



St. PETER'S UNIVERSITY

St. Peter's Institute of Higher Education and Research

(Declared Under Section 3 of the UGC Act, 1956)

AVADI, CHENNAI – 600 054

TAMIL NADU

M.Sc. (BIOINFORMATICS)

Code No. - 428

(Effective From 2009 – 2010)

(Distance Education)

Regulations and Syllabi

(I to IV Semester)

St. PETER'S INSTITUTE OF DISTANCE EDUCATION

Recognized by Distance Education Council and

Joint Committee of UGC – AICTE - DEC, New Delhi

(Ref. F. No. DEC/SPU/CHN/TN/Recog/09/14 dated 02.04.2009 and

Ref.F.No.DEC/Recog/2009/3169 dated 09.09.2009)

St. PETER'S UNIVERSITY
St. PETER'S INSTITUTE OF DISTANCE EDUCATION
Chennai – 600 054.

Code No. – 428
M.Sc. (BIOINFORMATICS)
(Distance Education)

Regulations and Syllabi
(Effective from 2009 – 2010)

- 1. Eligibility:** A Candidate with a Bachelor's Degree in Science in the disciplines of Genetics, Biology, Biochemistry, Biotechnology, Physics, Chemistry, Computer Science, Botany, Zoology, Microbiology, Mathematics, Statistics, Nutrition, Food Service Management & Dietetics, Agriculture, B.E/ B.Tech (Biotech), B.V.Sc, MBBS, BDS, B. Pharm. BPT & BCA from this University, or an examination of some other University accepted as equivalent thereto, are eligible for Admission to Two Year M.Sc. Programme in Bio Informatics.
- 2. Duration:** Two Years.
- 3. Medium:** English is the medium of instruction and examination.
- 4. Methodology:** The methodology of distance education includes the supply of self-instructional study materials in print format and in CD, face-to-face instruction for theory and practicals for a limited period during week ends and on holidays, provision of virtual class in phased manner, dissemination of information over e-mail, Student - Support Service at various Centres of the University, Continuous Assessment and End Assessment conducted by the University at various parts of India.
- 5. Weightage for Continuous and End Assessment:** There is no weightage for Continuous Assessment unless the ratio is specifically mentioned in the scheme of Examinations. The End Assessment (EA) has 100% weightage.
- 6. Credit System:** Credit system be followed with 36 credits for each Year and each credit is equivalent to 25 hours of effective study provided in the Time Table of the formal system.

7. Scheme of Examinations

First Semester

Code No.	Course Title	Credit	Marks	
			EA	Total
Theory				
109PBIT01	Biochemistry	4	100	100
109PBIT02	Biophysical Chemistry	4	100	100
109PBIT03	Biostatistics	4	100	100
109PBIT04	Elective-I: Cell Biology	3	100	100
109PBIP01	Practical -I: Theory and Practice of Computer Science and Programming Record	3	90	100
Total			18	500

Second Semester

Code No.	Course Title	Credit	Marks	
			EA	Total
Theory				
209PBIT01	Introduction to Bioinformatics	3	100	100
209PBIT02	Molecular Biology and Biotechnology	3	100	100
209PBIT03	Elective-II: Programming in JAVA	3	100	100
209PBIT04	Elective-III: Basic of Computer -aided drug design	3	100	100
209PBIP01	Practical - I: Biochemistry and Molecular Biology Lab Record	3	90	100
209PBIP02	Practical - II: Theory & Practice of Computer Programming PERL & CGI Record	3	90	100
Total			18	600

Third Semester

Code No.	Course Title	Credit	Marks	
			EA	Total
Theory				
309PBIT01	Genomics & Proteomics	3	100	100
309PBIT02	Algorithms for Computational Biology	3	100	100
309PBIT03	Structural Bioinformatics	3	100	100
309PBIT04	Elective-IV: Systems Biology	3	100	100
309PBIT05	Elective-V: Potential Applications and commercial aspects of Bioinformatics	3	100	100
309PBIP01	Practical-I: Tools and their Applications Bioinformatics Record	3	90 10	100
Total		18	600	600

Fourth Semester

Code No.	Course Title	Credit	Marks	
			EA	Total
Theory				
409PBIT01	Databases in Molecular Biology	4	100	100
409PBIT02	Elective-VI: Advanced Topics in Bioinformatics	4	100	100
409PBIT03	Elective- VII: Bioinformatics & Drug design	2	100	100
409PBIP01	Project & Viva-voce	8	100	100
Total		18	400	400

8. Passing Requirements: The minimum pass mark (raw score) be 50% in End Assessment.

9. Grading System: Grading System on a 10 Point Scale be followed with 1 mark = 0.1 and the conversion of the Grade point as given below.

$$\begin{aligned} \text{Overall Grade Point Average (OGPA)} &= \frac{\text{Sum of Weighted Grade Points}}{\text{Total Credits}} \\ &= \frac{\sum (EA)C}{\sum C} \end{aligned}$$

10. The Overall Grade: The Overall Grade and Classification of all successful candidates be arrived at from the Overall Grade Point Average as stipulated in the following conversion Table.

Grade	Over all Grade Point Average(OGPA)	Over all weighted Average marks	Classification
0	9.0 to 10.0	90 to 100	First Class
A	8.0 to 8.9	80 to 89	First Class
B	7.0 to 7.9	70 to 79	First Class
C	6.0 to 6.9	60 to 69	First Class
D	5.0 to 5.9	50 to 59	Second Class
F	0.0 to 4.9	0 to 49	Reappearance

The Grade Sheets of successful candidates provide particulars such as (1) Overall weighted Average Marks and (2) Overall Grade.

11. Pattern of the Question Paper: The question paper for the End Assessment will be set for three hours and for a maximum of 100 marks with following divisions and details.

Part A: 10 questions (with equal distribution to all the units in the syllabus). Each question carries 2 marks.

Part B: 5 questions with either or type (with equal distribution to all the units in the syllabus). Each question carries 16 marks.

The total marks scored by the candidates will be calculated to the maximum prescribed in the Regulations.

12. Syllabus

109PBIT01: BIOCHEMISTRY

Unit I

Carbohydrates: Classification, Structures-open chain forms, cyclic forms, glycosidic linkages, glycoprotein's-structures and physiological functions. Amino acids: Classification (based on nature and metabolism), Zwitter-ion, optical activity and chelate formation. Stereochemistry of amino acids. Classification structure and functions of lipids.

Unit II

Protein Chemistry: Peptide bond-formation and geometry; Classification of proteins based on shape, composition, function and stability; Denaturation of proteins, Cleavage of disulfide bonds and separation of polypeptide chains, complete hydrolysis of poly peptide chains, identification of C and N terminal residues, partial hydrolysis, Ordering of peptide fragments, assignment of the positions disulfide linkages. Protein folding pathways, Ramachandran Diagram.

