POST GRADUATE DIPLOMA IN BIOINFORMATICS (PGDBI)

SEM	COURSE CODE	COURSE	COURSE TITLE	HRS/ WEEK	CREDIT	CIA MARKS	SE MARKS	TOTAL MARKS
I	14PDBI1C1	CORE I	Fundamental of Bioinformatics	6	4	40	60	100
	14PDBI1C2	CORE II	Statistics for Bioinformatics	6	4	40	60	100
	14PDBI1C3	CORE III	Basic Structural Biology	6	4	40	60	100
	14PDBI1C4	CORE IV	Object Oriented Programming and Web Publishing	6	4	40	60	100
	14PDBI1C5P	COREV	C ++ Programming and Web Publishing - Practical	6	4	40	60	100
TOTAL				**30**	**20**	**200**	**300**	**500**
II	14PDBI2C6	CORE VI	Database Management Systems	6	4	40	60	100
	14PDBI2C7	CORE VII	Genomics and Proteomics	6	4	40	60	100
	14PDBI2C8	CORE VIII	Computational Biology	6	4	40	60	100
	14PDBI2C9	COREIX	Molecular Modeling and Drug Design	6	4	40	60	100
	14PDBI2C10P	CORE X	Bioinformatics - Practical	6	4	40	60	100
TOTAL				**30**	**20**	**200**	**300**	**500**
GRAND TOTAL				**60**	**40**	**400**	**600**	**1000**

SEMESTER I: CORE - I
FUNDAMENTAL OF BIOINFORMATICS

Course Code:14PDBI1C1 **Max. Marks : 100**
Hours / Week: 6 **Internal Marks : 40**
Credit: 4 **xternal Mark: 60**

Objectives:

Introduce the basics, models and applications of different biological sequence describe the database designing concepts and the languages used Describe the widely used relational database model and biological sequence databases.

UNIT I : **18 hours**

Bioinformatics – an Overview, Definition and History.Information Networks –Internet in Bioinformatics, #EMBnet – Commercial Databases and Software's#, Intranet and Internet Packages#.

UNIT II : **18 hours**

Languages – Basics of Programming, Perl – Basics, String handling, subroutines.HTML – Basics, Tags, Text handling, Image handling, Links, Frames and Tables.#XML – Basics, data binding and record sets#.

UNIT III: **18 hours**

Protein Information Resources – Biological Databases, Primary Sequence Databases, Composite Protein Sequence Databases, - #Secondary Databases – Prosite, Prints, Blocks Profiles and Identity#.

UNIT IV: **18 hours**

Genome Information Resources – DNA sequence Databases – EMBL DDBJ, Genbank GSDB (Genome, Sequence Database), #UniGene-Comprehensive microbial Resource#.

UNIT V: **18 hours**

Evolution of Bioinformatics – Scope – Potentials of Bioinformatics, Human Genome Project – #Bioinformatics in India – Future of Bioinformatics#.

Self-study portion

Text Books:

1. T.K. Attwood and D.J. Parry-Smith, Introduction to Bioinformatics, PearsonEducation Ltd., New Delhi, 2004.

2. Arthur M. Lesk, Introduction to Bioinformatics, Oxford University Press, NewDelhi, 2003.

3. D. Higgins and W. Taylor (Eds), Bioinformatics- Sequence, structure and databanks, Oxford University Press, New Delhi ,2000.

Unit I Chapter I Sections 1, 8-11. **T.B - 1**

Unit II Chapter IISections 6-9.T.**B- 2**

Unit III Chapter I Sections 1.2, 1.1, 3.2.**T.B- 3**

Unit IV Chapter VIII Sections 180-191. **T.B-3**

Unit V Chapter I Sections 1-23. **T.B-2**

Books for References:

1. S. R. Swindle, R.R.Miller and G.S.A.Myers (Eds.), Internet for the MolecularBiologist, Horizon Scientific Press, Wymondham, UK, 1996.

