

Annexure No.	45 B
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BHARATHIAR UNIVERSITY, COIMBATORE – 46
(w.e.f. 2007-2008)
M. Sc., BIOINFORMATICS (CBCS) WITH
COMPULSORY DIPLOMA IN GENOME TECHNOLOGY

I Introduction

Bioinformatics is an emerging scientific discipline representing the combined power of biology, mathematics and computers. Bioinformatics is needed to handle the enormous amount of data being generated by researchers identifying the lengthy DNA sequences of humans, plants, animals and microorganisms-life's blueprint and other biological data.

Stored digitally, in computers world wide, are trillions of pieces of information generated by emerging technologies in molecular biology. The amount of public DNA sequence data doubles every 12-14 months and will increase even more dramatically in the coming year. The resulting bottleneck-a wedge between having data and knowing what the data mean-must be overcome to facilitate breakthroughs in medicine, agriculture and environmental sciences.

Fortunately, biology and computer science are converging to unite raw data with powerful software tools and mathematical models. Bioinformatics represents a frontier in biological research and the best path toward finding meaning in a world of complex data.

II Goal

- Improve content and utility of chemical-biological databases
- Develop better tools and databases for comprehensive functional studies
- Develop and improve tools for representing and analyzing sequences similarity and variations
- Create mechanisms to support effective approaches for producing robust, exportable software that can be widely shared

III Bioinformatics and its scope

In last decade, bioinformatics has emerged as a new discipline. Bioinformatics uses advances in the area of computer science, information science, computer and information technology to solve complex problems in life sciences and particularly in biotechnology. Data capture, data ware housing and data mining have become major issues for biotechnologists and biological scientists due to sudden growth in quantitative data in biology such as complete genomes of biological species including human genome, protein sequences, protein 3D structures metabolic pathways databases, cell line and hybridoma information, biodiversity related information. Advancement in information technology,

particularly internet, is being used to gather and access ever increasing information in biology and biotechnology. Functional genomics, proteomics, discovery of new drugs and vaccines, molecular diagnostic kits and pharmacogenomics are some of the areas in which bioinformatics has become an integral part of research and development. The knowledge of multimedia databases, tools to carry out data analysis and modeling of molecular and biological systems on computer workstations as well as in a network environment has become essential for any student of bioinformatics. Bioinformatics, the multidisciplinary area has grown so much that one divides it into molecular bioinformatics, organal bioinformatics and species bioinformatics. Issues related to biodiversity and environment, cloning of higher animals such as Dolly and Polly, tissue culture and cloning of plants brought out that Bioinformatics is not only a support branch of science, but is also a subject that directs future course of research in biotechnology and life sciences. The importance and usefulness of bioinformatics is realized in last few years by many industries. Therefore, large bioinformatics R&D divisions are being established in many pharmaceutical companies, biotechnological companies and even in other conventional industries, dealing with biological. Bioinformatics is thus rated as number one career in the field of Biosciences. The need of trained manpower in this area is on increase but there are very few centers in the world where such training is given at present.

In short, bioinformatics deals with database creation, data analysis and modeling. Data capturing is done not only from printed material but also from network resources. Databases in biology are generally in the multimedia form organized in relational database model. Modeling is done not only on single biological molecule but also on multiple systems thus requiring a use of high performance computing systems.

IV Regulations

1. Eligibility for admission to M.Sc., Bioinformatics

A pass in any one of the following degree courses of UGC recognized Universities.

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 consist o

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. Scheme of Examination

As given in the respective Board

Distribution of marks	
Core	- 1800
Diploma	- 400
Total Marks	- 2200

5. 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 of 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.

6. Restriction to take the examinations

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

b) Candidate who fails in any of the papers shall pass the papers(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.

7. The medium of instruction and examinations

The medium of instruction and examinations shall be in English.

8. 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.

9. The minimum (Pass) Marks

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

10. 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.

11. 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 and 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 I the evening colleges also.

15. 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.

16. Transitory Provision

Candidates who have undergone the Course of Study prior to the academic Year 2007-2008 will be permitted to take the Examination under those Regulations for a period of four year 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 Time.

M. SC., BIOINFORMATICS
SCHEME OF EXAMINATION FOR CANDIDATES ADMITTED DURING THE
ACADEMIC YEAR 2007 - 2008 AND ONWARDS
(With project work - CBCS – University Department only).