Unit III

Enzymes- Active site, cofactors, Enzyme specificity, factors affecting enzyme activity. Enzyme kinetics- Michaelis – Menten equation, LB plot, Determination of K_m , Inhibitors, Allosteric enzymes, General mechanisms of action of enzymes, Regulation of enzyme activity, Enzymes on solid support- methods of enzyme immobilization, properties of immobilized Enzymes

Unit IV

Metabolic Pathways: Metabolism of glucose – glycolysis, TCA cycle, glycogenesis, glycogenolysis and gluconeogenesis, Pentose phosphate shunt, Protein metabolism- transamination, oxidative deamination and urea cycle. Interconnection of pathways, metabolic regulation

Unit V

Separation and Purification of Macromolecules-Extraction and purification of proteins and enzymes.

Centrifugation – differential, isopycnic and ultra centrifugation.

Chromatography-Gel filtration, ion-exchange chromatography, Affinity chromatography.

Electrophoresis-Principles, SDS-PAGE, Agarose Gel Electrophoresis, Capillary electrophoresis, 2D gel electrophoresis, isoelectric focusing.

RECOMMENDED TEXTS:

1. Lehninger, AL, Nelson, DL, Cox, M, M M (2004), "**Principles of Biochemistry**", 4th edition, W.H. Freeman & Co., New York.
2. Berg, JM, Stryer, L, Tymoczko, JL (2002), "**Biochemistry**" 5th edition, W.H. Freeman & Co., New York.
3. Voet, D, Voet, JG, Pratt, C.W. (2005) "**Fundamentals of Biochemistry**" 2nd edition, John Wiley & Sons, USA.

REFERENCE BOOKS:

1. Voet, D (2004), "**Biochemistry**", 3rd edition, Wiley, USA.
2. Horton, R, Moran, L, Scrimgeour, G, Perry, M, Ravon, D (2005) "**Principles of Biochemistry**", 4th edition, Prentice-Hall of India, Kolkata.
3. Satyanarayana, U (2005) "**Biochemistry**", Books Allied (P) Ltd, Kolkata.
4. Talwar, GP, Srivastava LM, (Editor) (2003) "**Textbook of Biochemistry and Human Biology**", 3rd edition, Prentice-Hall of India Pvt Ltd, New Delhi.
5. Palmer, T (2004) "**Enzyme: Biochemistry, Biotechnology, Clinical Chemistry**" Affiliated-East-West Press, India.

109PBIT02: BIOPHYSICAL CHEMISTRY

Unit I

Classical and quantum mechanics: Elementary introduction to Lagrangian and Hamiltonian formulation of mechanics – breakdown of classical mechanics – Planck theory of blackbody radiation – photoelectric effect – Bohr model of the atom – atomic spectra – De Broglie theory of matter waves – Schrodinger wave equation – interpretation of wave function – atomic orbitals – molecular orbitals – hybrid orbitals – valency of carbon atom – covalent bond – bond order – resonance structure of benzene – partial double bond character of peptide bond.

Unit II

Thermodynamics and energetics: Thermodynamics systems – laws of thermodynamics – statement and applications – concepts of entropy and enthalpy – chemical potentials – free energy – Gibb and Helmholtz free energy – ATP as energy currency in biological systems – free energy of hydrolysis of ATP and other organophosphates.

Unit III

Molecular mechanics and dynamics: Basic principles – molecular representations – force fields – atom-atom pair potentials – bond length and bond angle and torsion angle potential – van der Waals and electrostatic potential – hydrogen bonding terms – MM3, AMBER, GROMOS, ECEPP/3 force fields – minimization techniques – line search and elementary introduction to gradient techniques – concepts of molecular dynamics – introduction to time-step integration algorithms – dynamics protocols – equilibration and data collection – trajectories and their analyses – graphical representations of trajectories of geometrical parameters.

Unit IV

Protein and nucleic acid structure: Levels of protein structure – primary, secondary, tertiary and quaternary with examples – alpha helix, beta sheet and beta turn – domains and structural motifs – Rossmann fold, Immunoglobulin fold – Double helical structure of DNA – DNA polymorphism – RNA secondary and tertiary structure, with particular reference to tRNA and ribosomal RNA – Structure of macromolecular complexes – ribosome, viruses – TMV, TBSV and HIV

Unit V

X-ray crystallography and spectroscopy: Elementary description of crystallography – crystal growth, data collection, structure solution, refinement and interpretation – concept of resolution – IR spectroscopy – UV-Visible spectroscopy – hyperchromism and hypochromism – Raman spectroscopy – 'fingerprinting' using Raman spectra – complementarity of Raman and IR spectroscopy Fluorescence

spectroscopy – NMR spectroscopy – chemical shift – NOW – Fourier transform NMR spectroscopy - elementary introduction to COSY and NOESY – protein structure determination using NMR.

RECOMMENDED TEXTS:

1. Vasantha Pattabhi and N.Gautham (2001) '**Biophysics**' Narosa Publishing Company, New Delhi.
2. P.Narayanan (1999) '**Introductory Biophysics**' New Age Publishing Co., Mumbai, India.

REFERENCE BOOKS:

1. C.R. Cantor and P. Schimmel (1985) '**Biophysical Chemistry, Vol-I, II and III**' W.H.Freeman and Company, New York, USA.
2. D. Freifelder (1982) '**Physical Biochemistry**' W.H. Freeman and Company, New York, USA.
3. E. Ackerman, L.B.M. Ellis and L.E. Williams (1979) '**Biophysical Science**' Prentice Hall Inc., New Jersey, USA.
4. F.W. Sears, M.W. Zemansky and H.D. Young (1985). '**College Physics**' Addison Wesley Publishing Company, Massachusetts, USA.
5. C.N. Banwell (1983) '**Fundamentals of Molecular Spectroscopy**' Tata McGraw-Hill Publishing Company Lt., New Delhi, India.
6. G.M. Barrow (1962) '**Molecular Spectroscopy**' McGraw-Hill Book Company Inc., New York, USA.
7. D. Sherwood (1976) '**Crystals, X-rays and Proteins**' Longman Group Ltd., London, UK.
8. A.R. Leach (1996) '**Molecular Dynamics Simulation**' John Wiley and Sons, New York, USA.
9. J.M. Haile (1992) '**Molecular Dynamics Simulation**' John Wiley and Sons, New York, USA.
10. C. Branden and J. Tooze (1991) '**Introduction to Protein Structure**' Garland Publishing Company, New York, USA.

109PBIT03: BIOSTATISTICS

Unit I

Statistics – Scope –collection, classification, tabulation of Statistical Data – Diagrammatic representation – graphs – graph drawing – graph paper – plotted curve –Sampling method and standard errors –random sampling –use of random numbers –expectation of sample estimates – means – confidence limits – standard errors – variance.

