartlett publishers.

Paper-II **COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS**

Subject description :

This paper describes how to acquire information from biological databases, use of computational approaches to analyze this information, 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.

UNIT - I

Introduction to bioinformatics, classification of biological databases, Biological data formats, application of bioinformatics in various fields. Introduction to single letter code of amino acids, symbols used in nucleotides, data retrieval – Entrez and SRS.

UNIT - II

Introduction to Sequence alignment, Substitution matrices, Scoring matrices –PAM and BLOSUM. Local and Global alignment concepts, dot plot, dynamic programming methodology, Multiple sequence alignment –Progressive alignment. Database searches for homologous sequences –Fasta and Blast versions.

UNIT - III

Evolutionary analysis: distances - clustering methods – rooted and unrooted tree representation – Bootstrapping strategies

UNIT - IV

Fragment assembly-Genome sequence assembly. Gene finding method, Gene prediction - Analysis and prediction of regulatory regions.

UNIT - V

Concepts and secondary structure prediction –Probabilistic models:
Markov chain, Hidden Markov Models -Gene identification and other applications.

REFERENCES:

1. Andreqas D. Baxevanis, B. F. Francis Ouellette. **Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins** John Wiley and Sons, New York (1998).
2. S. C. Rastogi, Namita Mendiratta, Parag Rastogi. **Bioinformatics-concepts,skills, Applications**
3. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.
4. Richard Durbin, Sean Eddy, Anders Krogh, and Graeme Mitchison.**Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids** Cambridge University Press, 1998.
5. Bishop M.J., Rawlings C.J. (Eds.) **DNA and protein sequence analysis. A Practical approach** IRL Press, Oxford (1997).
6. Doolittle R.F. (Ed.) **Computer methods for macromolecular sequence analysis (Methods in Enzymology**, Vol. 266). Academic Press, San Diego (1996).
7. Teresa K. Attwood and David J. Parry-Smith. **Introduction to Bioinformatics.**

Paper-III **PROGRAMMING IN C AND PERL**

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.

UNIT-I

Introductory Concepts: History of C language- The process of learning a language – Characteristic features of C language-C character set–keywords and identifiers –Rules for naming a variable and a constant –Operators in C-Data types and qualifiers for data types-The first program in C-Explanation for the program-Turbo C Editor-Saving ,compiling and executing a C program.

UNIT-II

Instructions in C: I/O instructions –Control instructions (loop control, case control)-Conditional instructions (if, if-else and if- else-if)-Simple programs using instructions. The C preprocessor directives –Arrays in C-Numerical arrays and Character arrays –String manipulations-Simple programs in Numerical and Character arrays.

UNIT- III

User –defined functions –Uses of a function –Simple programs in functions-A recursive function
–Simple programs using recursive function –Pointers in C-Pointer operations-Simple programs in pointers. Basics of pointers and arrays-Simple programs using pointers and arrays, Basics of functions, pointers and arrays, Simple programs in functions, pointers and arrays.

UNIT-IV

Structures and Enumerations, File handling in C-Opening, Updating and Closing a file, Command Line Arguments –Simple programs in files and command line Arguments.

UNIT-V

PERL: Introduction, Basic Operators and Control Structures, Scalars, Lists, Hashes, File Manipulation, Pattern Matching and Regular Expressions, Subroutines, Text and String Processing

REFERENCES:

1. **Let us C**-Yashavant P.kanetkar_BPB Publications.
2. **Programming Perl** - Tom Christiansen, Larry. Wall Orielly Publications

Paper-IV

MOLECULAR INTERACTIONS

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.
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UNIT-I
Fundamentals of atomic and molecular orbitals:
Theory of atomic and molecular orbitals; Linear combination of atomic orbitals; Quantitative treatment of valency bond theory and molecular orbital theory; Resonance structures; σ-bonds and π-bonds.

UNIT-II
Fundamentals of chemical bonding and non-bonding interactions:
Electrovalent bond, stability of electrovalent bond. Co- valent bond – partial ionic character of co-valent bonds. Shape of orbitals and hybridization. Co-ordination bond, Vander Waals forces; Metallic bond. Molecular geometry- VSEPR Theory.

