TAMIL NADU VETERINARY AND ANIMAL SCIENCES UNIVERSITY

U.O.No.60014/R.I/Spl.BOM-73/2011   Office of the Registrar,
No.3912/R.I/Spl.BOM-73-4/50-14-VAS-2/2011   Madhavaram Milk Colony, Chennai-51.

Dated: 15.4.2011.

PROCEEDINGS

Sub: TANUVAS – Board of Management – Seventy Third Special Meeting held on 17.3.2011 – Starting of M.Sc. degree programme in Bioinformatics and the course contents, admission requirement and eligibility, annual intake, fees, academic regulations, staff, budget, etc – Approved – Orders – Issued.

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ORDER:

The Board of Management in its Seventy Third Special Meeting held on 17.3.2011 considered the recommendation of the 50ᵗʰMeeting of the Academic Council held on 9.3.2011 and approved the starting of M.Sc. degree programme in Bioinformatics and the course contents, admission requirement and eligibility, annual intake, fees, academic regulations, staff, budget, etc. as detailed in the Annexure-1 with the following conditions:

1. The requirement of Assistant Professor to be minimized to two and is to be made by deployment.

2. The fees prescribed for other Postgraduate courses (viz.) M.V.Sc., M.FSc., & Ph.D." shall be applicable for Bioinformatics also, instead of offering it on a self-sustaining mode.

2) Section 'C', Registrar's Office, TANUVAS shall take necessary action in the matter.

/BY ORDER OF THE VICE-CHANCELLOR/

Encl: Annexure-1.

REGISTRAR.

To
Section 'C', Registrar's Office, TANUVAS.
Cc: The Finance Officer, TANUVAS.
Cc: Section 'E', Registrar's Office, TANUVAS.
Cc: Stock File/U.S.O File/Spare-2.

ANNEXURE – 1
M.Sc DEGREE PROGRAMME IN BIOINFORMATICS

PREAMBLE

The end of the twentieth century has seen an explosion of information discovered from living organisms, especially in areas of molecular biology and genetics. The greatest challenge facing the molecular biology community today is to make sense of the wealth of data that has been produced by the genome and proteome sequencing projects.

Traditionally, molecular biology research was carried out entirely at the experimental laboratory bench but the huge increase in the scale of data being produced in this genomic era has seen a need to incorporate computers into this research process which resulted in the birth of new discipline, Bioinformatics.

Bioinformatics is a new emerging discipline that has emerged from the requirements to elucidate the biologically useful information. The focus of bioinformatics is dealing with the flood of information, coming from academic, industry and government labs and turning it into useful knowledge.

AIM

The aim of the course is to provide students with high quality Post Graduate Education in Bioinformatics, which meets the needs of Biotechnology, Genetics, Biochemistry, Microbiology and Pharmaceutical industries for Research and Development

JUSTIFICATION

Biological research today requires a different approach. In modern biology, everything is being conducted on a much larger scale than some time ago. There are currently more than1000 biological / molecular databases, each containing large volumes of data.

The sheer volumes and complexity of these facts translate into means that computers must be used for the efficient utilization of the resources available. For example, it will simply not be possible for a human researcher to analyze (in a reasonable amount of time) the results of a microarray experiment containing 20000 individual data points, much less comparing one experiment with 10 other similar experiments from around the world, each with 20000 data points.

Bioinformatics researches are constantly improving the efficacy of biological research, and with further advances in informatics, along with bioinformaticians applying the advances to biological research questions and challenges which will contribute to efficient biological experimentation in the future.

Bioinformatics has several uses in modern biology, and new novel methods of employing techniques from statistics, mathematics and informatics (to name but a few) are constantly being introduced.

The first challenge facing the bioinformatics community today is the intelligent and efficient storage of the mass of data. It is then their responsibility to provide easy and reliable access to

this data. The data itself is meaningless before analysis and the sheer volume present makes it impossible for even a trained biologist to interpret it manually. Therefore, incisive computer tools must be developed to allow the extraction of meaningful biological information.

The Bioinformatics department at Madras Veterinary College is conducting "Post Graduate Diploma in Bioinformatics" since 2004. So far, 18 students have completed the course and are well placed in several reputed institutions/companies like SRMC, SIET, Biocon, Infosys etc.