Unit II

Measures of central tendency – measures of dispersion – skewness, kurtosis, moments – Correlation and regression – correlation table – coefficient of correlation – Z transformation – regression – relation between regression and correlation

Unit III

Probability – Markov chains applications – Probability distributions – Binomial (Gaussian distribution) and negative binomial, compound and multinomial distributions – Poisson distribution – Normal distribution – graphic representation – frequency curve and its characteristics –measures of central value, dispersion, coefficient of variation and methods of computation – Basis of Statistical Inference –Sampling Distribution – Standard error – Testing of hypothesis – Null Hypothesis –Type I and Type II errors.

Unit IV

Tests of significance for large and small samples based on Normal, t, z distributions with regard to mean, variance, proportions and correlation coefficient – chi-square test of goodness of fit – contingency tables – χ^2 test for independence of two attributes – Fisher and Behrens 'd' test – 2×2 table – testing heterogeneity – $r \times c$ table – chi-square test in genetic experiments – partition $X 2$ – Emerson's method – Tests of significance –t tests – F tests – Analysis of variance – one way classification – Two way classification, CRD, RBD, LSD.

Unit V

Spreadsheets – Data entry –mathematical functions – statistical function – Graphics display – printing spreadsheets – use as a database word processes – databases – statistical analysis packages graphics/presentation packages.

RECOMMENDED TEXTS:

1. Zar, J.H. (1984) "**Bio Statistical Methods**", Prentice Hall, International Edition.
2. Sundar Rao P. S.S., Jesudian G. & Richard J. (1987), "**An Introduction to Biostatistics**", 2nd edition,. Prestographik, Vellore, India.
3. Warren, J; Gregory, E; Grant, R (2004), "**Statistical Methods in Bioinformatics**", 1st edition, Springer.

REFERENCE BOOKS:

1. Milton, J.S.(1992),. "**Statistical methods in the Biological and Health Sciences**", 2nd edition, McGraw Hill.
2. Rosner, B (2005), "**Fundamentals of Biostatistics**", Duxbury Press.

ELECTIVE SUBJECT

109UBIT04: CELL BIOLOGY

Unit I

Architecture of prokaryotic and eukaryotic cells and tissues. Biomembranes and the subcellular organization of eukaryotic cells. Cell motility and shape, Eukaryotic cytoskeleton- microfilaments-microtubules - intermediate filaments, Cell division-mitosis and meiosis, eukaryotic cell cycle and its regulation.

Unit II

The mitochondrion- structure, electron transport chain, oxidative phosphorylation, Chemiosmotic process. Chloroplasts-photosynthesis-photosystems, Calvin cycle, Dark reactions.

Unit III

Intracellular traffic- membrane transport-principles, active transport, ion channels. Protein sorting-an overview of targeting proteins to mitochondria, nucleus, endoplasmic reticulum, lysosomes and plasma membrane.

Unit IV

Cell signaling-Hormone-receptor interactions, G protein-coupled receptors and their effectors, Second messengers, Receptor tyrosine kinases, MAP kinase pathways. Cell-cell interactions in development.

Unit V

Basic immunology- Types of immunity-innate, acquired, active and passive, antigen-antibody reactions, elements of the immune system: T cells, B cells, antigen presenting cells, helper and suppressor cells, natural killer cells, cell-mediated and humoral immunity.

RECOMMENDED TEXTS:

1. C. Gerald Karp (Editor) (2005) **"Cell and Molecular Biology: Concepts and Experiments"**, 4th edition, Wiley Publishing Co, USA.
2. Lodish, H, Scott, M.P, Matsudaira P, Darnell, J, Zipursky, L, Kaiser, CA, Berk, A, Krieger, M, (2003) **"Molecular Cell Biology"**, 5th edition, W.H. Freeman and Co, New York.

REFERENCE BOOKS:

1. Alberts, B; Johnson, A; Lewis, J; Raff, M; Roberts, K; Walter, P (2002) **"Molecular Biology of the Cell"**, 4th edition, Garland Science, Taylor and Francis group, USA.
2. Verma, PS; Agarwal,VS (2005) **"Cell Biology, Genetics, Molecular Biology, Evolution and Ecology"**,14th edition, S.Chand & Company Ltd, New Delhi.
1. Alberts, B; Johnson, A; Lewis, J; Raff, M; Bray, D; Hopkin,mK; Roberts, K; Walter, P (2003), **"Essential Cell Biology"** ,2nd edition, Garland Science, Taylor & Francis Group, USA.
2. Becker, WM ; Klein smith, LJ Hardin (2005),**"World of the Cell"** 6Th edition, Benjamin Cummings.

109PBIP01: THEORY AND PRACTICE OF COMPUTER SCIENCE AND PROGRAMMING (PRACTICALS)

Unit I

Program structure-components of a program-program compilation and execution-flow charts-arrays (single and multi dimensional) and string functions-user defined functions and function categories-input/output devices

Unit II

Mathematical foundations-Data structures-reasoning about correctness-complexity analysis-implementation techniques

Unit III

Internet- communication types on the internet-hypertext, www, client programs-accessing internet resources via a web browser- static and dynamic web pages-wireless application protocol, network computing and grid computing-downloading using ftp-examples

Unit IV

UNIX-understanding the UNIX system-fundamentals of using the UNIX system- mastering the special features of the UNIX system.

Text processing: commonly used UNIX commands-resources for users of the UNIX system-interacting with the UNIX system-essentials of system administration-octal equivalents to ASCII-different file editors-handling files-introduction to Linux

Unit V

C++ programming- introduction to programming in C++ - The ASCII code-C++ keywords-C++ operators-C++ types-conditional statements and integer types-interaction and floating types.

Functions-arrays-pointers and references-strings-classes-overloading-operators-A string class-composition and inheritance-stream I/O - simple programs which demonstrates inheritance, operator overloading and polymorphism

REFERENCE BOOKS:

1. Hubbard, John (2000) "**Programming with C++**", Schaum's outline series, Tata McGraw Hill International.
2. Thomas, Rebecca and Jean Yates (1987), "**A user Guide to the UNIX system**," Tata McGraw Hill International.
3. Arnold Robbins & Daniel Gilly, (1999) "**Unix in a Nutshell**", O'Rielly and Associates.
4. Kay. A Robbins, Steven Robbins, Kay. Ret. Robbins and Steve Robbins (1999), "**The C programming language**", Prentice- Hall.

209PBIT01: INTRODUCTION TO BIOINFORMATICS

Unit I

Basics of computing: Introduction to operating systems – WINDOWS, UNIX, LINUX; Advantages of security installation; Use of internet; Graphics – visualization techniques; softwares and hardwares; Computer networking – LAN, WAN, MODEM, Optical Vs electronic networking, firewalls; Ethernet and TCP/IP family of protocols.