UNIT-III
Folding pathways: Principles of protein folding, hydrophobic interactions, electrostatic interactions, non-bonded interactions. Beta turns, gamma turns, types of helices, disulphide bridge.

UNIT –IV

Molecular interactions: protein-protein, protein-DNA, DNA-Drug, Protein-Lipid, Protein-Ligand, Protein-Carbohydrate interaction, Metalloproteins, Pi … Pi interactions, C-H…Pi interactions.

UNIT-V
Spectroscopy: Principles, Theory, Instrumentation and Application of UV, IR, NMR and Circular dichroism (CD) to macro molecules.

REFERENCES:

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. Winter, m. j. 1996. **Chemical Bonding**. Oxford University Press, Inc., New York. 91 pp.
4. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.

I YEAR

PRACTICAL-I: C & PERL PROGRAMMING

1. Program to carry out basic arithmetic operations (+,-,*, /, %)
2. Program to find whether a given number is prime or not
3. Program to find the biggest of 2/3 numbers
4. Program to print a series of odd/even numbers
5. Program to find factorial of an integer
6. Program to check whether a string is palindrome or not
7. Arrange a series of numbers/strings in ascending/descending order
8. Program to find factorial of an integer using function recursion

Perl programming

1. Program to convert DNA to RNA
2. Program to convert DNA to RNA using subroutines
3. Program to calculate reverse complement of DNA sequence.
4. Program to read Protein Sequence data from a file
5. Program to reading and translating a FASTA file
6. Program to search for Motif
7. Program for translation of DNA to protein
8. Program for translation of DNA in all six reading frames.

PRACTICAL-II

DATABANKS AND SEQUENCE ANALYSIS

- Biological Databanks- Sequence Databases, Structure Databases, Specialized Databases
- Data retrieval tools and methods
- Molecular visualization
- Gene structure and function prediction (using GenScan, GeneMark)
- Sequence similarity searching (NCBI BLAST)
- Protein sequence analysis (ExPASy proteomics tools)
- Multiple sequence alignment (Clustal)
- Molecular phylogeny (PHYLIP)
- Sequence analysis using EMBOSS or GCG Wisconsin Package

Paper-V

GENOMICS & PROTEOMICS

Subject description :
This paper deals with genome map, comparative genomics, structural genomics, functional genomics, protein structure prediction and function and various tools for analysis of proteins.

Goals:
To make the students to familiar with genome map, comparative genomics, structural and functional genomics and Proteomics —extensively used in drug discovery, and in learning various tools for analysis of proteins

Objectives:
To understand the genome architecture and extracting information like gene function, gene regulation, protein evolution and targets for drug designing.

UNIT I
Annotation of the Genome

- Various approaches in gene prediction

ORF prediction, Gene prediction in prokaryotes, Gene prediction in eukaryotes, Pattern discrimination, Evaluation of gene prediction method, Prediction of promoter sequences.

- **Genome analysis**

Chromosome rearrangement, Compositional analysis, Clustering of genes, Composite genes.

UNIT II
Functional Genomics
Gene expression analysis by cDNA micro arrays, SAGE, Strategies for generating ESTs and full length inserts; EST clustering and assembly; EST databases (DBEST, UNIGENE); Expression and regulation of entire set of genes, Sporulation Vs Vegetative condition in yeast and *Bacillus.*

UNIT III
Comparative Genomics

- **Purpose and Methods of comparison**

Methods of comparison, Comparison at Nucleotide level, Breakpoints level, Gene cluster level.

- **Applications of comparative Genomics**

Predicting function, Predicting regulatory elements, Analysis of conserved strings.

UNIT-IV

- **Principles of Protein classification:**

Based on Structural features, Phylogenetic relationship, CATH - Classification by Class, Architecture, Topology, Homology, SCOP - Structural Classification Of Protein, FSSP - Fold classification based on structure - structure alignment, MMDB - Molecular Modeling Database, SARF - Spatial arrangement of backbone fragments

UNIT - V
Proteome analysis

- 2D Electrophoresis

Immobilized pH gradient, Sample preparation, First dimension criteria, second dimension criteria, Stabilization, Detecting protein on gel, Electro blot, Image analysis, Digital imaging, Spot detection and quantification, Gel matching

