BHARATHIAR UNIVERSITY, COIMBATORE.

M. Sc BIOTECHNOLOGY DEGREE COURSE WITH COMPULSORY DIPLOMA (AFFILIATED COLLEGES)

(Effective from the academic Year 2009-2010)

SCHEME OF EXAMINATIONS – CBCS PATTERN

Semester	Study Components	Course title	Ins. Hrs/ week	Exam			Credit
				CIA	Uni. exam	Total	
I	**Paper I**	Cell & Molecular Biology	4	25	75	100	4
I	**Paper II**	Biochemistry	4	25	75	100	4
I	**Paper III**	Microbiology	4	25	75	100	4
I	**Paper IV**	Biophysics & Biostatistics	4	25	75	100	4
I	**Paper V**	Molecular Genetics	4	25	75	100	5
I		Practical I	3	-	-	-	-
I		Practical II	4	-	-	-	-
I	**Elective**	Diploma Paper I	3	25	75	100	3
II	**Paper VI**	Immunology & Immunotechnology	5	25	75	100	5
II	**Paper VII**	Genetic Engineering	4	25	75	100	4
II	**Paper VIII**	Microbial Biotechnology	4	25	75	100	4
II	**Paper IX**	Plant Biotechnology	4	25	75	100	4
II		Practical I	5	40	60	100	4
II		Practical II	5	40	60	100	4
II	**Elective**	Diploma Paper II	3	25	75	100	3
III	**Paper X**	Animal Biotechnology	5	25	75	100	4
III	**Paper XI**	Medical Biotechnology	5	25	75	100	5
III	**Paper XII**	Environmental Biotechnology	5	25	75	100	4
III	**Paper XIII**	Bionanotechnology	5	25	75	100	4
III		Practical III	5	-	-	-	-
III	**Elective**	Diploma Paper III	5	25	75	100	3
IV		Practical III	5	40	60	100	5
IV		Project	20	-	-	200*	10
IV	**Elective**	Diploma Paper IV	5	25	75	100	3
		Total				2200	90

* For Project report - 80%; Viva-voce - 20% (Project is pertain to the field of Biotechnology)

List of Group Elective/Diploma papers (Colleges can choose any one of the Group/Diploma papers as electives)

	Group A Compulsory Diploma in Bioprocess technology	Group B Compulsory Diploma in Computational Biology	Group C Compulsory Diploma in System Biology
Paper I / Sem I	Fundamentals of fermentation technology	Introduction to Bioinformatics & Molecular Biology databases	Developmental Biology
Paper II / Sem II	Fundamentals of Bioprocess technology & Biochemical Engineering	Biological Sequence Alignment	Metabolic Engineering
Paper Iii / Sem III	Downstream processing	Structural Bioinformatics	Molecular System Biology
Paper IV / Sem IV	Bioethics, Biosafety and IPR	Genomics Proteomics	Glycomics

Note :

1. The Syllabus for the above papers (except Elective Diploma papers Group B & Group C) be the same as prescribed for the academic year 2008- 09.
2. The syllabus for the Diploma papers Group B & Group C are furnished below :

GROUP B. DIPLOMA IN COMPUTATIONAL BIOLOGY

Description

Computational biology is relatively a new field in involved in the development of algorithms and statistical techniques to the interpretation, classification and understanding of biological datasets. These typically consist of large numbers of DNA, RNA, or protein sequences. Sequence alignment is used to assemble the datasets for analysis. Comparisons of homologous sequences, gene finding, and prediction of gene expression are the most common techniques used on assembled datasets; however, analysis of such datasets have many applications throughout all fields of biology.

GROUP B. DIPLOMA IN COMPUTATIONAL BIOLOGY

Paper I. Introduction to bioinformatics and Molecular Biology Databases

Unit I. Introduction to bioinformatics.

The dawn of sequencing: Protein sequencing and nucleic acid sequencing, The biological sequence/structure deficit, Genome projects, Human genome project, Goal and scope of bioinformatics, Applications of bioinformatics.

Unit II. Biological Information Networks.

The European molecular biology network (EMBnet)- Hinxton Hall, MIPS, UCL and The National centre for biotechnology information (NCBI). Information retrieval systems: SRS and Entrez. Submitting sequences: Bankit at NCBI, Sequin from NCBI, Webin from EBI and Sakura from DDJB.