It has been proposed to start a "M.Sc degree course in Bioinformatics" for the benefit of students community to open new avenues and augment employment potentials. The M.Sc degree course is designed to meet the requirements of students from the range of scientific backgrounds who are specially interested in the study of computational and scientific developments in Bioinformatics and the application of this knowledge, skills and tools to the fields of molecular and biological sciences. This course could be started as an inter-disciplinary course encompassing the existing facilities at Bioinformatics Centre along with Animal Biotechnology, Animal Genetics and Breeding, Animal Husbandry Statistics and Computer Applications, Veterinary Biochemistry and Library Sciences departments of MVC.

ADMISSION REQUIREMENT & ELIGIBILITY
Any graduate with a minimum qualification of B.V.Sc., B.V.Sc & AH, M.B.B.S, B.D.S., B.F.Sc or B.Sc. degree in any branch of Agriculture / Life Sciences / Genetics / Biochemistry / Biotechnology / Bioinformatics / Microbiology / Pharmacology / or equivalent of Indian or foreign university. The mark eligibility shall be decided by the University from time to time

ANNUAL INTAKE:
Ten students. Increase in number of seats in future shall be decided by the University.

FEES
As decided by the University from time to time. The programme is to be run on self sustaining mode.

ACADEMIC REGULATIONS
As per the TANUVAS Academic Regulations for PG Programmes - 2009

AVAILABLE INFRASTRUCTURE
Hardware	:	IBM servers, PIV HCL and Lenovo desktops
Software	:	Discovery Studio, Bio-Suite and other free wares used in the field of Bioinformatics like Rasmol, SPDBV, MEGA, Phylip, Bioedit, Modeller, Ribbons etc.
Wetlab	:	The wetlab at Bioinformatics Centre is equipped with PCR, Hot air Oven, Deep freezer, Incubator, Laminar air flow etc., to carry out molecular biology research works

AVAILABILITY OF RESOURCE PERSONS
The faculties available in Bioinformatics Centre along with the faculties in Animal Biotechnology, Animal Genetics and Breeding, Animal Husbandry Statistics and Computer

Applications, Veterinary Biochemistry and Library Sciences departments of MVC will be utilized for M.Sc. Bioinformatics course.

HUMAN RESOURCES AND BUDGET REQUIREMENT:

Post	Required	Subject Specialization	Present Position	Additional Human Resources Required	Additional Budget Requirement (Rs.)
Professor and Head	One	Bioinformatics / Veterinary or Animal Sciences with knowledge of Computer Science	One: Dr.P.Dhanapalan, Ph.D.	-	-
Associate Professor	One	Bioinformatics / Veterinary or Animal Sciences with knowledge of Computer Science / Biotechnology / Genetics	-	One	-
Assistant Professor	Four	Bioinformatics / Veterinary or Animal Sciences with knowledge of Computer Science (Two)	-	Two	-
		Genetics / Biotechnology (One)	Dr.S. Sureshkannan	One	-
		Computer Science / Information Science (One)	One: Dr. P.L.Sujatha, Ph.D. (as Assistant Librarian)	-	-

(All Posts by Deployment)

Additional Budget Requirement per year:
1. Man power   Rs. 20,00,000/- (By deployment)
2. Non-Recurring   Rs.   Nil
3. Recurring   Rs.   1,00,000/-

    Total   **Rs. 1,00,000/-**

BIOINFORMATICS – COURSE CONTENTS (AS PROVIDED BY THE ICAR)
Course Structure – at a Glance
CODE COURSE TITLE CREDITS

BIF 601*	INTRODUCTION TO BIOINFORMATICS	2+1
BIF 602*	ADVANCED BIOINFORMATICS	2+1
BIF 603*	TECHNIQUES IN BIOINFORMATICS	0+2
BIF 604**†	BIOLOGICAL CHEMISTRY	3+0
BIF 605**†	STATISTICS FOR BIOINFORMATICS	2+1
BIF 606	CONCEPTS IN COMPUTING	2+2
BIF 607**†	PROGRAMMING LANGUAGES FOR BIOINFORMATICS	2+2

BIF 608**†	BASIC MOLECULAR BIOLOGY	3+0
BIF 609**†	MATHEMATICS FOR BIOINFORMATICS	2+0
BIF 610**	GENETICS & IMMUNOLOGY	3+0
BIF 611	INTRODUCTION TO DATABASE SYSTEMS	2+1
BIF 612	COMPUTATIONAL & SYSTEM BIOLOGY	2+2
BIF 613	BIOMOLECULAR SEQUENCE ANALYSIS	1+1
BIF 614**†	DYNAMIC WEB-DESIGN	1+2
BIF 615	BIOLOGICAL DATABANKS & DATA MINING	1+2
BIF 616	MOLECULAR MODELLING & DRUG DESIGN	2+2
BIF 617	COMPARATIVE AND FUNCTIONAL GENOMICS	2+1
BIF 618	PHARMACOGENOMICS & IPR	2+1
BIF 691	MASTER'S SEMINAR	1+0
BIF 699	MASTER'S RESEARCH	20

* To be offered to the students other than those of M.Sc. Bioinformatics
** May be taken as Minor/Supporting course
† To be offered from respective departments. The syllabi are attached for reference only. Actual contents may be seen from the corresponding department(s).