REFERENCES

1. Bioinformatics Sequence and Genome Analysis. 2001. David W. Mount. Cold Spring Harbor laboratory Press.
2. Inna Dubchak et al. 2000, Active conservation of noncoding sequences revealed by three way species comparisons. *Genome Research*. **10**, 1304-1306

3. Proteomics. S.R. Pennigton and M.J. Dunn. 2002. Viva Books Private Limited. New Delhi. (for Units III and IV and V.)
4. Introduction to Protein Structure. Carl Branden and John Tooze 1999. Garland Publishing. New York. (for Units I and II)
5. Protein Evolution by Laszlo Patthy 1999. Blackwell Science
6. Shanmughavel, P. 2005. Principles of Bioinformatics, Pointer Publishers, Jaipur, India.

Paper-VI

II YEAR

SYSTEMS BIOLOGY

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.

UNIT - I

Introduction to Systems Biology

What is systems biology? Integrating Networks. Methods of study: Micro array – definition, types of array, micro array analysis : Hierarchical clustering, Self- organizing maps. Applications of micro arrays in system biology.

UNIT - II

Metabolomics & Metabolic Pathways

Digestion of proteins and protein metabolism, Transport metabolism, Carbohydrate metabolism – glycolysis, TCA cycle, PPP, glycogenesis, glycogenolysis, gluconeogenesis, PPP, ETC, Translating biochemical pathways 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 for database
  - Use of EST database - Unigene
  - Gene discovery
  - Primer design
  - Restriction mapping
  - Pharmacophore building
  - Position specific cloning
  - SNP database
  - Target identification
  - Epitope identification

REFERENCES

1. **Bioinformatics A Practical Guide to the Analysis of Genes and Proteins**. Ed. Andreas D. Baxevanis and B. F. Francis Ouellette. John Wiley & Sons, Inc., Publications (For Micro array).
2. Shanmughavel, P. 2006. **Trends in Bioinformatics,** Pointer Publishers, Jaipur, India.
3. **The underlying pathway structure of biochemical reaction networks.** Christopher H. Schilling *et. al*. 1998. PNAS. **95**:4193-8
4. **Towards metabolic phenomics: Analysis of Genomics Data Using Flux Balances**. Christopher H. Schilling *et. al*. 1999. *Biotechnology. Prog.* **15**: 288-295.
5. **The Minimal Gene Complement of *Mycoplasma genitalium.*** Claire M. Fraser *et. al*. 1995. *Science*, **270**: 397- 403.
6. **Molecular Classification of Cancer: Class Discovery and Class prediction by Gene Expression Monitoring.** Golub TR. *et. al*. 1999. . *Science*, **286**: 531 – 537.
7. **The *Escherichia coli* MG. 1655 *in silico* metabolic genotype: its definition, characteristics and capabilities.** Jeremy S. Edwards et. al. 2000. PNAS. **97**:5528-33.
8. **Whole cell simulation: a grand challenge of the 21st Century.** Masaru Tomita, 2001. *Trends in Biotechnology.* **19**: 205-210
9. **Cluster Analysis and Display of Genome – wide expression patterns.** Michael B.Eisen *et. al*. 1998, *Proc. Natl. Acad. Sci. USA.* **95**: 14863 – 14868.
10. **A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks.** Stephen Schuster *et. al*. 1999. *Nature Biotechnology*. **18**: 326-332.
11. **Of micro array and meandering data points.** Steven R. Gullans, 2000. . *Nature Genomics*. **26**: 4-5.
12. **A gene expression database for the molecular pharmacology of cancer.** Uwe Scherf *et. al*. 2000. *Nature genetics*, **24**: 236-244
13. **The transcriptional program in the response of Human Fibroblast to Serum** Viswanth R. Iyer 1999. *Science.* **283**: 83-87.

II YEAR

Paper-VII

PROGRAMMING IN VISUAL BASIC WITH RDBMS

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.

UNIT-I

Introduction: Data abstraction, Data models, Instances & schemes E-R Model: Entity and entity sets, Relations and relationship sets, E-R diagrams, Reducing E-R diagrams to tables. Network Data Model: Basic concepts, Hierarchical Data Model: Basic concepts. Introduction to distributed database processing.