Unit III. Databases.

What is a database? Types of databases: Relational databases and Object oriented databases. Databases management system. Structured query language (SQL). Biological databases.

Unit IV. Protein databases.

Primary sequence databases: PIR, MIPS, SWISS-PROT, The structure of SWISS-PROY entries, TrEMBL and NRL-3D. Composite protein sequence databases: NRDB, OWL, MIPSX and SWISS-PROT+TrEMBL. Secondary databases: PROSITE, The structure of PROSITE entries, PRINTS, BLOCKS, Profiles, Pfam and IDENTIFY. Composite protein pattern databse. Structure classification databases: SCOP, CATH and PDBsum.

Unit V. DNA databases.

DNA sequence databases: EMBL, DDBJ, GenBank, The structure of GenBank entries, dbEST and GSDB. Specialized genomic resources: *Sacharomyces* Genome Database (SGD), UniGene, TDB and ACeDB. Biological databases available on the web, Interconnection between biological databases, Pitfalls of biological databases.

GROUP B. DIPLOMA IN COMPUTATIONAL BIOLOGY

Paper II. Biological Sequence Alignment

Unit I. Pairwise sequence alignment.

Evolutionary basis of sequence alignment, Sequence homology versus sequence similarity, Sequence similarity versus sequence identity, Methods of sequence alignment, Scoring matrices, Comparison between scoring matrices, Statistical significance of sequence alignment.

UNIT II. Database similarity searching.

Database similarity searching: Unique requirements for database searching. Heuristic database searching, BLAST: Varients of BLAST, statistical significance, Low complexity regions and BLAST output format. FASTA, Comparison of BLAST nad FASTA. Database searching with Smith-Waterman method.

Unit III. Multiple sequence alignment.

The goal of multiple sequence alignment, Scoring function, Exhaustive algorithms, Heuristic algorithms, Databases of multiple alignments, Searching databases with multiple alignments, PSI_BLAST, Practical issues of multiple sequence alignment.

Unit IV. Secondary database searching.

Secondary databases, What is in a secondary databases: Regular expressions/rules/fuzzy regular expressions, Fingerprints, Blocks, Profiles and Hidden Markov Models.

Unit V. Protein motifs and domain prediction.

Identification of motifs and domains in multiple sequence alignment, Motif and domain databases using regular expressions, Motif and domain databases using statistical models, Protein family databases, Motif discovery in unaligned sequences, Sequence logos.

GROUP B. DIPLOMA IN COMPUTATIONAL BIOLOGY

Paper III. Structural Bioinformatics

Unit I. Protein Structure basics.

Amino acids, peptide formation, Dihedral angles, Hierarchy, Secondary structures, Tertiary structures, Determination of protein three dimensional structure, Protein structure database.

Unit II. Protein structure visualization, comparison, and classification.

Protein structure visualization tools: RasMol, Swiss-PDBViewer, Molscript, Ribbons, Grasp, WebMol, Chime and Cn3D. Protein structure comparison: Intermolecular method, Intramolecular method, Combined method and Multiple structure alignment. Protein structure classification: SCOP, CATH and comparison of SCOP and CATH.

Unit III: Protein secondary structure prediction.

Secondary structure prediction for globular proteins, secondary structure prediction for trans membrane proteins, coiled coil prediction.

Unit IV. Protein tertiary structure prediction.

Methods, Homology modeling, Threading and fold recognition, *Ab Initio* protein structural prediction, CASP.

Unit V. RNA structure prediction.

Types of RNA structures, RNA secondary structure prediction methods: *Ab Initio* approach, Dot Matrices, Dynamic programming and partition function Comparative approach, Performance evaluation.

GROUP B. DIPLOMA IN COMPUTATIONAL BIOLOGY

<u>Paper IV. Genomics and Proteomics</u>

Unit I. Genome mapping, assembly and comparison.

Genome mapping, Genome sequencing, Genome sequence assembly: Base calling and assembly programs, Genome annotation: Gene ontology, Automated genome annotation, Annotation of hypothetical proteins and Genome economy. Comparative genomics: Whole genome alignment, Finding a minimal genome, Lateral gene transfer, Within-genome approach and Gene order comparison.

