

Syllabus

Post Graduate Diploma in Bioinformatics (PGDBI)

2017-18



Since 1951

PG & Research Department of Biotechnology
JAMAL MOHAMED COLLEGE (Autonomous)

College with Potential for Excellence
Reaccredited (3rd Cycle) with 'A' Grade by NAAC
(Affiliated to Bharathidasan University)

Tiruchirappalli – 620 020.

Post Graduate Diploma in Bioinformatics (P.G.D.B.I)

PG Diploma Course Pattern from 2017 -2018 (Course Duration: I Year)

Sem	Course Code	Course	Course Title	Hours/ Week	Credit	CIA Mark	SE Marks	Total Marks
I	17PDBI1C1	Core - I	Fundamental of Bioinformatics	6	4	25	75	100
	17PDBI1C2	Core –II	Statistics for Bioinformatics	6	4	25	75	100
	17PDBI1C3	Core –III	Basic Structural Biology	6	4	25	75	100
	17PDBI1C4	Core –IV	Computer Programming	6	4	25	75	100
	17PDBI1C5/P	Core –V	C Programming and Web Publishing - Practical	6	4	25	75	100
	TOTAL				30	20	125	375
II	17PDBI2C1	Core –VI	Database Management Systems	6	4	25	75	100
	17PDBI2C2	Core –VII	Genomics and Proteomics	6	4	25	75	100
	17PDBI2C3	Core – VIII	Computational Biology	6	4	25	75	100
	17PDBI2C4	Core - IX	Molecular Modeling and Drug Design	6	4	25	75	100
	17PDBI2C5/P	Core – X	Bioinformatics - Practical	6	4	25	75	100
	TOTAL				30	20	125	375
GRAND TOTAL				60	40	250	750	1000

**SEMESTER I: CORE - I
FUNDAMENTAL OF BIOINFORMATICS**

Subject Code:17PDBI1C1
Hrs / Week: 6
Credit: 4

Max Marks: 100
Internal Marks: 25
External Marks : 75

***Objective:** To offer basic understanding of Bioinformatics and its applications to molecular biology, clinical medicine and other disciplines.*

18 Hours

Unit I:

Bioinformatics – an Overview, Definition – Scope and History of Bioinformatics Networks – Internet in Bioinformatics, #EMBNET – Commercial Databases and Software's, # Intranet and Internet Packages. Role of Bioinformatics.

18 Hours

Unit II

Languages – Basics of C Programming, Array, Structure and Function. Perl – Basics, String handling. HTML – Basics, Text handling, Image handling, Links and Tables. #XML – Basics, data binding and record sets#.

18 Hours

Unit III

Introduction to Biological database – Protein Information Resources – Biological Databases, Primary Sequence Databases, Protein Sequence Databases, and Nucleotide Sequence Database - #Secondary Databases, Metabolic pathway databases#.

18Hours

Unit IV

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

18 Hours

Unit V

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

Self-study portion

Text Books :

1. Attwood T.K and D.J. Parry-Smith, Introduction to Bioinformatics, Pearson Education Ltd., New Delhi (2004).
2. Arthur M. Lesk, Introduction to Bioinformatics, Oxford University Press, New Delhi (2003).

Unit I Chapter I Section 1, 8-11. T.B - 1

Unit II Chapter II Section 6- 9. T.B - 2

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

Unit IV Chapter VIII Section 180-191 T.B -3

Unit V Chapter V Section 1-23. T.B - 2

Books for References:

1. Swindell, S.R., R.R. Miller and G.S.A. Myers (Eds.), Internet for the Molecular Biologist, Horizon Scientific Press, Wymondham, UK, (1996).
2. Andrea Cabibbo, Richard Grant and Manuela Helmer-Citterich (Eds.), The Internet for Cell and Molecular Biologists (2nd Edn.), Horizon scientific Press, Norwich, UK (2004).

**SEMESTER I: CORE II
STATISTICS FOR BIOINFORMATICS**

Subject Code:17PDBI1C2
Hrs / Week: 6
Credit: 4

Max Marks: 100
Internal Marks: 25
External Marks : 75

Objective

To improve their ability to analyze the statistical data to optimize.

18 Hours

Unit I

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

18 Hours

Unit II

Probability – Frequency Theory of Probability – Limitations – View of Probability – Addition
Theorem – Multiplication Theorem - #Baye's Theorem and related problems#.

18 Hours

Unit III

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

18 Hours

Unit IV

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

18Hours

Unit V

Sampling Distributors – Large and small sample tests – Theories of probability, Student's t^2 test,
 X^2 test, F-test – and chi square test for goodness of fit #. Normal test and their applications#.

Self-study portion

Text Books:

1. Gupta S.C and V.K. Kapoor, Fundamentals of Mathematical Statistics, 11th Edition, Sultan Chand & Sons, New Delhi, 2002.
2. Pillai R.S.N and V. Bagavathi and S. Chand Statistics (1984).