SEM.	CODE	SUBJECT AND PAPER	INSTRUC/ WEEK	Credits	UNIVERSITY EXAMINATIONS	
					Duration in Hrs.	Max. @Marks
I	07BIC01	Paper-I : Cell and Molecular Biology	5	4	3	100
	07BIC02	Paper-II : Computational methods for Sequence analysis.	5	4	3	100
	07BIC03	Paper-III : Programming for Bioinformatics	5	4	3	100
	07BIE01	Paper-IV : Basics of Mathematics & Statistics.*	5	4	3	100
	07BIDTI	PG Diploma – Theory I	2	-	3	100
	07BIDPI	PG Diploma – Practical I #	2	-	-	-
II	07BIC04	Paper-V : Programming in Visual basic & RDBMS	5	4	3	100
	07BIC05	Paper-VI : Molecular interactions	5	4	3	100
	07BIC06	Paper-VII : Biophysics and crystallography	5	4	3	100
	07BIE02	Paper. VIII : Numerical methods & Optimization techniques.*	5	4	3	100
	07BIP01	Practical – I : Wet Lab – Protein, Nucleic Acid, Immunology and Pharmacology**	5	4	6	100
	07BIP02	Practical –II : Computer programming**	5	4	6	100
	07BIDT2	PG Diploma – Theory II	2	3	3	100
	07BIDP1	PG Diploma – Practical I #	2	-	6	50
III	07BIC07	Paper-IX : Genomics.	5	4	3	100
	07BIC08	Paper-X : Proteomics.	5	4	3	100
	07BIC09	Paper-XI : Molecular modeling & Computer aided drug design.	5	4	3	100
	07BIE03	Paper-XII : Systems biology*	5	4	3	100
	07BIP03	Practical-III : Biological Databanks & Sequence analysis **	5	4	6	100
	07BIP04	Practical – IV : Computer aided drug design **	5	4	6	100
	07BIDT3	PG Diploma – Theory III	2	-	3	100
	07BIDP2	PG Diploma – Practical II #	2	-	6	50
IV	07BIPW	Project work, Viva-voce (150+50).	-	8	-	200 ##

- * Electives
- ** Practical I & II should be conducted at the end of Second semester.
Practical III & IV should be conducted at the end of fourth semester.
- @ End semester examinations: 60 marks; internal: 40 marks in which monthly tests 20 marks (best two among three tests); monthly assignments 10 marks (best two among three assignments).
- # Dip. Practical I and II should be conducted at the end of fourth semester
- ## Project evaluation- external examiner-100 marks; internal= 50 marks; viva both by external and internal examiners= 50 marks

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
	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
	07BIDP2	Practical II	rDNA Technology	2	6	50

Subject title : CELL AND MOLECULAR BIOLOGY

Course number : 07BIC01 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 concepts of molecular biology that are basic to bioinformatics.

Unit I :

Biology of cells: Cells as a unit of life, structure of prokaryotic and eukaryotic cells. An overview of organelles (Mitochondria, chloroplasts, ER, Golgi, ribosomes, lysosomes and peroxisomes, nucleus and nucleolus). Differences and similarities in plant and animal cells. Cellular membrane: structure, transport, channels, carriers, receptors, endocytosis, membrane potentials.

Unit II:

DNA replication; Transcription and Translation.

Cell-cell interactions and signal transductions: Intercellular junctions, signaling by hormones and neurotransmitters; receptors, G-proteins, protein kinases and second messengers. Protein traffic in cells.

Unit III:

Cell Cycle and regulation – Mitosis, Meiosis.

Mutation – Types of mutations, types of mutagenic agents and their molecular mechanism; DNA repair; Chromosomal types and structure; Mechanism by which genome undergoes changes, recombination, mutation, inversion, duplication, and transposition.

UNIT-IV

Molecules of Life: Introduction to carbohydrates-Monosacharides and their derivatives, Disacharides, Polysacharides.

Proteins –Structure of aminoacids, Different levels of organization-Primary, secondary tertiary and Quarternary structures.

Nucleic acids – Purines, pyrimidines, Nucleosides and Nucleotides, Different structural form of DNA, denaturation and renaturation of DNA

Lipids-Structure and function of Fatty acids, Triacylglycerols, sphingolipids, steroids and glycerophospholipids.

Water, small molecules-Alkaloids, glycosides, phenols, oligopeptides, Flavonoids, and terpenoids

UNIT-V

Enzymes: Units 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.