Unit II. Functional Genomics.

Sequence based approaches: EST, EST index construction and SAGE. Microarray based approaches: Oligonucleotide design, Data collection, Image processing, Data transformation and normalization, Statistical analysis to identify differentially expressed genes and Microarray data classification. Comparison of SAGE and DNA Microarrays.

Unit III. Proteomics

Technology of protein expression analysis: 2D-PAGE, Mass spectrometry protein identification, protein identification through database searching, Differential in-gel electrophoresis and Protein Microarrays. Post translational modification: Prediction of disulphide bridges and Identification of posttranslational modifications in proteomics analysis. Protein sorting.

Unit IV. Protein-protein interactions.

Experimental determination of protein-protein interaction, Prediction of protein-protein interactions: prediction interactions based on domain fusion, predicting interactions based on gene neighbors, predicting interactions based on sequence homology, predicting interactions based on phylogenetic information and prediction interactions using hybrid methods.

Unit V. Applications of proteomics.

Medical proteomics-disease diagnosis: Biomarkers, Biomarker discovery using 2DGE and mass spectrometry and Biomarker discovery and pattern profiling using protein chips. Pharmaceutical proteomics-drug development: The role of proteomics in target identification, Proteomics and target validation, Proteomics in the development of lead compounds and Proteomics and clinical development. Proteomics and Plant biotechnology: Proteomics in plant breeding and genetics, Proteomics for the analysis of genetically modified plants and Proteomics and the analysis of secondary metabolism.

References

1. Xiong J. (2006). Essential bioinformatics. Cambridge, UK: Cambridge University Press.
2. Goodman N. (2002). Biological data becomes computer literature: New Advances in Bioinofrmatics. Curr. Opin. Biotechnol. 13: 68-71.
3. Hagen J.B. (2000).The origin of bioinformatics. Nat. Rev. Genetics. 1: 231-236.
4. Apweiler R. (2000). Protein sequence databases. Adv. Protein Chem. 54: 31-71.
5. Hughes A.E. (2001). Sequence databases and the internet. Methods Mol. Biol. 167: 215-223.
6. Stein L.D. (2003). Integrating biological databases. Nat. Rev. Genet. 4: 337-45.
7. Batzoglou S. (2005). The many faces of sequence alignment. Brief. Bioinformatics. 6: 6-22.
8. Xuang X.(1994). On global sequence alignment. Comput. Appl. Biosci. 10: 227-235.
9. Pearson, W.R. (1996). Effective protein sequence comparison. Methods Enzymol. 266: 227-258.
10. Spang R. and Vingron M. (1998). Statistics of large scale sequence searching. Bioinofrmatics. 14: 279-284.
11. Mullan L.J. (2002). Multiple sequence alignment- The gateway to further analysis. Brief. Bioinform. 3: 303- 305.
12. Brenden C, and Tooze J.(1999). Introduction to protein structure, 2nd ed. New York: Garland publishing.

13. Baker D. and Sali A. (2001). Protein structure prediction and structural genomics. Science 294: 93-96.
14. Stekel D. (2003). Microarray bioinformatics. Cambridge, UK: Cambridge university press.
15. Huynen M.A., Snel B., Mering C. and Bork P.(2003). Function prediction and protein networks. Curr. Opin. Cell Biol. 15: 191-198.
16. Attwood T.K. and Parry-Smith D.J. (2003). Introduction to bioinformatics, Singapore, Pearson education.
17. Twyman R.M.(2004). Principles of proteomics, York: Garland Science/Bios Scientific publishers.

GROUP C : DIPLOMA IN SYSTEM BIOLOGY

Paper I: DEVELOPMENTAL BIOLOGY

Subject description: The goals of this course are: to learn the major morphological changes that occur in animals from the fusion of eggs and sperm to birth, to understand how changes in gene expression can produce changes in developmental processes, and to relate development to evolution

UNIT I: Basic concepts of development

Potency, commitment, specification, induction, competence, determination and differentiation; morphogenetic gradients; cell fate and cell lineages; stem cells; genomic equivalence and the cytoplasmic determinants; imprinting; mutants and transgenics in analysis of development.