Unit II

Data warehousing, data capture, data analysis; Introduction to Nucleic Acid and Protein Sequence Data Banks; Nucleotide databases (Genbank, EMBL, DDBJ); Protein databases (Swiss-Prot, Tr-EMBL, PIR_PSD, Expasy); Derived Databases (Prosite, PRODOM, Pfam, PRINTS); Sequence submission Methods and tools (Sequin, Sakura, Bankit); Sequence retrieval systems (Entrez & SRS); Sequence File Formats and Conversion tools; Genome (NCBI, EBI, TIGR, SANGER), Metabolic Pathway database (KEGG, EMP, EcoCyc, BioCyc and MetaCyc); Specialized database (IMGT, Rebase, COG, LIGAND, BRENDA); Structural database.

Unit III

Internal and external co-ordinate system; Generation of co-ordinates of biopolymers in Cartesian and cylindrical polar co-ordinate system; Genome Anatomy, Prokaryotic genomes structures, Eukaryotic genomes structures, Gene density, Gene Ontology, Gene Order (synteny), Plasticity zone, Gene Network, tandem repeats, Transposable elements, Pseudo genes, Gene Clusters, Segmental duplication, non-coding conservation, Comparative genomics, Importance of Full Genome Alignments, Concepts & applications of Suffix tree in comparative genomics, Algorithms for BLAST2, Mega Blast, Mummer.

Unit IV

Analysis of protein and nucleic acid sequences, multiple alignment programs, Development of programs for analysis of nucleic acid sequences, Pairwise Sequence Alignment - Similarity, Identity and Homology, Global Alignment, Local Alignment; database search methods and scoring matrices ; Dynamic Programming, Heuristic approach, Scoring Matrices and Affine Gap costs; Detailed method of derivation of the PAM & BLOSUM Matrices; Differences between Distance & Similarity Matrix; Assessing the Significance of Sequence Alignments.

Multiple Sequence Alignment - Multiple alignment programs, Development of programs for analysis of nucleic acid sequences, Conversion of various file formats; Phylogenetic Analysis - Concept of dendrograms; Strings and Evolutionary trees; Ultra metric trees and Ultra metric distances; Additive - Distance trees; Methods of Construction of Phylogenetic trees-Maximum Parsimony Method, Maximum likelihood method and Distance Methods, Reliability of trees.

Unit V

Analysis of structures and correctness of structures, Submission of data to PDB: atomic coordinates and electron density maps; Anatomy of Proteins - Ramachandran plot, Secondary structures, Motifs, Domains, Tertiary and quaternary structures; Calculation of conformational energy for bio-macromolecules; Methods for Prediction of Secondary and Tertiary structures of Proteins - Knowledge-based structure prediction, Fold recognition, Ab initio methods for structure prediction; Methods for comparison of 3D structures of proteins; Molecular interactions of - Protein – Protein, Protein – DNA, Protein – carbohydrate, DNA – small molecules etc.; Docking of Molecules; Molecular Design.

RECOMMENDED TEXTS:

1. Lesk, A.M. (2002) **"Introduction to Bioinformatics"**, 1st Edition, Oxford University Press, Oxford, UK.
2. N. Gautham (2006) **"Bioinformatics"**, Narosa Publishing Company, New Delhi.
3. Westhead, D. R., Parish, J.H and Twyman, R.M (2003) **"Instant Notes Series – Bioinformatics"** 1st Edition, Viva Books Private Limited, New Delhi, India.
4. Bernhard Haubold and Thomas Wiehe (2006) **"Introduction to Computational Biology – An Evolutionary Approach"** Birkhauser Verlag, Switzerland.

REFERENCE BOOKS:

1. Krane, DE; Raymer, ML (2003), **"Fundamental concepts of Bioinformatics"**, Benjamin Cummings.
2. Ignacimuthu, S (2005) **"Basic Bioinformatics"**, 1st Edition, Narosa Publishing House, New Delhi, India.
3. P. Baldi and S. Brunak (2003) **"Bioinformatics"** Affiliated East-West Press, New Delhi, India.

209PBIT02: MOLECULAR BIOLOGY AND BIOTECHNOLOGY

Unit I

DNA is the genetic material-structure –DNA polymerases-replication – telomerases, DNA repair mechanisms, genetic recombination –Holliday model, transposons and retroposons.

Unit II

Gene expression;-Prokaryotic and Eukaryotic RNA polymerases, Initiation of transcription, termination of transcription, regulation of gene expression, lac operon and tryptophan operon, hormonal regulation of gene expression, translation-gene regulatory proteins, DNA methylation.

Unit III

Post transcriptional modifications-RNA splicing and ribozymes, gene control in development
Translation-initiation, elongation and termination, inhibitors, post translational modifications

Unit IV

Cloning and expression vectors-plasmids-cosmids-phages-viruses-YAC, BAC- Molecular probes-gene library-restriction enzymes-restriction mapping-southern, northern, western blotting-screening of cDNA libraries

Unit V

Antisense RNA technology-DNA finger printing-foot printing-gene amplification-Basic PCR-its modifications-RT- PCR- applications-RAPD. Introduction to nano technology, commercial applications of nanotechnology. Immunotechnology- Hybridoma technology –production of Interferon – vaccines – DNA vaccines.

RECOMMENDED TEXTS:

1. Benjamin Lewin (2004) "**Genes VIII**" ,8th edition, Pearson Education International.
2. Glick,BR; Pasternak, JJ (2003), "**Molecular Biotechnology;Principles and Applications of Recombinant DNA**",3rd edition,American Society of Microbiology.
3. Satyanarayan, U (2005) "**Biotechnology**", Books and Allied (Pvt) Ltd Calcutta.

REFERENCE BOOKS:

1. Watson, J; Zoller, M; Gilman, M; Witkowski, J (1992), "**Recombinant DNA**",2nd edition, W.H. Freeman.
2. Old,RW ; Primrose, SB (1994), "**Principles of Gene Manipulation-An Introduction to Genetic Engineering**" 5th edition, Blackwell Science.
3. Brown ,TA (2001) "**Gene Cloning and DNA analysis-an introduction**",4th edition, Blackwell Science.
4. Poole,C; Owens, FJ (2003) "**Introduction to Nanotechnology**", John Wiley and Sons.

209PBIT03: ELECTIVE SUBJECT PROGRAMMING IN JAVA

Unit I

An introduction to JAVA programming – OOPS and JAVA - Java basics - Working with objects – creating classes and application in JAVA- More about methods Conditionals and Loops

Unit II

Array and strings - Java applets Basics – Threads – Streams and I/O

Unit III

Graphics, fonts and color – Simple animation – More animation, Images and sound – Managing simple events and interactivity – creating user Interfaces with AWT Windows, Networking and other Tidbits – Modifiers, Access control and class Design.

