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

SEM	Course Code	Course	Course Title	Hrs / Week	Credit	CIA Mark	SE Mark	Total Marks
I	20PDBI1C1	Core I	Fundamental of Bioinformatics	6	4	25	75	100
	20 PDBI1C2	Core II	Statistics for Bioinformatics	6	4	25	75	100
	20PDBI1C3	Core III	Basic Structural Biology	6	4	25	75	100
	20PDBI1C4	Core IV	Computer Programming	6	4	25	75	100
	20PDBI1C5P	Core V	C Programming and Web Publishing – Practical	6	4	25	75	100
TOTAL				**30**	**20**	**125**	**375**	**500**
II	20PDBI2C1	Core VI	Database Management Systems	6	4	25	75	100
	20PDBI2C2	Core VII	Genomics and Proteomics	6	4	25	75	100
	20PDBI2C3	Core VIII	Computational Biology	6	4	25	75	100
	20PDBI2C4	Core IX	Molecular Modelling and Drug Design	6	4	25	75	100
	20PDBI2C5P	Core X	Bioinformatics - Practical	6	4	25	75	100
TOTAL				**30**	**20**	**125**	**375**	**500**
GRAND TOTAL				**60**	**40**	**250**	**750**	**1000**

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

Programme Specific Outcome

At the end of the programme, students will be able to:

- Explain the fundamental principles of Bioinformatics and statistical applications in bio informatics.
- Outline the process of generation, manipulation and representation of molecules for drug modeling.
- Describe the basic structure of biological molecules, process of acquiring the structures and the interaction between the molecules.
- Develop and apply basic computer programming to build biological algorithms and models to study their relationships.
- Deduce the interrelationship between genomics and Proteomics, techniques involved in analyzing proteomics and its applications.

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
I	20PDBI1CC1	Core -I	FUNDAMENTAL OF BIOINFORMATICS	6	4	100	25	75

Course Outcomes

At the end of the course, students will be able to:

1. Identify the scope of Computational Biology and Bioinformatics.
2. Ability to design programs with interactive Input and Output program c.
3. Demonstrate the biological information. Retrieval methods for DNA sequence.
4. Gain the knowledge Major Biological Databases and Information.
5. Determine the analysed molecular biology, clinical medicine and other disciplines.

UNIT I: 18 hours

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.

UNIT II 18 hours

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#.

UNIT III 18 hours

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

UNIT IV 18 hours

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

UNIT V 18 hours

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:

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

T.B 2 .Arthur M. Lesk, Introduction to Bioinformatics, Oxford University Press, NewDelhi2003.

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 Reference:

1. S.R.Swindell,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.

Web Source

1. https://www.epictraining.ca/course/15958/biological databases/-distance
2. https://bioinformatics.mit.edu/

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	Code		Title of the Paper			Hours				Credits
I	20PDBI1CC1		FUNDAMENTAL OF BIOINFORMATICS			6				4
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)				
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓	✓	✓	✓	✓	✓		✓	✓	✓
CO2	✓	✓	✓	✓		✓	✓	✓	✓	✓
CO3	✓	✓	✓	✓		✓	✓	✓	✓	✓
CO4	✓	✓	✓	✓		✓		✓	✓	✓
CO5	✓	✓	✓	✓	✓	✓		✓	✓	✓
Number of Matches = 44, Relationship : High										

Prepared by: **Checked by:**

1. Dr.K.Gobalan - 1. Dr. J. Sebastin Raj

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
I	20PDBI1CC2	Core - II	STATISTICS FOR BIOINFORMATICS	6	4	100	25	75

Course Outcomes

At the end of the course, students will be able to:

1. Determine the category of measures of central tendency, dispersion and correlation for analysis of data.
2. Improve the new concepts of probability and random variables.
3. Identify the application some standard distributions and their properties.
4. Gain the knowledge about frequency theory of probability and its related problems.
5. Intellectual about the rule's coefficient of association.

Unit I **18 hours**

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

Unit II **18 hours**

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

Unit III **18 hours**

Theoretical Distributions – Binomial, Poisson and Normal – Importance of Normal Curve # 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 – 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:

T.B 1: Pillai R.S.N and V. Bagavathi and S. Chand Statistics, 1984.