BIF 601 INTRODUCTION TO BIOINFORMATICS 2+1
Objective
To impart an introductory knowledge about the subject of Bioinformatics to the students studying any discipline of science.
Theory
UNIT I

Introduction, biological databases – primary, secondary and structural, Protein and Gene Information Resources – PIR, SWISSPROT, PDB, genebank, DDBJ. Specialized genomic resources.
UNIT II

DNA sequence analysis, cDNA libraries and EST, EST analysis, pairwise alignment techniques, database searching, multiple sequence alignment.
UNIT III

Secondary database searching, building search protocol, computer aided drug design – basic principles, docking, QSAR.
UNIT IV

Analysis packages – commercial databases and packages, GPL software for Bioinformatics, web-based analysis tools.
Practical
i. Usage of NCBI resources
ii. Retrieval of sequence/structure from databases
iii. Visualization of structures
iv. Docking of ligand receptors
v. BLAST exercises.
Suggested Readings
Attwood TK & Parry-Smith DJ. 2003. Introduction to Bioinformatics. Pearson Education.
Rastogi SC, Mendiratta N & Rastogi P. 2004. Bioinformatics: Concepts, Skills and Applications. CBS.

BIF 602 ADVANCED BIOINFORMATICS 2+1
Objective
To understand the usage of advanced techniques in Bioinformatics
Theory
UNIT I

Biological databases, database hierarchies, sequence and structure databases. Pairwise sequence alignment and database similarity searching: global and local alignments, matrices, gap penalties and statistical significance.

UNIT II

Multiple sequence alignment and phylogenetic analysis, Microarray technology: applications, analysis of data, clustering analysis. Pharmacogenomics: introduction, applications, Genome for medicine, current and future perspectives.

UNIT III

System modeling and metabolomics – concepts and principles. Nutrigenomics: system biology in nutrition and health arena.

UNIT IV

Genome annotation, EST clustering, protein modeling and design.

Practical

i. Development of small database

ii. Phylogenetic analysis

iii. Microarray data analysis (sample data from open sources).

iv. Other practical exercises based on above topics.

Suggested Readings

Baxevanis AD & Ouellettee BFF. 2001. Bioinformatics: a Practical Guide to the Analysis of Genes and Proteins. Wiley Interscience.

Mount DW Cold. 2001. Bioinformatics: Sequence and Genome Analysis. Spring Harbor

Stekel D. 2003. Microarray Bioinformatics. Cambridge University Press.

Tomita M & Nishioka T. 2005. Metabolomics: The Frontier of Systems Biology. Springer Verlag.

Wong SHY. 2006. Pharmacogenomics and Proteomics: Enabling the Practice of Personalized Medicine. American Association for Clinical Chemistry.

BIF 603 TECHNIQUES IN BIOINFORMATICS 0+2

Objective

To explore the usage of various Open source software for Bioinformatics applications

Practical

UNIT I

Gene Information Resources: GenBank, EMBL, Protein Information Resources: Swiss-Prot, BLOCKS, Gene Prediction Tools: GENSCAN, GRAIL

UNIT II

Structural Databases: PDB, CSD, RELIBASE, REBASE, File Format Converter Tools: BABEL, ReadSeq, NCBI Resources

UNIT III

Visualization tools – RasMol, QMol, Swiss PDB, Pymol, Modelling Tools: MODELLER, SwissPDB, Geno3D, Docking Tools: Chimera, Dock, AutoDock, GRAMM, Hex, Argus Lab.

UNIT IV

Proteomics Tools: EXPASY, CDART, 3D-Structure Optimization Tools, Sequence Analysis Tools: BLAST, FASTA, EMBOSS, TCOFFEE, Phylogenetic Analysis Tools: Phylip, NTSYS, CLUSTALW/CLUSTALX, BIOEDIT

Suggested Readings

Software Manuals and Help files

BIF 604 BIOLOGICAL CHEMISTRY 3+0

Objective

This is intended to prepare the non-biology students for basic concepts of biological structures and functions as well as recapitulate the knowledge of biology students.