UNIT IV

Packages and Interfaces – Exception and Managing errors – Multithreading.

UNIT V

Using Native Methods and Libraries – Under the Hood – Java programming tools – Working with Data structures and Java

RECOMMENDED TEXTS:

1. Patrick Niemeyer, P; Knudsen, J (2002) **Learning JAVA**, 2nd edition, O'Reilly Publishers.
2. Liang, YD (2002) **"Introduction to JAVA Programming"**, 4th edition, Prentice Hall.

Reference Books:

1. Crawford, W; Farley, J (2005), **"Java in a nutshell"** ,3rd edition, O'reilly Publishers.

ELECTIVE SUBJECT (EXTRA DISCIPLINARY)
209PBIT04: BASICS OF COMPUTER – AIDED DRUG DESIGN

Unit 1

Drug Discovery: Introduction, Conventional drug design approaches, irrational vs. rational, various steps of drug design process-Lipinski rule-pharmacophore kinetics and dynamics-ADME properties, Lipinski rule-Examples uses of computer based drug discovery-benefits

Unit 2

Introduction to Bioinformatics: What is bioinformatics-sequence database and their uses -analysis of sequence-multiple sequence analysis-secondary structure prediction-uses of different bioinformatics tools and applications

Unit 3

Biomacromolecular structure and function: Various levels of protein structure, Ramachandran Plot, Protein folding, Structure of DNA-protein-protein interaction, protein-DNA interactions-enzyme kinetics-inhibitors

Unit 4

Introduction to molecular modeling: Molecular structure, bonding, Various types of Forces responsible for stabilization of biomolecules and their interaction-Potential energy surface-force field-molecular mechanics method -Structure activity relationship- de novo drug design pharmacophore-and docking- scoring

Unit 5

Quantitative structure activity relationship: QSAR, concept, and properties of organic molecules- various descriptors used in the QSAR, multiple linear regression, and its applications to drug design

RECOMMENDED TEXTS:

1. Gautham N (2006) **"Bioinformatics"**, Narosa Publishing Company, New Delhi.
2. Vasantha Pattabhi and N. Gautham (2001) **'Biophysics'** Narosa Publishing Company, New Delhi.
3. Lesk, A.M. (2002). **"Introduction to Bioinformatics"**, 1st Edition, Oxford University Press, Oxford, UK.
4. Andrew R. Leach (2001) **"Molecular Modeling: Principles and Applications"** Printice-Hall.
5. Charifson P.S (1997) **"Practical Application of Computer Aided Drug Design"** Dekker, New York.

209PBIP01: BIOCHEMISTRY & MOLECULAR BIOLOGY LAB (PRACTICALS)

Unit I

Preparation of Buffers, determination of pH, Assay of protein by Lowry's method and Bradford method, Assay of glucose by orthotoluidine method, Assay of DNA Enzyme assay: Determination of specific activity of alkaline phosphates, Effect of pH and substrate concentration on alkaline phosphatase activity

Unit II

Cell fractionation and Isolation of cell organelles, Disruption of cells, Isolation of sub-cellular organelles, Isolation of plasmid DNA, Amplification of DNA by PCR.

Unit III

Chromatographic techniques: Gel filtration, Ion-exchange and Thin layer chromatography

Unit IV

Electrophoretic techniques: SDS PAGE and Agarose gel electrophoresis, molecular weight determination of plasmid DNA, Western Blotting and Southern blotting.

Unit V

Immunological methods based on antigen-antibody – Precipitation reaction based assays, Agglutination based tests, Enzyme linked immunosorbent assay (ELISA)

REFERENCE BOOKS:

1. Wilson, K; Walker, J (Editors) (2005) **"Principles and techniques of Biochemistry and Molecular Biology"** 6th edition, OUP.
2. Sambrook, J; Russel, DW (2001) **"Molecular Cloning"**, 3rd edition, Cold Spring Harbor Laboratory Press,.
3. Sadasivam, S; Manickam, A (1996) **"Biochemical Methods"**, 2nd edition, New Age International Pvt Ltd.

209PBIP02: THEORY AND PRACTICE OF COMPUTER PROGRAMMING – PERL & CGI (PRACTICALS)

Unit I

Introduction to Perl 5; Variable Types; Data Types Operators; File Test Operators; Control Structures; Subroutines, Hash Traversal Functions; Other Useful Functions; Regular Expressions.

Launching External Programs; Special Variables; File Functions; Special Conditionals; Command Line Args; Basic I/O.

Unit II

How Perl Replaces Other Utilities; Packages; Environment Variables, Signals; Getopts and Timelocal Libraries; Perl Debugging, Setuid/setgid Perl Scripts; Random Number Generation, CGI

Unit III

Introduction; Creating a static HTML files by a Perl Programme, Creating a Web Page "on the fly" by a CGI – Programme, Guidelines for HTML page generation by a CGI-Program

Unit IV

Receiving CGI – programme arguments from the URL, Using CGI.pm for parsing the query string, Receiving CGI-program arguments from a Web

Unit V

HTML-structure tags-tag attributes-linking to other web pages-preparing images for the web page-adding more style to the web page-developing pages for the institution, laboratory details

REFERENCE BOOKS:

1. Doyle Paul, Micheal O Foghlu, David Harlan, Shelly Powers, Matthew D. Healy; (1996). **"Using Perl for Web Programming"**.
2. James. D. Tosdall. (2000) ,**"Beginning Perl for Bioinformatics"** 1st edition, O'Rielly and Associates.
3. Larry Wall, Tom Christiansen Jon Orwant, (2000). **"Programming Perl "** 3rd edition, O'Rielly and Associates.
4. Randall. L. Schwartz & Tom Phoenix.(2000). **" Learning Perl "**1st edition, O'Rielly and Associates.
5. Scott Guelich, Shishir Gundavaram, Gunther Birzneits and Linda Mui,(2000),**"CGI Programming"** ,2nd edition, O'Rielly and Associates.

THIRD SEMESTER

309PBIT01: GENOMICS AND PROTEOMICS

Unit I

Organization of the prokaryotic and eukaryotic genomes – Genetic linkage maps and physical maps – current sequencing technologies – partial sequencing – gene identification – gene prediction rules and softwares, sequence assembly, Human Genome Project

Unit II

Gene therapy – pathway regulatory networks – drug discovery – management of chemical libraries - Microarrays – genes in metabolic pathways – microarrays in drug toxicity testing and metabolic pathways.

Unit III

Life cycle of a protein – functional protein families – Gene _expression – EST (Expressed sequence tag) – mass spectrometry – application of proteomic mining, expression profiling, network mapping and mapping protein modification.

Unit IV:

Extracting proteins from biological samples – protein separation before and after digestion using PAGE, preparative IEF, and HPLC – Tandem LC approaches for peptide analysis – protein digestion technique – Mass spectrometry for protein – protein sequence analysis by TMS data, Software for Mass Spectrometry data analysis.