Unit I Chapters 9 Sections 121 - 129. **T.B-1**

Unit II Chapters 18 Sections 686-695. **T.B-1**

Unit III Chapters 19 Sections 735 - 748 **T.B-1**

Unit IV Chapters 5 Sections 35-42. **T.B-2**

Unit V Chapters 1 Sections 222-224. **T.B-2**

Books for Reference:

1. Gupta, S.P., Statistical Methods, Sultan Chand & Sons, 1996.
2. Forthofer, L., 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**

Subject Code:17PDBI1C3
Hrs / Week: 6
Credit: 4

Max Marks: 100
Internal Marks: 25
External Marks : 75

Objective:

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

18 Hours

Unit I

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

18 Hours

Unit II

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

18 Hours

Unit III

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#.

18 Hours

Unit IV

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

18 Hours

Unit V

Principles of Structural Organization and Conformational Analysis. Prediction of protein structure - Modeling homology, Chou and Fasman method. #Basic Principles of X-ray Diffraction Studies, NMR, Mass Spectroscopy in Identifying Protein Conformation#.

Self-study portion

Text Books:

1. Van Holde., Principles of Physical Biochemistry –Prentice Hall. 2006
2. Horst Friebolin Witey., Basic one & two dimensional NMR sepectroscopy–VCH – 1990.

Unit I Chapters I Sections 3-27. **T.B-1**

Unit II Chapters III Sections 149-209. **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:

1. Lechninger., David L.Nelson, Michael M. Cox., Principles of Biochemistry –3rd Edition Macmillan worth Publishers. (2000)
2. Principles of Protein structure, G.E.Shultz and R.H.Schirmer, Springer –verlag, New York. (2002)

**SEMESTER I: CORE IV
COMPUTER PROGRAMMING**

Subject Code:17PDBI1C4
Hrs / Week: 6
Credit: 4

Max Marks: 100
Internal Marks: 25
External Marks : 75

Objective

This subject presents the fundamentals of programming techniques namely sequence of execution and selection of blocks to be executed, repetition of execution, etc with the help of c programming language.

18 Hours

Unit I

Block diagram of computer (input and output devices) generation – advantages and limitations of computers – Basics of operating systems DOS, Windows NT and XP, UNIX – #Application software's#.

18 Hours

Unit II

Introduction to internet, service on internet – internet tools, HTML, text formatting –Adding images – Tables – Frames to web pages. Web services – WWW, URL, DNS – Servers, WEB servers, Browsers, IP Addressing, Communication Technology – Networking: LAN, #WAN and MAN, wireless communication#.

18 Hours

Unit III

Identifiers and keywords – Constants, Variables and data types – #Operations and Expression – Data input and output#.

18 Hours

Unit IV

Control structure – If and Switch statement – While, Do – While and for statements – Goto statement, #Arrays - 1 D array -2 D array#.

18 Hours

Unit V

Web Publishing Internet – WWW – Designing web site – Basics of creating a web page with HTML – Linking – Text formatting – #Adding Images and background to HTML pages – Tables – Image maps#.Function – User defined functions – Defining and assessing functions – Passing arguments - Functions prototypes – character strings – string functions – recursion – storage classes – structure – union.

Self-study portion

Text Books:

1. Balagurusamy E., Object Oriented Programming with C++” — TMH-2000.
2. Monica D’Souza & Jude D’Souza “Web Publishing” — TMH– 2001.

Unit I Chapters III Sections 1-37.T.B-1

Unit II Chapters II Sections49-210.T.B-1

Unit III Chapters IV Sections 65-175.T.B-1

Unit IV Chapters VI Sections 2-59. T.B-2

Unit V Chapters VII Sections 11-109. T.B-3

Books for Reference:

1. Robert Lafore., Object Oriented Programming in C++ - Galgotia.2000.
2. Yeshwant Kanetkar., let us C++ — BPB. 2001
3. Steve Wright., Instant HTML Programmer’s Reference — WROX Press Ltd.2011

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

Subject Code:17 PDBI 1C5/P
Hrs / Week: 6
Credit: 4

Max Marks: 100
Internal Marks: 25
External Marks : 75

Objectives

This paper includes analyzed some of the basic programs in C++ and Web based applications.

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. Balagurusamy E., Object Oriented Programming C++. (Third Edition 2006).
2. Jitender A., 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. Jitender Kumar Chakra, Programming with C and C++. (Second Edition 2006).
3. Yes want Kantar., let us C++ – BPB. (2000)
4. Steve Wright ., Instant HTML Programmer’s Reference — WROX Press Ltd. 2011.

**SEMSTER II: CORE VI
DATABASE MANAGEMENT SYSTEMS**

Subject Code:17PDBI 2C1

Hrs / Week: 6

Credit: 4

Max Marks: 100

Internal Marks: 25

External Marks : 75

Objective

This course is to make students learn about concepts of databases, database management data warehousing and security.