Theory

UNIT I

The molecular logic of living organisms; Cells and composition of living matter; Carbohydrates: monosaccharides, oligosaccharides, polysaccharides, proteoglycans and glycoproteins; Lipids: fatty acids, acylglycerols, phospholipids, sphingolipids, cholesterol and membranes.

UNIT II

Structure and function of Proteins and nucleic acids; Enzymes: details of enzyme nomenclature and classification; units of enzyme activity; coenzymes and metal cofactors; temperature and pH effects; Michaelis-Menten kinetics; Inhibitors and activators; active site and catalytic mechanisms; covalent and noncovalent regulations; isoenzymes.

UNIT III

Organization of metabolic systems: enzyme chains, multienzyme complexes and multifunctional enzymes; anaplerotic sequences and amphibolic pathways; pacemaker enzymes and feedback control of metabolic pathways; shuttle pathways; energy charge.

UNIT IV

Oxidation of glucose in cells: high energy bond, glycolysis, citric acid cycle and oxidative phosphorylation, metabolism of lipids, proteins and nucleic acids, signal transduction.

Suggested Readings

Geoffrey LZ, Michael Gregory E & Sitz T. 1997. Biochemistry. McGraw-Hill.
Nelson DL, Cox MM & Ocorr MOK. 2005. Lehninger's Biochemistry. WH Freeman & Co.
Voet D & Voet JG. 1997. Biochemistry. John Wiley & Sons.

BIF 605 STATISTICS FOR BIOINFORMATICS 2+1

Objective

To understand the basic principles of statistics and mathematics and their applications in relation to Biological system.

Theory

UNIT I

Introduction to Statistical Bioinformatics, Principles of sampling from a population; Random sampling

UNIT II

Frequency distributions: Graphical representations and Descriptive measures; Standard Probability Distributions; Correlation and regression analysis.

UNIT III

Hypothesis testing; Markov Models, Cluster Analysis: Hierarchical and Non-Hierarchical methods.

UNIT IV

Phylogenetic Analysis Tools: Maximum Likelihood, Parsimony methods.

Practical

i. Computational exercises on Random Sampling
ii. Construction and representation of frequency distributions
iii. Descriptive measures
iv. Probability distribution.

Suggested Readings

Gupta SC & Kapoor VK. 2000. Fundamentals of Mathematical Statistics: A Modern Approach. S. Chand & Co.
Warren JE & Gregory RG. 2005. Statistical Methods in Bioinformatics. Springer.

BIF 606 CONCEPTS IN COMPUTING 2+2

Objective

The **Objective** of this course is to introduce the basic concepts of computing with introduction to OS, graphics, networking and client-server technologies.

Theory
UNIT I

Fundamentals of Computing; Introduction to Operating Systems: WINDOWS, UNIX/Linux operating systems; Computer Security (hacking, cracking), Computer Viruses.

UNIT II

Computer Graphics: Visualization techniques - Software and Hardware, Interactive Graphics; Viewing in three dimension; Raster algorithms; Rendering; Animation; Image Processing with emphasis on biological systems.

UNIT III

Computer Networking, Security of the network, Fire-walls, Network Goals, Applications Network, Network architecture, Hierarchical networks, Ethernet and TCP/IP family of protocols

UNIT IV

Use of INTERNET and WWW, Internet services.

Practical
i. MS-Windows

ii. Linux, UNIX

iii. Network design

iv. Internet search

v. Graphics and animation.

Suggested Readings
David FR. 1997. Procedural Elements for Computer Graphics. WCB/McGraw-Hill.

Foley JD & Van Dam A. 1982. Fundamentals of Interactive Computer Graphics. Addison-Wesley.

James FK & Keith WR. 2006. Computer Networking: A Top-Down Approach Featuring the Internet. Prentice Hall.

Siever E. 2005. Linux in a Nutshell. O'Reilly.

BIF 607 PROGRAMMINGLANGUAGESFORBIOINFORMATICS 2+2

Objective
Programming is a very significant area for bioinformatics and this course gives an understanding for logics of programming and command-line and graphical GDIs.

Theory
UNIT I

Programming in C: Pointers, pointers to functions, macro programming in C, graphs, data structure - linked list, stack, queue, binary trees, threaded binary trees.

UNIT II

File and exception handling in C, Programming in Visual Basic: Introduction to Application Development using Visual Basic; Working with Code and Forms.

UNIT III

Variables, Procedures and Controlling Program Executor; Standard Controls; Data Access Using Data Control; Connecting to Database using VB.