UNIT-II

Data definition languages – Data Manipulation language, Data Control language, Data and String Functions, Union and intersect operator, Sub queries, Normal Form, Introduction to PL/SQL , Data types in SQL, Simple PL/SQL programs.

UNIT-III

Visual Basic: Introduction to Client / Server technology, Introduction to Visual Basic features, Data types, Strings, Variant, Constant, Data Arrays, looping and iterative statements.

UNIT-IV

Simple controls, Command buttons, text boxes, labels, list box, drive list box, directory list box, file list box, combo box, check box, timer control, functions in Visual Basic.
Introduction to data connectivity, different database connectivity approaches, simple connectivity program using data control.

UNIT-V

Menu creation, MDI forms, VB scripting, Introduction to ASP.

REFERENCES

1. **Database System Concepts**. Silberschatz, Tata Mac-Graw Hill Publications.
2. **Database system organization**. J.M.Martin, Princeton-Hall.
3. **Introduction to Database Systems**. C.J.Date
4. **Introduction to Database Systems**. J.M.Martin, Princeton-Hall.
5. **Parallel and Distributed Databases**. Wilteach et.al.
6. **Using Visual Basic**. Que Series. 2001
7. **Visual Basic 6 From the Ground Up**. Gary Cornell Tata Mc-Graw Hill

Paper-VIII

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN

Subject description :

This paper deals with molecular modeling, quantum mechanics, molecular mechanics pertaining to drug discovery.

Goals:

Provide a broad and thorough 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.

UNIT-I

Introduction to the concepts of molecular modeling. Molecular structure and internal energy. Application of molecular graphics

UNIT-II

Introduction to Computational Quantum mechanics- One electron atoms, 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

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. **Monte Carlo Simulation methods**- Monte Carlo simulation of molecules.

UNIT-V

Macromolecular modeling. Design of ligands for known macromolecular target sites. Drug – receptor interactions. Classical SAR/QSAR studies and their implications to the 3-D modeler. Molecular Docking. Structure-based drug design for all classes of targets.

REFERENCES:

1. Andrew,R. Leach **Molecular modeling: Principles and applications** Prentice Hall Publications
2. Shanmughavel, P. 2005. **Principles of Bioinformatics,** Pointer Publishers, Jaipur, India.
3. Shanmughavel, P. 2006. **Trends in Bioinformatics,** Pointer Publishers, Jaipur, India.
4. Tamar Schlick **Molecular Modeling and Simulatio**n Springer Publications
5. Rauter, C. Horn, K. (1984). X-ray crystallography and drug design, Elsevier.
6. Matthew F. Schlecht. **Molecular modeling on the PC**
7. William B. Smith **Introduction to theoretical organic chemistry and molecular modeling**
8. N. Claude Cohen. **Guidebook one molecular modeling in drug design**.
9. Yvonne C. Martin. **Designing Bioactive molecules three dimensional techniques and applications.**
10. Leo, Albert, Hockma, D. H. **Exploring QSAR** - Hansch, Corwin.

II YEAR

PRACTICAL III

PROGRAMMING IN VB WITH RDBMS

1. Create Tables, queries, and Simple PL/SQL Programs.
2. Construct user interface with manipulation and validation
3. Provide Database Connectivity and hence produce Reports.

Mini project using Visual Basic and RDBMS

PRACTICAL IV

COMPUTER AIDED DRUG DESIGN

- Small molecule building, using ISIS DRAW and CHEM SKETCH
- Homology Modeling using SPDBV
- Model structure refinement using SPDBV
- Model validation using What Check and Pro Check
- Docking using DOCK or AUTODOCK or HEX

REFERENCE:

Bioinformatics a Practical Approach by K. Mani and N. Vijayaraj, Aparna Publications, Coimbatore.