Metabolism of glucose: glycolysis, TCA cycle, glycogenesis, glycogenolysis and gluconeogenesis, pentophosphate shunt, ETC. Digestion of protein and protein metabolism, nitrogen balance: transamination, oxidative deamination and urea cycle. Lipid metabolism: beta oxidation. Interconnection of pathways, metabolic regulations.

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. David. E. Sadava **Cell Biology: Organelle Structure and Function** Jones & Bartlett publishers.
4. Shanmughavel, P. 2005. **Principles of Bioinformatics**, Pointer Publishers, Jaipur, India.

Subject title : **COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS**

Course number : 07BIC02 **Number of lecture hours: 5**

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 aminoacids, 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: Needleman and Wunsch algorithm. Smith–Waterman algorithm. Statistics of alignment score. Multiple sequence alignment. Progressive alignment. Database search for similar sequences using FASTA and BLAST Programs.

UNIT-III

Evolutionary analysis: distances, Cladistic and Phenetic methods. Clustering Methods. Rooted and unrooted tree representation. Bootstrapping strategies, Use of Clustal and PHYLIP.

UNIT-IV

Gene finding methods. Gene prediction: Analysis and prediction of regulatory regions. Fragment assembly. Genome sequence assembly, Restriction Mapping, Repeat Sequence finder.

UNIT-V

Concepts of secondary structure prediction of RNA and Protein. Probabilistic models: Markov chain, Hidden Markov Models-other applications.

REFERENCES

1. **Bioinformatics – Concepts, Skills, Applications**". S.C. Rastogi, Namita Mendiratta, Parag Rastogi.
2. **Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.** Andréa's D. Baxevanis, B.F. Francis Ouellette.
3. **Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids.** Richard Durbin et al.
4. **Computer Methods for Macromolecular Sequence Analysis.** Doolittle R.F. (Ed.) (Methods in Enzymology, VOL. 266).
5. Shanmughavel, P. 2005. **Principles of Bioinformatics**, Pointer Publishers, Jaipur, India.
6. **DNA and Protein Sequence Analysis. A Practical approach.** Bishop M.J. Rawlings C.J. (Eds.).
7. **Introduction to Bioinformatics.** Teresa. K. Atwood and David J. Parry-Smith.

Subject title : PROGRAMMING FOR BIOINFORMATICS

Course number : 07BIC03 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.

UNIT-I:**Programming in C**

Introduction, Data types, Operators, Expressions, Control Flow, Structures, Input and Output, Functions, Pointers and References, String Processing, File Handling

UNIT-II**Programming in C++**

Basic concepts of OOPS-Introduction to C++, C vs C++-data types, variables, constants, operators and statements in c++- Functions in c++- function prototype-definition-inline functions-overloaded functions.

UNIT- III**Programming in PERL**

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

UNIT-IV**BioPERL Programming**

General Bioperl classes, Sequences (Bio::Seq Class, Sequence Manipulation), Features and Location Classes (Extracting CDS), Alignments (AlignIO), Analysis (Blast, Genscan), Databases (Database Classes, Accessing a local Database)

UNIT-V**Python Programming**

Overview, Data structures, Control Flow, Modules, Basic I/O, Exception Handling, Regular Expressions, File Manipulation, Classes, Standard library

REFERENCES:

1. The C Programming Language, B.W.Kernighan and D.M. Ritchie 2nd Edition. Prentice Hall of India.
2. Programming Perl – Larry Wall, Tom Christiansen & John Orwant 3ed 2000- O’ Reilly
3. Programming Python – Mark Lutz – 2nd Ed., O’ Reilly
4. E. Balagurusamy - “Programming in C++ ” - Tata Mc. Graw Hill Edition
5. Byron Gottfried, - “Programming with C” (Schaum's Outline Series) - Tata
6. McGrawHill Publishing Company - 1998.
7. Object oriented programming with c++ -Robert Laffore -Waite series.
8. Programming Perl - Tom Christiansen, Larry. Wall Orielly Publications

Subject title : BASICS OF MATHEMATICS AND STATISTICS

Course number : 07BIE01 Number of lecture hours: 5

Subject description :

This paper includes Basic mathematics and statistics

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.