2. S.C. RastogiNamitaMendirattaParagRastogi. (Bioinformatics Concepts, Skills & Applications, 2003.

SEMESTER I: CORE - II
STATISTICS FOR BIOINFORMATICS

Course Code:14PDBI1C2Max Marks: 100
Hours/Week: 6Internal Mark: 40
Credit: 4 External Mark : 60

OBJECTIVES:

To gain knowledge in measures of central tendency and dispersion to appropriately choose, define and/or derive probability distributions such as the binomial, poison and normal distribution to solve engineering problems.

UNIT I : 18 hours

Measures of central Tendency – Arithmetic Mean – Median – Mode – Quartiles –Range – #Quartile deviation – #Mean deviation – Standard Deviation#.

UNIT II : 18 hours

Probability – Addition Theorem – Multiplication Theorem - #Baye's Theorem and related problems#.

UNIT III : 18 hours

Theoretical Distributions – Binomial, Poisson and Normal – #fitting of the Distributions and its properties - Z-score, P-value and E-value#.

UNIT IV : 18 hours

Theory of Attributes – Introduction – Dichotomy – Consistency of Data –Independence of Attributes – Association of Attributes – #Rules coefficient of Association#.

UNIT V : 18 hours

Sampling Distributors – Large and small sample tests – Student's t^2 test, X^2 test, F-test – and #Normal test and their applications#.

 # # Self-study portion

Text Book:

1. S.C. Gupta and V.K. Kapoor, Fundamentals of Mathematical Statistics, 11th Edition, Sultan Chand & Sons, New Delhi, 2002.
2. Glover & Mitchell. (An Introduction to Biostatistics), 2002.

Unit I Chapters VI Sections 77-80. **T.B-1**

Unit II ChaptersIIISections 58-76**. T.B-1**

Unit III Chapters I Sections 1.2, 1.1, 3.2. **T.B-1**

Unit IV Chapters IV Sections 35-42.**T.B-2**

Unit V Chapters I Sections 222-224. **T.B-2**

Books for Reference:

1. S.P.Gupta, Statistical Methods, Sultan Chand & Sons, 1996.
2. L. Frothier, Introduction to Biostatistics, Academic Press, 1995.
3. Robert R. Sokal and F.J. Rohlf, Introduction to Biostatistics (Biology- Statistics Series), W.H. Freeman & Company, New York, 1987.

SEMESTER I: CORE - III
BASIC STRUCTURAL BIOLOGY

Course code:14PDBI1C3 **Max Marks :100**
Hours/Week : 6 **Internal Marks :40**
Credit : 4 **External Marks :60**

Objective:

To study cell structure and functions of organelle functions and understand the mechanism of cellular transport within and outside the cell membrane.

UNIT I : **18 hours**

Cell Structure and Ultra cell structure of Pro and Eukaryotic cells – Cell wall – cell membrane – Biomembranes – Organelles. – Diffusion – #Active and Passive Transport – #Osmoregulation#

UNIT II : **18 hours**

Carbohydrates – Classification Types – Structure – Function.Lipids – #Classification Types – Structure – Function#.

UNIT III : **18 hours**

Introduction and Physiochemical Properties of Nucleic Acids – DNA and RNA.Watson and Crick Model of DNA and the different forms of DNA.RNA structure – #Principles and Prediction.Gene Structure#.

UNIT IV : **18 hours**

Classification of amino Acids.Classification and three-Dimensional structure of proteins. Overview of protein structure – Primary, Secondary, Tertiary and Quaternary structures – J helix, #K Pleated sheet, #Ramachandran plot and bonds stabilizing protein structure#.

UNIT V : **18 hours**

Principles of Structural Organization and Conformational Analysis.Prediction of Protein structure – Fold Recognition (threading), Comparative Modeling (homology), #The Chou and Fasmanmethod.#Basic Principles of X-ray Diffraction Studies, NMR, Mass Spectroscopy in Identifying Protein Conformation#.