18 Hours

Unit I

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

18 Hours

Unit II

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

18 Hours

Unit III

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

18 Hours

Unit IV

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

18 Hours

Unit V

Database security: Data Classification– Database access Control – Types of Privileges – Cryptography- Statistical Databases.- Distributed Databases- Processing. #Object Oriented Databases-XML Databases #.

Self-study portion

Text Book:

1. James Martin, Computer Database Organization, Prentice Hall of India. (2016)

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 Sections 16.1-16.8. **T.B-2**

Books for Reference:

1. James Martin, Principles of Database Management, Prentice Hall of India. 2012
2. Date C.J., An Introduction to Database systems, 3rd edition, Narosa Publishing House. 2004

**SEMSTER II: CORE VII
GENOMICS AND PROTEOMICS**

Subject Code:17PDBI 2C2

Hrs / Week: 6

Credit: 4

Max Marks: 100

Internal Marks: 25

External Marks : 75

Objective

This paper deals with genome map, comparative genomics and structural genomics, functional genomics and regulation.

18 Hours

Unit I

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

18 Hours

Unit II

Different types of genome maps and their uses, genetic and physical mapping techniques – Genomics – definitions – pharmacogenomics – taxicogenomics – #prokaryotic and eukaryotic genome – genome relationships – human genomics.

18 Hours

Unit III

Genomics Whole genome analysis – Physical methods of sequencing – automated sequencing – genome expression and analysis – serial analysis. #code micro assay and microchips.

8 Hours

Unit IV

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 toxicology, microbial drug ,tumour immunology, vaccine discovery, drug design.

18 Hours

Unit V

Proteome and technology – Primary attributes for protein identification – protein super families. 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. Doolittle RF Molecular evolution. Computer Analysis of Protein and Nucleic acid Sequences, Methods in Enzymology, Academic Press, New York. (1990).

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:

1. Faber K., Biotransformation in Organic Chemistry, Springer Verlag. 1992.
2. Gerbardt P. Murray RG, Wood WA, Kreig NR., Methods for General and Molecular Bacteriology – American Society for Microbiology Washington D.C., 1994.

**SEMSTER II: CORE VIII
COMPUTATIONAL BIOLOGY**

Subject Code:17PDBI 2C3

Hrs / Week: 6

Credit: 4

Max Marks: 100

Internal Marks: 25

External Marks : 75

Objective

The objective of this course is to make students learn about concepts of modeling of biological processes and their representation

18 Hours

Unit I

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

18 Hours

Unit II

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

18 Hours

Unit III

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

18 Hours

Unit IV

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

18 Hours

Unit V

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. Baxevanis AD., BFF Ouellette Bioinformatics: A practical guide to the analysis of genes and proteins– Wiley Interscience – New York. 2001
2. Stephen Misener & Stephen A. Krawetz, Bioinformatics: Methods and Protocols Humana Press, New Jersey. 2000.

Unit I Chapters III Sections 3-21.**T.B-1**

Unit II Chapters III Sections 20.3-4.21.**T.B-1**

Unit III Chapters III Sections 22-55.**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 Reference:

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

**SEMSTER II: CORE IX
MOLECULAR MODELING AND DRUG DESIGN**

Subject Code:17PDBI 2C4
Hrs / Week: 6
Credit: 4

Max Marks: 100
Internal Marks: 25
External Marks : 75

Objective

*It deals with molecular modeling, quantum mechanics, and molecular mechanics.
Provide a broad and thorough background in modeling tools and docking programs.*

18 Hours

Unit I

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

18 Hours

Unit II

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

18 Hours

Unit III

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

18 Hours

Unit IV

Historic development of drug discovery, Modern drug discovery Software tools for modeling bio-molecules. #Molecular electrostatic potentials, charge analyses. Protein conformations, folding and mutation through modeling#.

18 Hours

Unit V

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 Modelling: Principles and Applications (2nd Edition), Addison Wesley Longman, Essex, England, 1996.
2. Alan Hinchliffe, Molecular Modelling 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 7.1-7.9.**T.B.1**

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

Books for Reference:

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

**SEMESTER II: CORE X
BIOINFORMATICS – PRACTICAL**

Subject Code: 17PDBI 2C5/P
Hrs / Week: 6
Credit: 4

Max Marks: 100
Internal Marks: 25
External Marks : 75

Objectives

This practical describes to acquire information from biological databases. Use of computational approaches to analyze the information.

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 chemDraw 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. Small molecule building using chemSketch.
9. Metabolic pathway prediction
10. Docking Using Patch Dock.

Text Books:

1. Andreas D. Baxevanis, B.F. Francis Ouellette. Bioinformatics. A Practical Guide to the Analysis of Genes and Proteins. (Third Edition 2006).
2. Baxevanis A 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. Rastogi S.C., Namita Mendiratta Parag Rastogi. Bioinformatics Concepts, Skills & Applications. (First Edition 2003).
2. Teresa K. Attwood & David J. Parry Smith. Introduction to Bioinformatics. (1999).