UNIT I: BASIC MATHEMATICS

Matrix Algebra – Types – Determinants – Transpose – Conjugate – Inverse – Eigen values of matrices – Rank – Solving Simultaneous equations in three variables using matrices, Cayley – Hamilton theorem without proof – Verification and Computation of Inverse of a Matrix – Consistency of linear equations.

Vector – Addition, subtraction – Dot product – Cross product (up to 3 vectors) – Scalar triple product – Gradient – Divergence and Curl.

UNIT II: CALCULUS

Differentiation – Standard results – Derivatives of simple functions – Product Rule – Quotient Rule.

Partial Differentiation – Partial derivative of simple functions (3 variables case only) – Euler's Theorem.

Integration – Standard results – Integrals of simple functions – Definite Integrals – Indefinite Integrals – Integration by parts – Integration by substitution – Integration by partial fractions.

UNIT III: BASIC STATISTICS

Ungrouped data and Frequency distribution: Collection – Classification – Tabulation – graphical and diagrammatic representation of numerical data – Graphs – Histogram, Frequency curve.

Statistical Averages: Mean, Median, Mode, SD, Variance and Coefficient of variation.

Correlation and regression analysis: Types of correlation, Methods of studying correlation – Rank correlation – Simple linear regression – Regression Equations.

UNIT IV: PROBABILITY

Random experiment – Definitions of probability – Theorems of Probability: Addition rule – Multiplication Rule – Properties of probability – Conditional probability – Bayes Theorem – Simple Problems.

Random variables – Discrete and Continuous – Probability mass functions – Probability density functions – Cumulative density function and its properties – Distributions Function.

Theoretical distributions – Binomial, Poisson and Normal distributions – Basic ideas and their applications.

UNIT V: TEST OF HYPOTHESIS

Sampling: Population – Sample – Parameter – Statistic – Standard error – Hypothesis-Null Hypothesis – Alternative Hypothesis – Critical Region – Level of Significance – Errors in Sampling – One tailed and two test statistic-test of significance and its test procedure.

Test of significance for small samples: Tests based on normal distribution for Single mean, difference of two means - Tests based on t-distribution for single mean, difference of two means, paired test and observed correlation coefficient – F Test – Parametric and Non parametric tests - Chi-square (χ^2) test for goodness of fit.
Analysis of variance: One way and two way classifications.

REFERENCES:

1. **Calculus** - Volume I &II - T.K.Manickavachagam Pillai and Others.
2. **Applied Mathematics** - Raymond A.Barnett and Michael R.Ziegler.
3. **Fundamentals of Mathematical Statistics** - V.K.Kapoor and S.C.Gupta.
4. **Statistical Methods** - S.P.Gupta.
5. **Allied Mathematics** – P. R. Vittal, Margham Publishe

Subject Title : PROGRAMMING IN VISUAL BASIC WITH RDBMS

Course Number : 07BIC04 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.

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.

Subject title : MOLECULAR INTERACTIONS

Course number : 07BIC05 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.

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, role of chaperons, 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, Metalloprotein. 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. Stereochemistry of proteins and nucleic acids.

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. Ernest Eliel, 1996. **Stereochemistry of carbon compounds**, Prentice Hall
5. Shanmughavel, P. 2005. **Principles of Bioinformatics**, Pointer Publishers, Jaipur, India.

Subject title : BIOPHYSICS AND CRYSTALLOGRAPHY

Course number : 07BIC06 Number of lecture hours: 5

Subject description :

This paper emphasizes the biophysical techniques for 2D and 3D structure prediction.

Goals:

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

Objectives:

To get an insight into the biophysical techniques to analyze protein molecules

UNIT – I.

Introduction to protein structure: Physical and chemical properties of aminoacids and polypeptides. Theoretical and experimental methods for determination of size of proteins. Physical nature of non covalent interactions. Conformational properties of proteins, Ramachandarn Plot, Secondary, Super Secondary, tertiary and quaternary structure of proteins.

UNIT – II.

Protein structure modeling: Homology modeling, Threading, Fold recognition, Vector based method, neural network. Model refinement and validation. **Fuctional classification of proteins:** Cell surface receptors, GPCR's, Kinases, Channel proteins, Ubiquitin

UNIT - III.

Biophysical Techniques: Principles, Process and Applications of Thin layer chromatography, Column chromatography (ion exchange and affinity only), HPLC, Uni Directional and 2 D Electrophoresis, UV Visible spectroscopy, NMR and MALDI - TOF

UNIT – IV.