UNIT IV

Introduction to JAVA, variables, constants, control structures, input output, classes. Jar and Java applets.

Practical
i.Programming in C and Visual basic with special reference to database linking.

ii. Small Java applets

Suggested Readings
Brian WK & Ritchie DM. 1988. C Programming Language. Prentice Hall. Kanetkar. 2002. Let us C. BPB Publications.

Microsoft Developers Network (MSDN Digital Library).2006. Microsoft.

BIF 608 BASIC MOLECULAR BIOLOGY 3+0

Objective

To understand the basic concepts of molecular biology in order to relate to the structure and functions of biomolecules and to have an insight of chemical aspects of life.

Theory

UNIT I

Nucleic acids as hereditary material, Genome organization in prokaryotes and eukaryotes.

UNIT II

DNA replication, semi-conservative model, mechanism of replication in E.coli, differences in pro- and eukaryotic DNA replication.

UNIT II

Reverse transcription, Transcription in pro-and eukaryotes, post-transcriptional changes; Ribozymes, anti-sense RNA, micro-RNAs

UNIT IV

Genetic code and translation; differences in translation process in pro-and eukaryotes; Gene regulation in prokaryotes and eukaryotes.

Suggested Readings

Gupta PK. 2003. Cell and Molecular Biology. 2nd Ed. Rastogi Publications.

Lodish H. 2003. Molecular Cell Biology. 5th Ed. W.H. Freeman & Co.

Zhang MQ & Jiang T. 2002. Current Topics in Computational Molecular Biology. MIT Press.

BIF 609 MATHEMATICS FOR BIOINFORMATICS 2+0

Objective

To understand and apply fundamental concepts of mathematics as applicable in Biology and to acquaint about theoretical concepts of algebra and geometry and numerical methods.

Theory

UNIT I

Coordinate geometry with basic concepts of 2D and 3D geometry, Vector algebra – Addition and subtraction of vectors, Dot and cross product, Scalar triple product.

UNIT II

Matrix algebra: basic definitions, matrix operations, transpose of a matrix, inverse of matrix, eigen values, Boolean algebra. Geometric and Arithmetic Progression.

UNIT III

Solution of equation by bisection method, Iteration method, Newton Raphson method, numerical differentiation.

UNIT IV

Numerical integration- Trapezoidal rule, Simpson's 1/3 and 3/8 rules, Runga Kutta method of nth order. Fast Fourier transformation.

Suggested Readings

Babu CA & Seshan CR. 2006. New Engineering Mathematics. Narosa Publishing House.

Datta KB. 2002. Matrix and Linear Algebra. Prentice Hall.

Narayan S. 1980. Matrix Algebra. S Chand & Co.

Rao S. 2006. Numerical Methods for Scientists and Engineers. Prentice Hall.

BIF 610 GENETICS & IMMUNOLOGY 3+0

Objective

To learn the basic concepts of genetics and immunology.

Theory

UNIT I

Genetics-Science of genetics - objectives, terminologies, methods; Mendelian principles of inheritance, sex linked inheritance; Concept of linkage, linkage maps and recombination; Mutations -molecular, gene/point and chromosomal.

UNIT II

Phenotype and genotype relationships, role of environment, from gene to phenotype, gene interactions. Study of quantitative traits. Genetics of populations, genetics and evolution. Genetics and diseases.

UNIT III

Immunology -Overview of immune system, innate and acquired immune system; Structure and function of antibody molecule and TCR; Genetics of antibody diversity; MHC I and II, Polymorphism; Characteristics of B Cell and T Cell antigens; MHC Peptide interaction; Affinity maturation.

UNIT IV

Autoimmunity and molecular mimicry; Ligand - receptor interaction in the light of protein structure in immune system; Use of bioinformatics in immunology and vaccine development.

Suggested Readings

Johnson RL. 2006. Genetics. Twenty-First Century Books.
Male D. 2003. Immunology. Open University Worldwide.
Stansfield WD. 2002. Genetics. McGraw-Hill.

BIF 611 INTRODUCTION TO DATABASE SYSTEMS 2+1

Objective

To familiarize the concept of RDBMS and to apply the database techniques to biological databanks.

Theory

UNIT I

Data Abstraction; Data Models; Instances and 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.

UNIT II

Multimedia Databases - Basic Concepts and Applications; Indexing and Hashing; Basic concepts (ISAM, B+ Tree indexed files, B Tree indexed files, Static Hash functions, Dynamic Hash functions); Text Databases; Introduction to Distributed Database Processing, Data Security.