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Model Question Papers for SDE PG courses

FUNDAMENTALS OF BIOLOGICAL SYSTEMS

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

Answer any Five Questions (5 X 20 = 100)

Each questions carry equal marks

1.Describe about the various components of cell membrane
2.Discuss about the basic mechanism of initiation of transcription
3.Explain the structure of an antibody with a neatly labelled diagram
4.How cell cycle is regulated
5.Discuss about prokaryotic genome organization
6.Describe M.M equation and explain its significance
7.Give an overview of the immune system
8.Discuss the role of co-enzymes in enzyme catalysis

COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS

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

Answer any Five Questions (5 X 20 = 100)

Each questions carry equal marks

1. What are the various secondary structure databases? Write its uses.
2. What is Bioinformatics? Write about the applications of bioinformatics in various fields.
3. Write about sequence similarity search using BLAST and FASTA.
4. What is multiple sequence alignment? Write its applications.
5. Write the uses of Clustal and PHYLIP?
6. What are the methods used for evolutionary analysis.
7. Explain the various aspects of genome sequence assembly.
8. What are the applications of probabilistic models used for secondary structure prediction.

PROGRAMMING IN C AND PERL

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

Answer any Five Questions (5 X 20 = 100)

Each questions carry equal marks

1. Explain about functions in C.Write a function to sort an array
2. Explain switch… case with an example.
3. Write an overloaded function to overload arithmetic operators + and
4. Explain inheritance types in c++ with syntax.
5. Explain list manipulation in PERL with examples
6. Explain pattern matching in IN PERL.
7. Explain various applications of BIOPERL in Bioinformatics
8. Explain about Analysis in BIOPERL.

MOLECULAR INTERACTIONS

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

Answer any Five Questions (5 X 20 = 100)

Each questions carry equal marks

1. Discuss in detail about different types of chemical bonding with example. And discuss the advantages of non-bonding interactions over chemical bonding
2. Correlate hybridization and geometry of the molecules and comment on them
3. Compare atomic and molecular orbital. Molecular orbital theory is superior to Valence bind theory – comment
4. Describe different types of molecular interactions
5. Write a note on (i) Metalloprotein (ii) Intercalation (iii) Chaperons (iv) disulphide bridge
6. Explain the applications of NMR, CD, UR and IR in macromolecules
7. Bring out the importance of non-bonded interactions in bimolecular structures.
8. Explain the stereochemistry of protein and nucleic acids

GENOMICS & PROTEOMICS

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

Answer any Five Questions (5 X 20 = 100)

Each questions carry equal marks

1.Give an account of mouse genome database and snapshot the data content in MGD
2.How will you predict gene function employing the similarity in sequence?
3.Discuss about sequence repeats and its importance
4.Discuss ontological comparison
5.Explain about high and low resolution map
6.Discuss about hidden Markov with neat-labelled diagram
7.Explain about genomic organization of homosapiens and plasmodium
8.Explain gene clustering with one example.

SYSTEMS BIOLOGY

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

Answer any Five Questions (5 X 20 = 100)

Each questions carry equal marks

1 Highlight the techniques used to study the differential expression and regulation of genes in the prokaryotic systems
2. Explain microarray data analysis in detail
3. Outline the level of metabolic genotype understanding through the TCA cycle.
4. Minimal gene complement are necessarily studied for a whole cell simulation approach – Give your views in support of this
5. How will you identify the various pathological status of diseases through a simulation approach
6 Highlight on a comparative scale the role of binding surfaces and its relativity to relationship analysis between organisms
7. List out the varied applications of gene cluster analysis and its impact on taxonomy
8. Comment on EST and PDB databases and its advantages

PROGRAMMING IN VISUAL BASIC WITH RDBMS

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

Answer any Five Questions (5 X 20 = 100)

Each questions carry equal marks

1. Explain about RDBMS features and applications
2. How are data bases manipulated using RDBMS .Explain.
3. Write about various string functions of SQL
4. Write A PL/SQL program for creating a data base.
5. Explain client/server technology in detail.
6. How is client server communication taking place? Explain .
7. Write a VB program to create a report.
8. Write a program in VB TO implement a calculator

MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN

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

Answer any Five Questions (5 X 20 = 100)

Each questions carry equal marks

1. Write about molecular mechanics.
2. What are the main methods used to minimize energy of small molecules?
3. What is Monte- Carlo simulation?
4. Explain about the various methods used for conformational analysis.
5. How is 2D-3D database searching applied for pharmacophore identification?
6. What are the methods used for energy minimization? Write its applications.
7. Write about SAR/QSAR studies in modeling.
8. Explain structure based drug design?