Unit V:

Mining proteomics- protein expression profiling – identifying protein-protein interaction and protein complexes – mapping protein modification – new approaches in proteomics.

RECOMMENDED TEXTS:

1. Primrose, S.B. and Twyman, R.M. (2003). **"Principles of Genome Analysis and Genomics"**: 3rd edition, Blackwell Publishing Company, Oxford, UK.
2. Liebler, D.C. (2002). **"Introduction to Proteomics – Tools for the New Biology"**, 1st Edition, Humana Press Inc., New Jersey, USA.
3. Orengo, C.A., Jones, D.T. and Thornton, J.M. (2003). **"Bioinformatics – Genes, Proteins and Computers"**, 1st Edition, BIOS Scientific Publishers Limited, Oxford, UK.

REFERENCE BOOKS:

1. Mount, D.W. (2001). **"Bioinformatics – Sequence and Genome Analysis"**, 1st Edition, Cold Spring Harbor Laboratory Press, New York, USA.
2. West Head, D.R., Parish, J.H. and Twyman, R.M. (2003). **"Instant Notes Series – Bioinformatics"**, 1st Edition, Viva Books Private Limited, New Delhi, India.
3. Ignacimuthu, S. (2005). "Basic Bioinformatics", 1st Edition, Narosa Publishing House, New Delhi, India.
4. Lesk, A.M. (2002). **"Introduction to Bioinformatics"**, 1st Edition, Oxford University Press, Oxford, UK.

309PBIT02: ALGORITHMS FOR COMPUTATIONAL BIOLOGY

Unit I: Strings and Trees

Definitions – strings – substrings, superstrings, suffix and prefix strings – operations on strings – concatenation – delete operator – graphs – definitions – directed, connected, cyclic, complete graphs – trees and terminology – leaf, node, branch root – algorithms – big O notation – classification of algorithms – P, NP, NP-hard, NP – complete, with examples, Traveling Salesman, Hamilton Path – pseudo code algorithms for sorting, finding minimum/maximum.

Unit II: Sequence Alignment

Why align sequences – similarity v/s homology – heterologs, orthologs, paralog, xenolog – Karlin – Altschul statistics to estimate significance of an alignment – expectation values and Z values – sequence comparisons using dot matrices with examples – dynamic programming – details of Needleman – Wunsch, Smith – Waterman algorithms with worked out examples – hashing methods with worked out examples – BLAST and FASTA.

Unit III: Multiple sequence alignment, substitution matrices and Phylogenetic trees

Representing and scoring a multiple sequence alignment – dynamic programming for multiple sequence alignment – pitfalls – progressive or hierarchical alignment with worked out examples – substitution matrices – evolutionary models – PAM substitution matrices – BLOSUM substitution matrices – gap penalties – phylogenetic trees – distance matrix methods – UPGMA, neighbour joining, with worked out examples – maximum parsimony with worked out examples - maximum likelihood.

Unit IV: Pattern discovery and characterization in protein and DNA Sequences

Sequence pattern representations – deterministic patterns – regular expressions – probabilistic patterns – sequence logos – general methods of pattern classification – methods for proteins – hidden Markov models and application to analyses of protein sequences – general methods of gene discovery – using HMM, GeneMark – artificial neural networks – introduction and their use in gene discovery, GRAIL – Gene discovery using Fourier analysis, Genes can ,Bayesian Classifications

Unit V: Methods of analysis of bimolecular structures

Visualization and representation of molecular structure - computer graphics - methods of representing a three-dimensional object on a two-dimensional surface - methods of representing biological molecules - geometrical analyses - bond lengths, angles, hydrogen bonds, torsion angles, calculations of planes, the Ramachandran map - protein surface and solvent accessibility - protein structure comparisons - superposition techniques - distance matrices - dynamic programming using distance matrices - COMPARE - nucleic acid structural parameters.

REFERENCE BOOKS:

1. Mount D.W. **Bioinformatics. Sequence and Genome Analysis.** (Cold Spring Harbor, 2000).
2. Baxevanis A.D. **Bioinformatics: A practical guide to the analysis of genes and proteins** (John Wiley & Sons, 2nd Edn. 2001).
3. Attuvod T.K. Smith D.J. **Introduction to Bioinformatics** (Addison Wesley Longman Ltd ,1999).
4. Taylor, H.D **Bioinformatics: sequence structure and data banks** (Oxford Univ. Press,2000).

309PBIT03: STRUCTURAL BIOINFORMATICS

Unit I:

Structural features of biomolecules – techniques used to determine the structure of biomolecules – geometrical parameters – potential energy surfaces – molecular graphics – hardware and software requirements – Internet – mathematical concepts, molecular file formats

Unit II:

Structure prediction – secondary structure – homology modeling, fold recognition and ab initio 3D structure prediction – structure comparison and alignment – prediction of function from structure.

Unit III:

Molecular dynamic using simple models – simulations with continuous potentials – advantage of constant temperature and pressure simulation – solvent effects – analysis of conformational changes during molecular dynamic simulation.

Unit IV:

Molecular docking – structure based drug design – de novo approach – molecular similarity – quantitative structure-activity relationship – 3D pharmacophore derivation and matching – importance of molecular modeling in drug discovery, Cheminformatics and its applications, Combinatorial libraries and Chemical diversity

Unit V:

Protein stability and folding-SCOP-DALI-assignment of protein structures to genomes-determining gene function through conserved protein structure-prediction of protein function-approaches to protein structural genomics

RECOMMENDED TEXTS:

1. Lesk, A.M. (2002). **“ Introduction to Bioinformatics”**, 1st Edition, Oxford University Press, Oxford, UK.

REFERENCE BOOKS:

1. Mount, D.W. (2001). **“ Bioinformatics – Sequence and Genome Analysis”**, 1st Edition, Cold Spring Harbor Laboratory Press, New York, USA.
2. Westhead, D.R., Parish, J.H. and Twyman, R.M. (2003). **Instant Notes Series – Bioinformatics**, 1st Edition, Viva Books Private Limited, New Delhi, India.
3. Ignacimuthu (s.j.), S. (2005). **Basic Bioinformatics**, 1st Edition, Narosa Publishing House, New Delhi, India.

309PBIT04: SYSTEMS BIOLOGY

Unit I: Introducing computational Systems biology

Basic concepts of System biology, Enabling information and integration for systems biology, Databases for Systems biology, Natural language processing and ontology-enhanced biomedical literature mining for Systems Biology.

Unit II: Foundations of biochemical network analysis and modeling

Introduction to computational models of biochemical reaction networks, Biological foundations of Signal transduction and the Systems biology perspective, Reconstruction of metabolic network from genome information and its structural and functional analysis, Metabolic Flux analysis, GEPASI, Gopher

Unit III: Computer simulations of dynamic networks

Discrete approach to network modeling, Gene networks: Estimation modeling and simulation, Computational models for circadian rhythms: Deterministic Versus Stochastic approaches.