 # # Self-study portion

Text Books:

1. Principles of Physical Biochemistry – Van Holde, Prentice Hall.
2. Basic one & two dimensional NMR spectroscopy, Horst FriebolinWitey –VCH – 1990.
3. J. David Rawn Town State University (biochemistry). 2004.
Unit I Chapters I Sections 3-27.**T.B-1**
Unit II Chapters III Sections149-209.**T.B-1**
Unit III Chapters V Sections 665-975.**T.B-1**
Unit IV Chapters IV Sections 265-359. **T.B-2**
Unit V Chapters V Sections 101-109. **T.B-3**

Books for References:

3. Lechninger Principles of Biochemistry – David L.Nelson, MichaelM.cox.3rd Edition Macmillan worth Publishers.1990.
4. Principles of Protein structure, G.E.Shultz and R.H.Schirmer, Springer –verlag, New York.2004.

SEMESTER I:CORE- IV
OBJECT ORIENTED PROGRAMMING AND WEB PUBLISHING

Course Code:14PDBI1C4 **Max Marks: 100**
Hours / Week: 6 **Internal Mark: 40**
Credit: 4 **External Mark : 60**

Objectives:

Understand the program development life cycle Design algorithms to solve simple problems using computers Convert algorithms into HTML and C++ programs and execute.

UNIT I : **18 hours**

Object Oriented Programming with C++: Introduction to the basic concepts of C++ language – Tokens, Keywords, Identifiers, Data types, Variables, Manipulators – Expression and Control structures. #Functions: Main function – function prototyping – call by reference – function overloading – friend and inline functions.

UNIT II : **18 hours**

Classes and objects – Constructors and Destructors – Operator overloading – #Type conversions.

UNIT III : **18 hours**

Inheritance – Single inheritance – #multiple inheritance – Hierarchical, Hybrid inheritance – Polymorphism – Pointers – #Console I/O operations.

UNIT IV : **18 hours**

Files – classes for file stream operations – Opening, closing and processing files –End of file detection – File pointers – #Error handling during file operations – #Command line arguments – Exception handling.

UNIT V : **18 hours**

Web Publishing**:** Internet – WWW – Browser – Designing web site – Basics of creating a web page with HTML – Linking – Text formatting – #Adding Images and background to HTML pages – Tables – Image maps.

 # # Self-study portion

Text Books:

1. For Units 1 to 4 "Object Oriented Programming with C++" – EBalagurusamy – TMH.
2. For Unit 5 : "Web Publishing" – Monica D'Souza & Jude D'Souza – TMH– 2001.

Unit I Chapters I Sections 3-27.**T.B-1**
Unit II Chapters III Sections149-209.**T.B-1**
Unit III Chapters V Sections 265-275.**T.B-1**
Unit IV Chapters IV Sections 65-78. **T.B-2**
Unit V Chapters V Sections 101-109. **T.B-2**

Reference Books:

1. Object Oriented Programming in C++ - Robert Lafore, Galgotia
2. let us C++ - YeshwantKanetkar – BPB.
3. Instant HTML Programmer's Reference – Steve Wright – WROX Press Ltd.

SEMESTER I: CORE - V
C++ PROGRAMMING AND WEB PUBLISHING - PRACTICAL

Course Code:14PDBI 1C5P **Max. Marks: 100**
Hours / Week: 6 **Internal Marks: 40**
Credit: 4 **External Marks : 60**

Objectives

Understand the program development life cycle Design algorithms to solve simple problems using computers Convert algorithms into HTML and C++ programs and execute.Application of the programs in HTML and C++ using algorithms to solve and web design.

1. Factorial of a given number.
2. Sorting and merging two arrays of numbers.
3. Sorting names in alphabetical order.
4. Reversing a given string.
5. Checking for palindrome.
6. String Manipulation – String copy, String length, String concatenation, String comparison and String reverse.
7. Mean, median, mode and standard deviation calculations.
8. Storing and retrieving amino acid sequences using structure data types.
9. Swapping two values using pointers.
10. File Processing – Creation and simple processing.
11. Computing amino acid composition of a given protein sequence.
12. Enumerate RNA Secondary Structure.