UNIT II: Gametogenesis, fertilization and early development

Production of gametes, cell surface molecules in sperm-egg recognition in animals; embryo sac development and double fertilization in plants; zygote formation, cleavage, blastula formation, embryonic fields, gastrulation and formation of germ layers in animals; embryogenesis, establishment of symmetry in plants; seed formation and germination.

UNIT III: Morphogenesis and organogenesis in animals

Cell aggregation and differentiation in *Dictyostelium*; axes and pattern formation in *Drosophila*, amphibia and chick; organogenesis – vulva formation in *Caenorhabditis elegans;* eye lens induction, limb development and regeneration in vertebrates; differentiation of neurons, post embryonic development-larval formation, metamorphosis; environmental regulation of normal development; sex determination. Programmed cell death and aging.

UNIT IV: Morphogenesis and organogenesis in plants

Organization of shoot and root apical meristem; shoot and root development; leaf development and phyllotaxy; transition to flowering, floral meristems, floral development and senescence in *Arabidopsis* and *Antirrhinum.*

UNIT V: Techniques for the study of development
Microscopy - Study of gene expression by biochemical methods – Study of gene expression by *in situ* methods – Microinjection – Cell-labeling methods – Cell sorting.

References:

1. Essential developmental biology – Jonathan Michael Wyndham slack, Wiley-Blackwell, 2006.
2. Current topics in developmental biology – Geral P. Schatten, Academic press, 2006.
3. The origin of animal body plans: a study in evolutionary developmental biology – Wallace Arthur, Cambridge university press, 2000.
4. Developmental biology – Werner A. Muller, Springer, 1997.

GROUP C : DIPLOMA IN SYSTEM BIOLOGY

Paper II: METABOLIC ENGINEERING

Subject description: The paper applies the concepts of analytical methods for metabolic pathways in living organisms and systematic approach for genetic modification and process design are described. Analysis of the capability of cells for the production of industrially targeted products and rigidity of the control mechanism in metabolic pathways are discussed.

UNIT I:

Principles of metabolism, Resolution of metabolism, compartmentalization; Enzyme regulation of metabolism; Metabolic disorders and its consequences. Metabolic flux balance analysis; challenges and promise of metabolic engineering; Engineering of cental metabolism of *E. coli* an over view.

UNIT II:

Tools for metabolic engineering of *E.coli*: Metabolic engineering of *E. coli* for the production of aromatic compounds. Strategies for the production of Polyhydroxy alkanoates, Biodegradable polymers. Amino acid production: Metabolic engineering for process improvement for Antibiotics; Biosynthesis. The Generation of organic molecule diversity; Regulation of metabolism solvents production of *Clostridium acetobuylicum*.

UNIT III:

Role of downstream processing: Biomass separation – Intracelluar /Extracellular products – Membrane separation techniques – Precipitation method – Solvent extraction – Two phase separation – Affinity based enrichment for microbial product recovery

UNIT IV:

Metabolic engineering of yeast for substrate untilization and metabolic production. Metbolic engineering of mammalian cells molecular bioremediation: Metabolic engineering for biodegradation of recalcitrant pollutants. Engineering heterologous secretion in yeast.

UNIT V:

Metabolic engineering for the production of plant secondary metabolites. Molecular bioremediation. Online metabolic flux analysis for fermentation operation.

Metabolomics: data base for metabolites.

Reference:

1. Metabolic engineering by Sang Yup Lee, Eleftherios T. Papoutsakis Marcel Dekker, Inc. USA.
2. Product recovery in Bioprocess technology. Biotol Series, VCH, Oxford. 1998.

GROUP C : DIPLOMA IN SYSTEM BIOLOGY

Paper III: Molecular Systems Biology

Subject description: Biology is fast becoming an interdisciplinary science. There is accumulation of large amount of information in different areas of biology - on genome sequences of many organisms, genetic and biochemical interaction networks, cell interactions during development, and organismal response to environmental stimuli, along with molecular understanding of diseases. This has led to the emerging need for a holistic description of the working of biological systems at different scales.

UNIT I

Introduction - Genome sequences, annotation, sequence alignment - Expression profiling and scoring differential expression. Interpreting expression data using Gene Ontology: Modularity in biology, clustering and probing cancer with gene expression analysis. Basics of transcription: Solution thermodynamics, Structure-Function-Energy pyramid.