Unit IV: Multiscale representation of cells and Emerging phenotypes

Spatio-temporal Systems biology, Cytomics-from Cell States to predictive medicine, The IUPS Physiome project, E-Cell Concept. Genesis tool and its applications

Unit V: Applications and perspectives of Systems biology

Developments and trends of Systems biology, Long and medium term goals of Systems biology, the potential applications of Systems biology, Microarray analysis and gene networks, BRB Array tool

REFERENCE BOOKS:

1. Computational Systems Biology. By Andres Kriete, Roland Eils. Published by Academic Press, 2005, ISBN 012088786X.
2. Systems Biology: Applications And Perspectives. By Peter Bringmann. Published by Springer, 2007, ISBN 3540313389.
3. Systems Biology: Principles, Methods, and Concepts. By Andrzej K. Konopka. Published by CRC Press, 2007, ISBN 0824725204.
4. Systems Biology: Definitions and Perspectives. By Lilia Alberghina, Hans V. Westerhoff, Published by Birkhäuser, 2005, ISBN 354022968X.

309PBIT05: POTENTIAL APPLICATIONS AND COMMERCIAL ASPECTS OF BIOINFORMATICS

Unit I

Visualization of sequence data: What a sequence reveals about the biological function of a gene

Unit II

Applications of bioinformatics in drug discovery

Unit III

Genetic basis of disease Role of genetics in future approaches to healthcare, Genetic medicine, human disease and genes

Unit IV

Pharmacogenomics, Personalized medicine and gene-based diagnostics: Definition of personalized medicine, Conventional medicine versus personalized medicine, Role of genetics in development of personalized medicines

Unit V

Introduction to ethical issues, Legal, ethical and commercial ramifications of bioinformatics Ethical and Regulatory Aspects of Personalized Medicine

309PBIP01: TOOLS AND THEIR APPLICATIONS IN BIOINFORMATICS (PRACTICALS)

Unit I:

Bibliographic search on the Internet – PubMed: The students should search PubMed (www.ncbi.nlm.nih.gov) and obtain information about a particular topic, which may be suggested by the teacher.

Browsing database – Each student should independently access at least one database described in http://nar.oxfordjournals.org/content/vol34/suppl_1/index.dtl and describe its contents.

Unit II:

Blast search – Each student is given a specific protein or DNA sequence, which is used in the search through the Blast web page (www.ncbi.nlm.nih.gov)
PsiBlast – Each student is given a specific protein or DNA sequence, which is used in the search through the PsiBlast web page (www.ncbi.nlm.nih.gov).

Unit III:

Global alignment using Needleman – Wunsch (NW) algorithm – student is given a pair of sequences to perform a global alignment using the NW algorithm.

Dot Plot – student creates a Dot Plot display of a pair of sequences
Multiple sequence alignment – Each student creates an alignment of a set of 6 to 10 sequences and displays the results appropriately

Restriction Site analyses – Given a DNA sequence and a particular restriction enzyme, the student identifies the cleavage sites. Comparative genomics using Vista.

Unit IV:

Phylogenetic tree construction (UPGMA) – Given a set of 6 to 10 protein or DNA sequences, the student uses UPGMA to construct a phylogenetic tree.

Phylogenetic tree construction (Neighbour Joining) – Given a set of 6 to 10 protein or DNA sequences, the student uses Neighbour Joining to construct a phylogenetic tree.

Unit V:

Sequence conversions – The student converts a DNA sequence into the complementary RNA and vice versa. The student translates the DNA Sequence in all six reading frames to the protein sequence and a protein sequence and a protein into the respective DNA sequence, choosing an appropriate codon usage table Gene discovery – Given a large DNA sequence (such as e.g. a small portion of an eukaryotic genome) the student predicts all possible genes.

Protein structure calculations – Given a small protein/peptide structure, the student calculates and tabulates bond lengths, bond angles, and torsion angles, and identifies hydrogen bonds, Molecular surface calculations.

Ramachandran plot – Given a protein structure, the students creates and displays its Ramchandran plot Structural superposition – Given a pair of similar protein structures the student performs a structural superposition and calculates the similarities/differences Chemical library search, molecular format conversion Molecular dynamics simulation using simple models and continuous potentials, Molecular docking and interaction analysis, QSAR, pharmacophore search.

RECOMMENDED TEXTS:

1. K.Mani and N.Vijayaraj (2004) "**Bioinformatics – A Practical Approach**" Aparnaa Publication, Coimbatore, India.
2. C.Gibas and P.Jambeck (2001) "**Developing Bioinformatics computer Skills**" Shroff Publishers and Distributors Pvt. Ltd., Mumbai, India.

REFERENCE BOOKS:

1. It is expected that a computer laboratory is available, with necessary software and data.
2. The manual corresponding to the software would serve as Reference Book.

FOURTH SEMESTER

409PBIT01: DATABASES IN MOLECULAR BIOLOGY

Unit I: Database concepts

Databases in general – definitions and examples – computerized databases – advantages and disadvantages – need for database models and systems – examples of logical models – hierarchical, network and relational models – RDBMS – objected oriented models – primary and secondary (derived) databases – structure and sequences databases – growth of databases, Gene Ontology classifications

Unit II: Molecular Biology data types

Brief descriptions of the various types of data used in modern Molecular Biology and how they are obtained, stored, represented and retrieved – organisms – genome maps – DNA, RNA and protein sequences – RNA secondary structure – protein secondary and tertiary structure – DNA and protein sequence motifs – protein and RNA structure motifs – RNA and protein-protein interaction data – mutations and polymorphisms in sequences and structures – tissues and cells – populations.

Unit III: Primary sequence databases

DNA sequence databases – GenBank, EMBL, DDBJ – details of structure of GenBank – differences with and links to other databases – protein sequence databases – Swissprot, PIR – details of arrangement of data in Swissport – differences and links to other databases – TrEMBL database

Unit IV: Derived sequence database

Subcollections of data – FlyBase – AceDB, WormBase – comprehensive microbial genome, Omniome – organelle genome database, GOBASE – eukaryotic promoter database – Codon usage table database – Exon-Intron database – examples of protein sequence subcollections – GPCR sequence database – human unidentified gene-encoded large protein sequence database, HUGE – CluSTr and COGS – databases of protein sequence patterns and motifs – PRINTS, PROSITE, Pfam, ProDom.