***Web Publishing*:**

1. Create a web page for your University / College using HTML. The opening page should provide hyperlinks to other pages (add animation and sound effects appropriately).

2. Creating a web page to get protein sequence data and compute and display amino acid composition.

3. Creating a web page to get nucleic acid sequence data and compute and display base composition.

Text Books:

1. E.Balagurusamy(Third Edition 2006). Object Oriented Programming C++.
2. A. Jitender). Introduction to HTML."Web Publishing" – Monica D'Souza & Jude D'Souza – TMH– 2001. Third Edition (2008).

Practical

Practical 1 to 12:**T.B-1**
Practical 1 to 3:**T.B-2**

Books for References

1. Gary J.Bronson (A First Book of ANSI C Third Edition 2001).
2. Adapted by Jitender Kumar Chakra, Programming with C and C++. (Scond Edition 2006).
3. let us C++ - Yes want Kantar – BPB.
4. 3. Instant HTML Programmer's Reference – Steve Wright – WROX Press Ltd.

SEMESTER II:CORE - VI
DATABASE MANAGEMENT SYSTEMS

Course Code:14PDBI 2C6 **Max. Marks: 100**
Hours / Week: 6 **Internal Marks: 40**
Credit: 4 **External Marks : 60**

Objectives:

Introduce the basics, models and applications of different DBMS. Describe the database designing concepts and the languages used.

UNIT I : **18 hours**

Data base: Introduction – Basic Technology and Data Basics – #Objective of a Data base organization – Entities & Attributes.

UNIT II : **18 hours**

Data Models: Introduction – Schemes & Sub Schemes – Data base Management Systems – Tree Structures – Plex Structures – #Relational Databases – Normal Forms.

UNIT III : **18 hours**

Data Base Languages: Introduction – Data Description Languages – the CODASYL Data Description Language – #Query Languages – Data Dictionaries.

UNIT IV : **18 hours**

Physical Organization: Introduction – Criteria affecting physical organization –Differences between physical & logical organization – #Addressing Techniques –Index sequential organization – Hashing.

UNIT V : **18 hours**

Pointers – Chains & Ring Structures: Introduction – Physical representation of tree structures – #Physical representation of plex structures – Virtual & Storage hierarchies.

Self-study portion

Text Book:

1. James Martin, Computer Database Organization, Prentice Hall of India.
2. Ramon A Mata- Toledo I Pauline K Cushman. DebabrataSahoo (Database Management Systems). (2007).

Unit I Chapters I Sections 1.1-1.25.**T.B-1**

Unit II Chapters II Sections 2.1-2.61.**T.B-1**

Unit III Chapters IV Sections 4.1-4.44.**T.B-1**

Unit IV Chapters V Sections 5.1-5.24.**T.B-2**

Unit V Chapters XVI Sections16.1-16.8.**T.B-2**

Books for Reference:

1. James Martin, Principles of Database Management, Prentice Hall of India
2. C.J.Date, an Introduction to Database systems, 3rd edition, NarosaPublishing House.

SEMESTER II: CORE - VII
GENOMICS AND PROTEOMICS

Course Code:14PDBI 2C7 **Max. Marks: 100**
Hours / Week: 6 **Internal Marks: 40**
Credit: 4 **External Marks : 60**

Objective:

This paper deals with genome map, comparative genomics and structural genomics, functional genomics and regulation. The other part of the paper deals with protein structure prediction and functions and also various tools for analysis of proteins.

UNIT I : **18 hours**

The genetic material – Identification of genetic material, genetic code, concept of gene – operon concept – lac and trp operons, #promoters and repressors.