X-ray crystallography of small molecules; x-ray generation ; its application; unit cell and 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, hydrogen bonding

UNIT – V.

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 method, 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 methods.

REFERENCES:

1. Thomas. E. Creighton **Proteins Structures and Molecular Properties** Freeman and Company
2. Cantor and Schimmel **Biophysical Chemistry Part II Techniques for the study of biological structure and function** Freeman and Company
3. Thomas M Devlin **Textbook of Biochemistry** Wiley LISS Fifth edition
3. Stephen Neidle **Nucleic Acid Structure and Recognition**
4. Leonard Banaszak **Foundations of Structural Biology**
5. Philip E. Bourne **Structural Bioinformatics** John Wiley & sons
6. Shanmughavel, P. 2005. **Principles of Bioinformatics**, Pointer Publishers, Jaipur, India.

Subject title : **NUMERICAL METHODS & OPTIMIZATION TECHNIQUES**

Course number : **07BIE02** **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 optimization techniques.

Objectives:

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

UNIT-I: ERRORS IN MODELLING

Errors involved in the construction of a mathematical model of the real physical process - Errors in Numerical Calculations – Errors in the numerical approximation of the mathematical model (truncation errors) – Errors in a series approximation – Errors in the actual computation using a computer (round off errors).

UNIT-II: MINIMIZATION OR MAXIMATION OF FUNCTION**Problems with Minimum number of iterations**

One Dimensional Optimization: Golden section Method, parabolic interpolation and Brent's method in one dimension, one-dimensional search with first derivatives. Second-order Derivative: Newton-Raphson method,

Multidimensional Optimization: Univariate Method – Pattern Directions – Powell's Method – Conjugate directions – Algorithm – Quadratic Convergence - Downhill simplex method in multi dimensions, Indirect Search Methods – Gradient - Steepest decent(Cauchy) method – Conjugate gradient(Fletcher-Reeves) method - Procedure.

UNIT-III: RANDOMIZED MINIMIZATION TECHNIQUES

Monte-Carlo minimization.

Genetic algorithms – Representation of Design Variables – Representation of Objective function and Constraints – Genetic Operators.

Simulated annealing – Procedure – Features.

UNIT-IV: FOURIER TRANSFORM

Fourier Transform of Discretely Sampled Data – Discrete convolution – Periodic sequence and Circular convolution –Linear Convolution through circular convolution –Fast Fourier Transform(FFT) – Discrete in Time(DIT) – Discrete in Frequency(DIF) – Algorithm – Computation of inverse DFT - Simple problems.

UNIT-V: NUMERICAL SOLUTIONS OF ODEs

Solution by Taylor's series Method - Euler's Method – Modified Euler Method – Midpoint Method, Runge-Kutta Method, Predictor–Corrector Methods - Adam's-Moulton Method - Milne's Method – Simultaneous and Higher Order Equations, Methods to solve stiff equations (Implicit Euler Method and Explicit Euler Method).

REFERENCES:

1. **Sastry,S.S. (1993).** Introductory methods of numerical analysis. **Prentice hall of India pvt Ltd., New Delhi.**
2. **Chapra,S.C. / Raman and Canale, P.** Numerical methods for Engineers with personal computer applications.
3. **Venkatraman, M.K. (1999), International student Edition,** Numerical methods in science and engineering. **National publishing company, Chennai.**
4. T. Veerarajan, **Engineering Mathematics,** Tata Mc. Graw-hill Publishing Company.
5. Singiresu S. Rao, **Optimization Techniques** New Age International (P)Limited.

07BIP01**SEM.I & II****PRACTICAL – I. WET LAB – PROTEIN, NUCLEIC ACID,
IMMUNOLOGY AND PHARMACOLOGY****Subject description :**

This paper includes the isolation of protein, nucleic acid and some of the basics in immunology and pharmacology techniques.

Goals:

To understand the isolation of biomolecules and techniques related to pharmacology and immunology.

Objectives:

To make the student to learn the techniques which are basics to bioinformatics.