Unit V: Structural databases

Nature of structure data – coordinate systems – primary structure databases – PDB, CSD – details of arrangement of data in PDB with examples – access to PDB and CSD – derived structure databases – value-added subcollections, NDB – structural patterns and motifs – SCOP – CATH-FSSP-PALI-DSSP, Drug bank, ligand depot, Querying chemical databases

REFERENCE BOOKS:

Nucleic Acids Research (January 2008) Number 1. Database Issue. (This issue is available online for free and open access at the following url http://nar.oxfordjournals.org/content/vol34/suppl_1/index.dtl).

- N.Gautham (2006) '**Bioinformatics**' Narosa Publishing Company, New Delhi.
- V.R. Srinivas (2005) '**Bioinformatics: A Modern Approach**' Prentice-Hall of India Private Limited New Delhi, India.
- D.Mount (2000) '**Bioinformatics: Sequences and Genome Analysis**' Cold Spring Harbor Laboratory Press, Cold Spring Harbor, USA.
- D.Higgins and W.Taylor. (eds) (2000) '**Bioinformatics: Sequences, Structures and Databanks**' Oxford University Press, Oxford, UK.

409PBIT02: ADVANCED TOPICS IN BIOINFORMATICS

Unit I: Pharmacogenomics and Toxicogenomics

Definition of Pharmacogenomics & Toxicogenomics – case study in Alzheimer's diseases – safety metabolisms pharmacology – Exploitory Toxicology, Preclinical Toxicology, Pharmacokinetics & Metabolism

Unit II: Phylogenetic analysis and Comparative genomics

Relationship of phylogenetic analysis to sequence alignment, genome complexity and phylogenetic analysis – Maximum parsimony method, Distance methods. Reliability of phylogenetic predictions- Complications from phylogenetic analysis – Philip & Paup software's. DNA computers – Principle & working

Unit III: Nutrigenomics

Nutritional genetics – nutritional genomics-genetic nutrition-gene directed nutrition with reference to diabetes, cardiovascular diseases and obesity and neurogenomics-short notes on herbal informatics (medicinal foods)

Unit IV: Chemogenomics

Definition – Effect of chemicals on genes – delayed mutations – Interaction of molecules (small & Big) with DNA intercalation – case study with copper deficiency leading to diseases, Role of p53 – Oncogene changes

Unit V: Metagenomics and Molecular Evolutionary Pathways

Definition of metagenomics – application of genomics to cultured and uncultured microorganisms, metagenomics of microbial communities, clastistics – evolutionary relationships – evolution of nucleic acids, proteins and enzymes associated SNP's.

REFERENCE BOOKS:

1. Jacoby, E (2005) Chemogenomics- **Knowledge-based Approaches to Drug Discovery**, World Scientific.
2. Rothstein, MA ,(2003) **Pharmacogenomics**, Wiley-Liss.
3. Chakraborty, C ; Bhattacharya, A (2005) **Pharmacogenomics**, Biotech Publishers.
4. Rimbach,GH (2005), **Nutrigenomics**, CRC.
5. Hamadeh,HK:Afshari,CA (2004) Toxicogenomics : Principles and Applications Wiley-Liss.

ELECTIVE SUBJECT
409PBIT03: BIOINFORMATICS AND DRUG DESIGN

Unit I:

Introduction – Basics of combinatorial chemistry & natural product libraries – Chemical parameters in Drug design prod rugs & soft drugs – physico chemical parameters in Drug design – structure based drug design – Micro array and drug discovery.

Unit II:

Drug metabolism – Genome to drug discovery – Sequence analysis – Structure properties & computer identification of eukaryotic genes – analyzing regulatory regions in genomes.

Unit III:

Homology modeling – Molecular modeling using computers – CADD, protein-ligand docking in drug design – vaccine development through Bioinformatics, Lipinski's rule

Unit IV:

Target discovery – Target validation – Assay development – High through screening – Lead optimization – Drug substrate manufacture – Development of new drugs, subtractive genomics

Unit V:

Candidate drug nomination – clinical trial – Investigational new drug application – FDA, MDA, approval, patenting and formulations-Marketing.

REFERENCE BOOKS:

- Richard B. Silverman , **Organic chemistry of Drug Design & Drug action** Elsevier Science, Academic Press
- Wu-Pong Susanna, Rojanasakul, Youngest **Biopharmaceutical Drug Design and Development, Molecular modeling – Principles and Applications** ,Prentice Hall.
- R. Mannhold, H.Kubinyi, H.Timmerman, (Editors) **Bioinformatics – From Genomes to Drugs – Methods & Principles in medicinal chemistry Vol-14**
- H.Gerhard vogel, Wolfgang H **Drug Discovry & Evaluation. Pharmacological assays (with CD-ROM)**
- Eric M.Gordon ;James F.Kerwin (Editors)**Combinatorial chemistry & Molecular Diversity in drug discovery**

409PBIP01: PROJECT AND VIVA-VOCE

a. Topic

The topic of the Project shall be assigned to the candidate before the end of first year and a copy of the same should be submitted to the University for approval.

b. Advisory committee

Each guide shall have a maximum of five students in science and maximum of seven for all Arts subjects.

There will be an advisory committee consisting of the guide as chairman and one member from the same department or allied departments of the college and a third member should be from other college preferably from Aided / Government colleges in the case of self financing college and vice – versa.

c. No. of Copies

The students should prepare three copies of Project and submit the same for the evaluation by examiners. After evaluation one copy is to be retained in the college library and one copy is to be submitted to the University (Registrar) and one copy can be held by the student.

d. Format to be followed

The formats / certificate for Project to be submitted by the students are given below:

Format for the preparation of project work

- a. Title page
- b. Bonafide certificate
- c. Acknowledgement
- d. Table of content

Format of the certificate

CERTIFICATE

This to certify that the Project entitled.....

submitted in part fulfillment of the requirement of the degree of Master of Science / Master of Arts in To St. Peter's University, Distance Education, Chennai. is a record of bonafide research work carried out by under my supervision and guidance and that no part of the Project has been submitted for the award of any degree, diploma, fellowship or other similar titles or prizes and that the work has not been published in part or full in any scientific or popular journals or magazines.

Date:

Place:

Chairman, Advisory Committee,

Approved by

Chairman:

Members:

1.

2.

External Examiner

Guidelines for approval of PG guides for guiding students in their research for submitting Project.

1. M.Sc. (Part fulfillment) Guide

The person seeking for recognition as guide should have.

- i. M.Sc degree with first class / second class
- ii. Should have 3 years of active teaching / research experience.

2. They should have published atleast one research paper in a National journal authored solely or jointly. Procedure for submitting application for approval as guides

- a. The University will on request give prescribed application form.
- b. The filled in applications should be submitted before the close of said date by the University.
- c. such applications should be routed through the Principal of their respective institutions with specific recommendations.
- e. All relevant proofs should be submitted along with the applications.

3. Approval

The committee constituted for the purpose will scrutinize the applications and recommend for approval / rejection.

Orders will then be passed by the authority of the university and communicated to each member individually through the Principal.