UNIT III

MySQL/MS-Access -Select Statements; Data Definition Statements; Data Manipulation Statements; Data Control Statements; Other Database Objects (Views, Sequences, Synonyms); Introduction to Application Development using Visual Basic; Working with Code and Forms; Variables.

UNIT IV

Procedures and Controlling Program Executor; Standard Controls; Data Access Using Data Control; Connecting to Oracle Database using Visual Basic.

Practical

i. **Practical** exercise using MySQL
ii. Design of database in MS-Access and MySQL.
iii. Database linking.

Suggested Readings

Date CJ. 1986. Introduction to Database Systems. Addison-Wesley.
Korth H & Silberschatz A. 2002. Database System Concepts. McGraw-Hill.
Martin D. 1986. Advanced Database Techniques. MIT Press.

BIF 612 COMPUTATIONAL & SYSTEM BIOLOGY 2+2

Objective

To understand the computational aspects of structural biology; to familiarize the usage of software for 3D structures of nucleic acids and proteins and to translate the sequence to protein structure.

Theory

UNIT I

Methods of single crystal X-ray Diffraction of macromolecules, NMR of macromolecules Anatomy of Proteins - Ramachandran plot, Secondary structures, Motifs, Domains, Tertiary and quaternary structures.

UNIT II

Anatomy of DNA: A, B, Z DNA, DNA bending etc.; RNA structure; Structure of Ribosome; Principles of Protein Folding; Structural data banks - Protein Data Bank, Cambridge small molecular crystal structure data bank.

UNIT III

Methods for Prediction of Secondary and Tertiary structures of Proteins, DNA, RNA, Fold recognition, Ab initio methods for structure prediction; Homology modeling, Methods for comparison of 3D structures of proteins.

UNIT IV

Molecular interactions of Protein – Protein with special reference to signal transduction and antigen-antibody interaction, Protein - DNA, Protein - carbohydrate, DNA - small molecules. System modeling and metabolomics – concepts and principles.

Practical

i. Usage of softwares for above topics

ii. Molecular Visualization tools: RasMol, QMol, Swiss PDB, Pymol

iii. Biomolecular Interaction Databases: BIND, DIP;

iv. Structure Similarity Search Tools: CN3D, Vast Search

Suggested Readings

Fall CP. 2002. Computational Cell Biology. Springer.

Tsai CS. 2003. Computational Biochemistry. John Wiley & Sons.

Waterman MS. 1995. Introduction to Computational Biology: Maps, Sequences and Genomes. CRC Press.

BIF 613 BIOMOLECULAR SEQUENCE ANALYSIS 1+1

Objective

To understand the local and multiple alignment concepts and to carry out multiple sequence alignment.

Theory

UNIT I

Analysis of protein and nucleic acid sequences, multiple alignment programs,

UNIT II

Development of programs for analysis of nucleic acid sequences, Use of EMBOSS package.

UNIT III

Phylogenetic analysis – Elements of phylogenetic models, tree interpretation, tree data analysis, alignment – building data model.

UNIT IV

Extraction of phylogenetics data sets, Distance and character based methods.

Practical

i. EMBOSS

ii. File Format Converter Tools: BABEL, ReadSeq

iii. Phylogenetic Analysis Tools: Phylip, NTSYS, PAUP

iv. CLUSTALW/CLUSTALX.

Suggested Readings

Baxevanis AD & Ouellettee BFF. 2001. Bioinformatics: a **Practical** Guide to the Analysis of Genes and Proteins. Wiley Interscience.

Mount DW. 2001. Bioinformatics: Sequence and Genome Analysis. Spring Harbor, CSHL Press.

Nei M & Kumar S. 2000. Molecular Evolution and Phylogenetics. Oxford University Press.

Salemi M & Vandamme AM. 2003. The Phylogenetic Handbook – A **Practical** Approach to DNA and Protein Phylogeny. Oxford University Press.

BIF 614 DYNAMIC WEB-DESIGN 1+2
Objective
This course teaches the basic principles and application of various technologies used in creation of dynamic web content.
Theory
UNIT I
PERL: Strings, Numbers, and Variables. Variable Interpolation, Basic Input and Output, File handles, Making Decisions, Conditional Blocks, Loops, Combining Loops with Input, Standard Input and Output, Finding the Length of a Sequence File
UNIT II
Pattern Matching, Extracting Patterns, Arrays, Arrays and Lists, Split and Join, Hashes, A Real-World Example, BioPERL; Applications.
UNIT III
Creation, hosting and maintenance of web-site using HTML, XML, ASP, JSP.
UNIT IV
Creation, hosting and maintenance of web-site PHP, PERL and CGI.
Practical
i.Creation of Web-based applications, interactive and dynamic web-pages
ii. Connecting databases using CGI scripting
iii.Creation and maintenance of web-sites using HTML, XML, ASP, PHP, PERL and CGI
iv. Retrieval of specific information from web-sites using CGI scripts.
Suggested Readings
Moorhouse M & Barry P. 2004. Bioinformatics, Biocomputing and Perl: An Introduction to Bioinformatics. John Wiley & Sons.
Tisdall JD. 2001. Beginning Perl for Bioinformatics. O'Reilly.