UNIT II : **18 hours**

Genomics – definitions – pharmacogenomics – taxicogenomics – #prokaryotic and eukaryotic genome – genome relationships – human genomics.

UNIT III : **18 hours**

Genomics methodologies: Whole genome analysis – Physical methods of sequencing – automated sequencing – genome expression and analysis – serial analysis – #oligo NT array technology – #code micro assay and microchips.

UNIT IV : **18 hours**

Proteomics: Definition – Transcriptomics; Proteomics, metabolomics. Techniques of proteomics – 2D PAGE, Multidimensional protein identification (Mud PIT) Isotopically coded affinity Tag (ICAT), Mass spectrophotometer – (MALDI – TOF) MS. #Application of functional genomics in basic biology, target / marker identification, target valediction / toxicology, microbial drug resistance, tumour immunology, vaccine discovery, drug design.

UNIT V : **18 hours**

A brief account of genetic engineering –Vectors used in genetic engineering-Genomic DNA library-Cloning and modification methods-#Site Directed mutagenesis-Commercial applications

 # # Self-study portion

Text Books:

1. Baxevanis AD and B.F.F. Ouellette, Wiley Bioinformatics – A practical guide to the analysis of genes and proteins. (ed) – Interscience, New York, 2001.
2. S.R Pennington M.J Dunn (proteomics from protein sequence to function) .(2002)
3. T.A.Brown (Genomes). (2006).

Unit I Chapters I Sections 3-12.**T.B-1**
Unit II Chapters IV Sections 103-109.**T.B-2**
Unit III Chapters VIII Sections 197-206.**T.B-2**
Unit IV Chapters X Sections 207-220.**T.B-2**
Unit V Chapters VII Sections 151-166.**T.B-3**

Books for References:

3. Faber K (1992) Biotransformation in Organic Chemistry, Springer Verlag.
4. GerbardtP.Murray RG, Wood WA, Kreig NR (1994) Methods for General and Molecular Bacteriology – American Society for Microbiology Washington D.C.

SEMESTER II:CORE - VIII
COMPUTATIONAL BIOLOGY

Course Code:14PDBI 2C8 **Max. Marks: 100**
Hours / Week: 6 **Internal Marks: 40**
Credit: 4 **External Marks : 60**

Objectives

To acquire information from biological databases.Use of computational approaches to analyze this information. To interpret the results as a guide to experiments in Biology

UNIT I **18 hours**

Structure of DNA & Protein – Sequence analysis – pair wise sequence comparison – sequence queries against biological databases – BLAST and FASTA – #multifunctional tools for analysis.

UNIT II **18 hours**

Multiple sequence alignments, Phylogenetic alignment – profiles and motifs – distance and similarity – #evolutionary basis of sequence alignment – scores and gaps.

UNIT III **18 hours**

Protein structure visualization – tools structure – classification, alignment and analysis.Solvent accessibility and Interactions – Physico chemical properties, structure optimization.#Protein resource databases.

UNIT IV **18 hours**

Predicting Protein structure and function from sequence – Determination of structure – feature detection – secondary structure prediction – Predicting 3 D structure. #Protein modeling.

UNIT V **18 hours**

Genomics and Proteomics – Sequencing genomes – sequence assembly – genome on the web – annotating and analyzing genome sequences. #Proteomics – biochemical pathway databases – submitting sequence to the databases.

Self-study portion

Text Books:

1. Bioinformatics: A practical guide to the analysis of genes and proteins –2001 – AD Baxevanis& BFF Ouellette – Wiley Interscience – New York.
2. B Thiagarajan PA Rajalakshmi (Computational Biology). (2009)
Unit I Chapters I Sections 4.1.**T.B-1**
Unit II Chapters II Sections 2.1-2.2.**T.B-1**
Unit III Chapters III Sections 2.3-2.21.**T.B-1**
Unit IV Chapters V Sections 5.1-5.6.**T.B-2**
Unit V Chapters VII Sections 151-166.**T.B-2**

Books for References:

3. Bioinformatics: Sequence, structure and databanks – 2000 – Des Higgins & Willie Taylor – Oxford University Press.

SEMESTER II: CORE - IX
MOLECULAR MODELING AND DRUG DESIGN

Course Code:14PDBI 2C9 Max. Marks: 100
Hours / Week: 6Internal Marks: 40
Credit: 4External Marks: 60

Objective:

It deals with molecular modeling, quantum mechanics, and molecular mechanics. Pertaining to drug discovery. Provide a broad and thorough background in modeling tools and docking programs.