1. Isolation of Microbes (*fungi, bacteria and Actinomycetes*) from soil – serial dilution techniques.
2. Screening of microbes for enzymes (amylase) production plate and enzyme assay method.
3. Isolation / Extraction of intracellular and extra cellular enzymes
4. Construction of purification table for any one enzyme
5. Molecular weight determination (SDS - PAGE)
6. Native PAGE and elution of enzyme from the gel

Nucleic Acid Lab

7. Isolation of DNA from microbial and animal cells
8. Isolation of RNA from bakers yeast
9. Isolation of plasmid from bacterium
10. Restriction, digestion and ligation
11. PCR amplification

Immunology lab

12. Methods of bleeding
13. counting of blood cells- Haemocytometre count
14. Preparation of serum from blood
15. Blood grouping- Haemoagglutination
16. ELISA

Pharmacology Lab

17. Screening of microbes for antibiotic production
18. Antibiotic bioassay(Kirby Bauer method)
19. Extraction of any one pharmaceutical compound from medicinal plants (soxlet – extraction method)
20. Tissue culture technique for secondary metabolites production
21. Structure prediction of pharmaceutical compound by NMR

Subject Title : PRACTICAL - II. COMPUTER PROGRAMMING

Course Number : 07BIP02 Number of hours: 5

Subject description :

Some of the basic programs in MS- office, HTML, C and perl ,

Goals:

The use C and Perl and available modules for routinely performed bioinformatics tasks.

Objectives:

Ability to write simple Perl scripts. And develop web page

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 LI NUX.

Programming in C and PERL

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' characters of one array to another
- 8) Copy the last 'n' characters of one array to another
- 9) Copy the middle 'n' characters of one array to another
- 10) Concatenate two character arrays (String Concatenate)
- 11) Counting the numbers of Words, Lines and characters in an 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 occurrences 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(char by char)
- 20) Read data from the file and display it on the screen(char by char)
- 21) Display the content of all the files(Cat 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) Grep all files (Pattern match all the files)

PERL Programming

1. Program to store a DNA sequence
2. Program to concatenate DNA fragments
3. Program to convert DNA to RNA
4. Program to calculate reverse compliment 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 motifs in a protein sequence
15. Program to count nucleotides in a sequence
- 16 Program to find the percentage of hydrophobic amino acids in a sequence
- 17 Program to find the percentage of G and C in a DNA 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 DNAto RNA using subroutines
22. Program to find if a DNA is stable or not

VISUAL BASIC AND 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

Subject title : GENOMICS

Course number : 07BIC07 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 extracting information like gene function, gene regulation, protein evolution and targets for drug designing

UNIT – I

Definition of Genome, Genome sequencing, Genome map: Types of Genome maps and their uses, High and low-resolution map, Map elements, Polymorphic markers, Types of maps: Cytogenetic, Linkage map, Transcript map, Physical map, Comparative map, Integrated map, STS content maps, Map repositories: NCBI – Entrez Human genome map viewer, OMIM – Online Mendelian Inheritance in Man, Linkage map resources: CEPH reference pedigree, CHLC – Cooperative human linkage center, Radiation hybrid map resources. Practical uses of genome maps: Locating genomic regions, Target identification, Arrangement of genes, SNP diagnosis, Positional specific cloning,

UNIT – II

Genome Anatomies The anatomy of the Eukaryotic Genome –The special features of metaphase chromosomes, where are the genes in the genome? Families of genes, pseudogenes – Eukaryotic organelle genomes, Repetitive DNA content of the human genome.

Transcriptomes and Proteomes

Genome Expression in outline; The RNA content of the Cell– the Transcriptome – yeast and human; The Protein content of the cell - the link between the Transcriptome and the Proteome.

UNIT – III

Annotation of the Genome: Structural annotation (Locating coding regions and other structural elements of the gene). Various approaches in gene prediction: ORF prediction, Gene prediction in prokaryotes and eukaryotes, Hidden Markov Model, Pattern discrimination, Evaluation of gene prediction methods, 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. Analysis of Human Genome.

UNIT – IV**Comparative Genomics:**

Purpose and Methods of comparison, Tools for genomic comparison: Applications of Comparative Genomics, Reconstruction of metabolic pathway, Predicting regulatory elements, Identifying targets, examination of domain function, analysis of conserved strings.

Genome projects and Model Organism research -Yeast; Drosophila; C. elegans; and Mouse – a comparative analysis. Comparative genomics as an aid to gene mapping and in the study of human diseases.

UNIT – V**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*.