BIF 615 BIOLOGICALDATABANKS&DATAMINING 1+2
Objective
To understand the biological databases – types and formats and to learn the retrieval, deposition and analysis of sequences and structures from biological databanks.
Theory
UNIT I
Data warehousing, data capture, data analysis; Introduction to Nucleic Acid and Protein Data Banks; Nucleic acid sequence data banks: Genbank, EMBL nucleotide sequence data bank.
UNIT II
AIDS Virus sequence data bank, rRNA data bank, Protein sequence data banks: NBRF-PIR, SWISSPROT, Signal peptide data bank; Database Similarity Searches.
UNIT III
BLAST, FASTA, PSI-BLAST algorithms; Pair wise sequence alignment NEEDLEMAN and Wunsch, Smith Waterman algorithms; Multiple sequence alignments - CLUSTAL, Patterns, motifs and Profiles in sequences.
UNIT IV
Derivation and searching; Derived Databases of patterns, motifs and profiles: Prosite, Blocks, Prints-S, Pfam, etc.; Primer Design.
Practical
i.Gene Information Resources
ii.Protein Information Resources
iii.Structural Databases
iv.Sequence Analysis and Database Similarity Search Tools: BLAST, PHI-BLAST, PSI-BLAST, FASTA, EMBOSS, CLUSTAL, TCOFFEE

v. Use of similarity, homology and alignment tools.

Suggested Readings

Letovsky S. (Ed).1999. Bioinformatics: Databases and Systems. Kluwer.

LeÛn D & Markel S. 2003. Sequence Analysis in a Nutshell: A Guide to Common Tools and Databases. O'Reilly.

NCBI(www.ncbi.nlm.nih.gov). PUBMED (www.pubmedcentral.nih.gov) and database web-sites.

BIF 616 MOLECULAR MODELLING AND DRUG DESIGN 2+2

Objective

To understand the Modelling of small molecules; to understand the computational chemistry principles and to familiarize the role of computers in drug-discovery process.

Theory

UNIT I

Concepts of Molecular Modelling, Molecular structure and internal energy, Application of molecular graphics,

UNIT II

Energy minimization of small molecules, Use of Force Fields and MM methods, Local and global energy minima. Techniques in MD and Monte Carlo. Simulation for conformational analysis, Ab initio, DFT and semi-empirical methods.

UNIT III

Design of ligands, Drug-receptor interactions, Classical SAR/QSAR, Docking of Molecules;

UNIT IV

Role of computers in chemical research; Structure representation, SMILES; Chemical Databases, 2D and 3D structures, reaction databases, search techniques, similarity searches; Chemoinformatics tools for drug discovery.

Practical

i. Modelling Tools: MODELLER, Geno3D

ii.Docking Tools: Chimera, Dock, MOE, AutoDock Tools, GRAMM, Hex, ArgusLab;

iii. 3D-Structure Optimization Tools: CHEMSKETCH, CHEM 3D, ISIS Draw, CHEMDRAW

Suggested Readings

Bunin BA. 2006. Chemoinformatics: **Theory**, Practice and Products. Springer.

Gasteiger J & Engel T. 2003. Chemoinformatics: A Textbook. Wiley-VCH.

Hinchliffe A. 2003. Molecular Modelling for Beginners. John Wiley & Sons.

Leach AR. 1996. Molecular Modelling: Principles and Applications. Longman.

BIF 617 COMPARATIVE AND FUNCTIONAL GENOMICS 2+1

Objective

To understand the genomic and proteomic concepts and to learn the usage of various algorithms and programmes in analysis of genomic and proteomic data.

Theory

UNIT I

A brief account of recombinant DNA technology, PCR and molecular marker techniques. Genomics - Whole genome analysis, Comparative and functional genomics,

UNIT II

Pathway analysis, Repeat analysis, Human genetic disorders, Candidate gene identification, Linkage analysis, Genotyping analysis.