UNIT II

Physiochemical basis of protein folding & protein interactions: Structural biology of protein-DNA interactions: molecular cooperativity as the foundation of complex regulatory interactions.

Molecular recognition of protein-DNA interactions: from basic principles, to calculation, to engineering: Network motifs, simple building blocks of complex networks.

UNIT III

Microscopy-based measurements of transcription, network properties, just-in-time transcription and the p53-Mdm2 feedback loop: Basics of chromatin structure. High-throughput TF-DNA interaction measurements and modeling the sequence-specificity of TFs. Modeling the condition-specific activity of TF's: Engineering principles of gene regulatory networks

UNIT IV

Comparative genomics of non-coding sequence - Application to discovering cis-regulatory elements in 3' UTRs. Evolution of modularity and transcriptional networks : Inferring mechanisms for mRNA stability regulation from high-throughput mRNA expression data - transcriptome, non-coding RNA, ribozymes, micro RNAs.

UNIT V

Overview of translation cycle, biomolecular players, comparison of prokaryotic/eukaryotic translation cycles - RNA structure, dynamics, and function: Structures of the ribosome and representative structures of translation factors. cryo-EM models of translational complexes. mRNA as a major regulator of its own expression: Riboswitches within the 5'-UTR, hairpins and pseudo knots involved in frameshifting and stop-codon readthrough within the coding sequence, micro RNAs within the 3'-UTR - Limitations of transcriptional profiling; Translational profiling: High-throughput polysomal transcript analysis.

Reference:

1. An introduction to systems biology: Design principles of biological circuits – Uri Alon, CRC Press, 2006
2. Introduction to systems biology – Sangdun choi, Humana press, 2007
3. Systems biology: definitions and perspectives – Lilia Alberghina, Hans V. Westerhoff, Birkhauser press, 2005.

GROUP C : DIPLOMA IN SYSTEM BIOLOGY

Paper IV: Glycomics

Subject Description:

Glycomics is an integrated systems approach to structure-function relationships of glycans. The basis of the paper is to identify and discuss the basic science of

1. Glycomics / Glycobiology at the genetic and cellular level.

2. Identify and discuss the clinical applications of Glycomics / Glycobiology.

3. Identify and discuss the economic implications of Glycomics / Glycobiology for the future.

Unit I: Carbohydrates

IUPAC Nomenclature of Carbohydrates; CFG Nomenclature; Cell surface carbohydrates: Introduction – Structure of *N*-glycans – Cell specific expression of *N*-glycans – *O*-glycans – Role of cell surface carbohydrates. Carbohydrate recognition in leukocyte-endothelial cell interaction: Oligosaccharides in lymphocyte homing – dependent cell adhesion mediated by E-selectin and P-selectin.

Unit II: Mammalian glycosylation

Introduction - Carbohydrate biosynthesis; Congenital disorders of glycosylation (CDG): Biosynthetic pathways in CDG pathogenesis; Structural characterization of glycosaminoglycans; Computational modeling in glycosylation; Glycosylation in native and engineered insect cells.

Unit III: Lectins

Genomics Resource for Animal Lectins, 3D structure of lectins, CFG-GBP-DB Glycan binding protein, LectinDB: Plant lectin Database, SugarBindDB: Bacterial lectin Database; Prediction of glycosylation sites

Unit IV: Glycoproteomics

Chemoenzymatic synthesis of glycan libraries - Metabolic labeling of glycans with azido sugars for visualization and glycoproteomics. Functional proteomic profiling of glycan-processing enzymes - Identification of ligand specificities for glycan-binding protein using glycan arrays.

Unit V: Database Resources

Carbohydrate databases , Bacterial Carbohydrate Structure DataBase, Glycan topology description , Glycan MS tools, Glycan NMR tools, Glycan 3D modeling, Glycans in PDBs, Glycan Processing Pathways & Enzymes, CFG- Microarray Data Glycogene chip

References:

1. Glycobiology – Minoru Fukuda, Academic press, 2006
2. Handbook of carbohydrate engineering – Kevin J. Yarema, CRC press, 2005.
3. Molecular and cellular glycobiology – Minoru Fukuda, Ole Hindsgaul, Oxford university press, 2000.