REFERENCES

1. **Active Conversation of Non-coding Sequences revealed by three way species comparisons.** Inna Dubchak et al. 2000. Genome Research. 10, 1305–1306.
2. **Bioinformatics A Practical Guide to the Analysis of Genes and Proteins.** Ed. Andreas D. Baxeavanis and B.F. Francis Ouellette. A. John Wiley & Sons, Inc., Publications (For mapping and comparative Genomics and COG and other database repositories).
3. **Bioinformatics Sequence and Genome Analysis.** 2001. David W. Mount. Cold Spring Harbor Laboratory Press.
4. Shanmughavel, P. 2005. **Principles of Bioinformatics**, Pointer Publishers, Jaipur, India.
5. Shanmughavel, P. 2006. **Trends in Bioinformatics**, Pointer Publishers, Jaipur, India.
6. **Comparative genetics.** Ann Gibbons, 1998. Science. 281: 1432 – 1434.
7. **Encyclopedia or Escherchia coli genes and Metabolism.** Peter D. Karp et al. 1996. Eco-Cyc: Nucleic Acids Research. 10: 86-90.
8. **Structural Genomics and its importance for Gene Function Analysis.** Jeffrey et al. 2000. Nature Biotechnology. 18:283 – 287.
9. **The COG database: New developments in phylogenetic classification of Proteins from complete genomes.** Roman Tatusov et al. 2001. Nucleic Acids Research. 29:22-28.
10. **The Comprehensive Microbial Resource.** Jeremy D. Peterson et.al. 2001. Nucleic Acids Research. 29: 123 – 125.
11. **The Molecular Biology Database Collection: Updated Compilations of Biological Database Resources.** Baxeavanis A.D. 2001. Nucleic Acids Research. 29 p 1-10.
12. **Genomes.** T.A. Brown, 2001. Taylor and Francis Group.

Subject title : PROTEOMICS

Course number : 07BIC08 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 in learning various tools for analysis of proteins.

Objectives:

Taxonomy, structure-function relationship and functional aspects of the entire set cell.

UNIT – I

Protein classification: Structural elements and terminology, Helix, Sheet, Strand, Loop and coil, Active site, Architecture, Blocks, Class and Domains, Fold, Motif, PSSM, Profile. Principles of 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 – II

Protein structure prediction: Use of sequence pattern, leucine zipper, coiled coil, transmembrane, signal peptide, cleavage site. Secondary structure prediction: Chou – Fasman / GOR method, Neural network, nearest neighbor method, tertiary structure prediction, threading profile, contact potential, modeling.

UNIT – III

Analytical protein and peptide separations - Complex protein and peptide mixtures, Extracting proteins from biological samples, Protein separation before digestion: 1D and 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. Data Analysis – Database for 2D gel.

UNIT – IV**Tools of Proteomics-**

Mass Spectrometry for protein and peptide analysis:

- MALDI-TOF Analyzers
- ESI Tandem MS instrument
- Tandem Mass Analyzers
- The Triple Quadrupole Mass Analyzer
- The Ion Trap Mass Analyzer
- Q-TOF & Fourier Transform–Ion Cyclotron Resonance MS Instrument

UNIT – V

Functional Proteome Analysis: Integrated Proteome Analysis - Phage antibody as tool, Protein expression analysis, High throughput analysis for proteomics. Automation of proteomic analysis. Proteomics in plant breeding: Objectives, principles and methods, Genetic diversity analysis, Distribution of varieties, lines and cultivars, Mutant characteristics, Variability between organ and developmental stage, Identification of abiotic stress, Genetic mapping of protein markers.

REFERENCES

1. Daniel C. Leible, (2002), **Introduction to Proteomics: Tools for New Biology**, Humana Press, Totowa, NJ.

2. Branden, Carl and Tooze John. 1999. **Introduction to Protein Structure** (2nd Ed.), Garland Publishing, NY, USA.
3. Mount, David, W., (2001); **Bioinformatics: Sequence and Genome Analysis**, Cold Spring Harbor Lab. NY, USA
4. Pennington, S, (Editor), M. J. Dunn (Editor); (2001); **Proteomics: From Proteins Sequence to Function**, Springer Publications
5. Palzkill, Timothy; (2002); **Proteomics**, Kluwer Academic Publishers
6. Suhai, Sandor, (ed)., (2000); **Genomics and Proteomics : Functional and Computational Aspects**, Plenum Pub. Corp.
7. Shanmughavel, P. 2005. **Principles of Bioinformatics**, Pointer Publishers, Jaipur, India.

Subject title : MOLECULAR MODELING AND COMPUTER AIDED DRUG DESIGN

Course number : 07BIC09 **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 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 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.