UNIT I **18 hours**

Recent advances in drug design methodologies, Biomolecular structure, Structure activity relationship, #Pharmacokinetics, #structure-based drug design.

UNIT II **18 hours**

Pharmacophoric pattern, ADME Properties, quantitative structure activity relationship, #Use of genetic algorithms and principle component analysis in the QSAR equations.

UNIT III **18 hours**

Molecular modeling, quantum mechanical and molecular orbital methods, introduction to semi-empirical, molecular mechanics and abintiotechniques.#Simulation techniques, potential energy surfaces, docking and modeling substrate – receptor interactions.

UNIT IV **18 hours**

Software tools for modeling bio-molecules. #Molecular electrostatic potentials, charge analyses.Protein conformations, folding and mutation through modeling.

UNIT V **18 hours**

Use of Genomics and Proteomics for understanding diseases at molecular level strategies for target identification and #lead design.

 # # Self-study portion

Text Books:

1. Andrew Leach, Molecular Modeling: Principles and Applications (2nd Edition), Addison Wesley Longman, Essex, England, 1996.
2. Alan Hinchliffe, Molecular Modeling for Beginners, John-Wiley, 2003.

Unit I Chapters XI Sections 12.1.**T.B-1**

Unit II Chapters X Sections 10.1-10.9.**T.B-2**

Unit III Chapters VIII Sections 8.1-8.9.**T.B-2**

Unit IV Chapters VII Sections 7.1-79.**T.B.1**

Unit V Chapters I Sections 1.1-1.10.**T.B-1**

Books for References:

3. N. Cohen (Ed.), Guide Book on Molecular Modeling in Drug Design, Academic Press, San Diego, 1996.

SEMESTER II: CORE - X
BIOINFORMATICS – PRACTICAL

Course Code:14PDBI 2C10PMax.Marks: 100
Hours / Week: 6Internal Marks: 40
Credit: 4External Marks : 60

Objective:

Information from biological databases. Use of computational approaches to analyze the information. Interpret the results as a guide to experiments in biology.

1. Multiple alignments- using CLUSTAL W
2. Phylogenetic Analysis using NJ plot.
3. BLAST, FASTA programs for sequence database search.
4. Small molecule building using che1nDraw or chem. Sketch.
5. Evaluation of protein structure by Swiss PDB viewer and by other molecular visualization tools.
6. Calculation of phi – psi angles - Ramachandran plot.
7. Homology modeling of a given protein sequence.
8. Comparative genomic analysis.
9. Metabolic pathway prediction
10. Docking Using Patch Dock.

Text Books:

1. Andreas D.BaxevanisB.F.Francis Ouellette (Third Edition 2006). Bioinformatics. A Practical Guide to the Analysis of Genes and Proteins.
2. 4. A. Baxevanis and B.F. Ouellette. Bioinformatics: A practical Guide to the Analysis of Genes and Proteins, Wiley-Inter science, Hoboken, NJ (1998).

Practical:

1. Practical: 1 to 10. **T.B-1**

Books for References

1. S.C. RastogiNamitaMendirattaParagRastogi (First Edition 2003). Bioinformatics Concepts, Skills & Applications.
2. Teresa K.Attwood& David J. Parry Smith (1999). Introduction to bioinformatics.
3. Arthur M.Lesk (Internal Student Edition Second Edition (2005). Introduction to Bioinformatics.

****