UNIT III

Concepts of Pharmacogenomics Proteomics -Introduction to basic Proteomics technology, Bio-informatics in Proteomics, Gene to Protein Function: a Roundtrip,

UNIT IV

Analysis of Proteomes, Analysis of 2-D gels, Protein to Disease and vice versa, Human Genome and science after Genome era. SAGE.

Practical

i. Gene Prediction Tools: GENSCAN, GRAIL, FGENESH

ii.NCBI Genomic Resources

iii.Proteomics Tools: EXPASY, CDART

Suggested Readings

Azuaje F & Dopazo J. 2005. Data Analysis and Visualization in Genomics and Proteomics. John Wiley & Sons.

Jollès P & Jörnvall H. 2000. Proteomics in Functional Genomics: Protein Structure Analysis. Birkhäuser.

BIF 618 PHARMACOGENOMICS & IPR 2+1

Objective

To understand the translation of Bioinformatics into commercial gains; to familiarize the concepts of microarray – data acquisition and analysis and learn the IPR issues in Biological sciences with special emphasis on bioinformatics.

Theory

UNIT I

Bioinformatics companies, Genomes, transcriptomes and proteomes – their applications in medicine and agriculture, disease monitoring, profile for therapeutic molecular targeting.

UNIT II

Diagnostic drug discovery and genomics. Pharmacogenomics and its application. SNPs and their applications. Microarray and genome wide expression analysis: Introduction to basic microarray technology, Bioinformatics in microarrays, Getting started – target selection.

UNIT III

Customised microarray design, Image processing and quantification, Normalization and filtering, Exploratory statistical analysis, Public Microarray data resources.

UNIT IV

Patenting and data generation from patent literature for commercial benefits. IPR, and bioinformatics. Bioinformatics patents.

Practical

i. Microarray Analysis Tools: MAGICTool

ii. Stanford Microarray Database

iii. Gene Expression Omnibus

iv. Creation of an On-line company.

Suggested Readings

Blalock EM. 2003. A Beginner's Guide to Microarrays. Springer.

Catania M. 2006. An A-Z Guide to Pharmacogenomics. American Association for Clinical Chemistry.
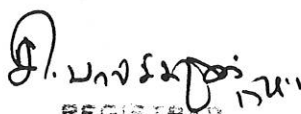
Chakraborty C & Bhattachary A. 2005. Pharmacogenomics. Biotech Books.

Stekel D. 2003. Microarray Bioinformatics. Cambridge University Press.

List of Journals

- Bioinformatics - Oxford University Press
- BMC Bioinformatics - BioMed Central
- Briefings in Bioinformatics - Oxford University Press
- Briefings in Functional Genomics and Proteomics - Oxford University Press
- Computers in Biology and Medicine – Elsevier
- Journal of Bioinformatics and Computational Biology (JBCB) – World Scientific Publishers
- Journal of Biomedical Informatics – Elsevier
- Journal of Computational Biology - Mary Ann Liebert, Inc. publishers

- Journal of Molecular Modelling – Springer
- Nucleic Acids Research – Oxford Press
- Protein Engineering, Design and Selection (PEDS) – Oxford Press e-Resources
- Bioinformatics.Org: The Open-Access Institute - http://bioinformatics.org/
- European Molecular Biology Network - http://www.embnet.org/
- European Bioinformatics Institute -http://www.ebi.ac.uk/
- The European Molecular Biology Laboratory - http://www.embl.org/
- International Society for Computational Biology - http://www.iscb.org/
- National Center for Biotechnology Information - http://www.ncbi.nlm.nih.gov/
- ExPASy Proteomics Server - http://us.expasy.org/
- Mouse Genome Informatics - http://www.informatics.jax.org/
- Center for Molecular Modeling - http://cmm.info.nih.gov/modeling/
- RCSB PDB - http://www.rcsb.org/pdb
- Bioinformatics resources -
- http://www.biochem.ucl.ac.uk/bsm/BCSB/bioinfo_resources/bioinform_res.htm
- South African National Bioinformatics Institute - http://www.sanbi.ac.za/
- Swiss Institute of Bioinformatics - http://www.isb-sib.ch/
- Protein Structure Prediction Center - http://predictioncenter.llnl.gov/
- Programs for Genomic Applications -http://www.nhlbi.nih.gov/resources/pga/
- Computational Molecular Biology At NIH - http://molbio.info.nih.gov/molbio/
- Gene Ontology Home - http://www.geneontology.org/
- All About The Human Genome Project (HGP) - http://www.genome.gov/
- UCSC Genome Browser - http://genome.ucsc.edu/

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