REFERENCES

1. **Molecular Modeling: Principles and Applications.** Andrew R. Leach
2. **Basic principles and applications** Hans-x
3. **Designing bioactive molecules three-dimensional techniques and applications.** Yvonne C. Martin.
4. **Exploring QSAR.** Leo, Albert, Hockma, D.H.– Hansch, Corwin.
5. **Principles of Bioinformatics,** Shanmughavel, P. 2005 , Pointer Publishers, Jaipur, India.
6. Shanmughavel, P. 2006. **Trends in Bioinformatics,** Pointer Publishers, Jaipur, India.

Subject title : SYSTEMS BIOLOGY

Course number : 07BIE03 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.

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 systems biology.

UNIT – II**Metabolomics & Metabolic Pathways**

Digestion of proteins and protein metabolism, Transport metabolism, Carbohydrate metabolism – metabolism of glucose – glycolysis, TCA cycle, glycogenesis, Pentose phosphate shunt, Electron transport, Interconnection of pathways, metabolic regulation. Translating biochemical networks into linear algebra.

UNIT – III

Whole cell simulation: Principle and levels of simulation - Virtual Erythrocytes, Pathological analysis. Flux Balance Analysis

UNIT IV

Relationship analysis: Predicting ligand-binding function, Use of gene cluster, detecting protein – protein interaction.

UNIT – V

Creative Bioinformatics: Novel use for database. Use of EST database – Unigene, gene discovery, Primer design, Restriction mapping, 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. **Nanofabrication towards Biomedical applications.** Ed. Challa S. S. R. Kumar, Joseph Hornes, Carola Leuschner. Wiley-VCH Verlag GmbH & Co.
3. Shanmughavel, P. 2005. **Principles of Bioinformatics**, Pointer Publishers, Jaipur, India.
4. Shanmughavel, P. 2006. **Trends in Bioinformatics**, Pointer Publishers, Jaipur, India.
5. **The underlying pathway structure of biochemical reaction networks.** Christopher H. Schilling *et. al.* 1998. *PNAS*. **95**:4193-8
6. **Towards metabolic phenomics: Analysis of Genomics Data Using Flux Balances.** Christopher H. Schilling *et. al.* 1999. *Biotechnology. Prog.* **15**: 288-295.
7. **The Minimal Gene Complement of *Mycoplasma genitalium*.** Claire M. Fraser *et. al.* 1995. *Science*, **270**: 397- 403.
8. **Molecular Classification of Cancer: Class Discovery and Class prediction by Gene Expression Monitoring.** Golub TR. *et. al.* 1999. . *Science*, **286**: 531 – 537.
9. **The *Escherichia coli* MG. 1655 *in silico* metabolic genotype: its definition, characteristics and capabilities.** Jeremy S. Edwards *et. al.* 2000. *PNAS*. **97**:5528-33.
10. **Whole cell simulation: a grand challenge of the 21st Century.** Masaru Tomita, 2001. *Trends in Biotechnology*. **19**: 205-210
11. **Cluster Analysis and Display of Genome – wide expression patterns.** Michael B.Eisen *et. al.* 1998, *Proc. Natl. Acad. Sci. USA*. **95**: 14863 – 14868.
12. **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.
13. **Of micro array and meandering data points.** Steven R. Gullans, 2000. . *Nature Genomics*. **26**: 4-5.
14. **A gene expression database for the molecular pharmacology of cancer.** Uwe Scherf *et. al.* 2000. *Nature genetics*, **24**: 236-244
15. **The transcriptional program in the response of Human Fibroblast to Serum** Viswanth R. Iyer 1999. *Science*. **283**: 83-87.

Subject title : PRACTICAL III BIOLOGICAL DATABANKS AND SEQUENCE ANALYSIS

Course number : 07BIP03 Number of hours: 5

Subject description :

This paper includes data retrieval from 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:

- Biological Databanks Sequence Databases, Structure Databases, Specialized Databases
- Data retrieval tools and methods
- Database file formats
- 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 (PHYLP)
- Analysis of protein and nucleic acids sequences,
- Sequence analysis using EMBOSS or GCG Wisconsin Package

REFERENCE:

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

Subject title : PRACTICAL IV – COMPUTER AIDED DRUG DESIGN

Course number : 07BIP04 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:

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 AMBER

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**

CaPO₄ 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