T.B 2: Gupta S.C and V.K. Kapoor, Fundamentals of Mathematical Statistics, 11th Edition, Sultan Chand & Sons, New Delhi, 2002.

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. Robert R. Sokal and F.J. Rohlf, Introduction to Biostatistics (Biology- Statistics Series), W.H. Freeman & Company, New York, 1987.

2. Forthofer, L., Introduction to Biostatistics, Academic Press, 1995.

3. Gupta, S.P., Statistical Methods, Sultan Chand & Sons, 1996.

Web Source

1. https://nptel.ac.in/courses/statistics 102103012/s

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	**Code**		**Title of the Paper**			**Hours**			**Credits**	
I	**20PDBI1CC2**		**STATISTICS FOR BIOINFORMATICS**			**6**			**4**	
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)				
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓		✓	✓	✓		✓	✓	✓	✓
CO2	✓		✓	✓	✓			✓	✓	✓
CO3	✓		✓	✓	✓			✓	✓	✓
CO4	✓		✓	✓	✓			✓	✓	✓
CO5	✓	✓	✓	✓	✓	✓		✓	✓	✓
Number of Matches = 38, Relationship : High										

Prepared by: **Checked by:**

1. Dr. K. Gobalan - 1. Dr. T. Nargis Begum

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
I	20PDBI1CC3	Core - III	BASIC STRUCTURAL BIOLOGY	6	4	100	25	75

Course Outcomes

1. Acquire the basic and fundamental concepts of cell biology.
2 .Explain the knowledge in basic energy sources.
3. Apply the principle, Physiochemical properties, structure of nucleic acids.
4. Appraise the basic science of Protein structure including mechanisms.
5. Formulate the key experimental processes required to evaluate protein structure, functions and to apply them to solve biochemical problems.

Unit I **18 hours**

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

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.#Ramachandran plot and bonds stabilizing protein structure#.

Unit V **18 hours**

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. Horst FriebolinWitey, Basic One & Two dimensional NMR sepectroscopy–VCH – 1990.

2. Van Holde, Principles of Physical Biochemistry –Prentice Hall. 2006

Books for Reference:

1.Lehninger, David L. Nelson, Michael M. Cox., Principles of Biochemistry –3rd Edition Macmillan worth Publishers, 2000.

2. G.E.Shultz and R.H.Schirmer,Principles of Protein structure, Springer –Verlag, New York. 2002.

Web Source

1. https://nptel.ac.in/courses/102103012/

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	Code			Title of the Paper			Hours			Credits
I	20PDBI1CC3			BASIC STRUCTURAL BIOLOGY			6			4
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)				
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓	✓		✓	✓		✓	✓		✓
CO2	✓			✓	✓		✓	✓	✓	✓
CO3	✓		✓	✓	✓		✓	✓	✓	✓
CO4	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
CO5	✓	✓			✓	✓	✓	✓	✓	✓
Number of Matches = 40, Relationship : High										

Prepared by:
1. Dr. T. Nargis Begum

-

Checked by:
1.Dr. J. Sebastin Raj

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
I	20PDBI1CC4	Core - IV	COMPUTER PROGRAMMING	6	4	100	25	75

Course Outcomes

At the end of the course, students will be able to:

1. Develop the foundation for higher studies in the field of Computer Application.
2. Ability to design programs with Interactive Input and Output
3. Gain ability to develop responsive web applications
4. Explore different web extensions and web services standards.
5. Acquire knowledge and skills for creation of web site considering both client and server-side programming.

Unit I **18 hours**

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#.

Unit II **18 hours**

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#.

Unit III **18 hours**

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

Unit IV **18 hours**

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

Unit V **18 hours**

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:

T.B 1: Balagurusamy E., Object Oriented Programming with C++" — TMH-2000.

T.B.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-2

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.

Web Source

1. https://ocw.mit.edu/courses/computer program /7-06- -spring-2007.
2. https://ocw.mit.edu/courses/biology/7-06-computer application-spring-2010/

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	**Code**			**Title of the Paper**			**Hours**		**Credits**
I	**20PDBI1CC4**			**COMPUTER PROGRAMMING**			**6**		**4**
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)			
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
CO2	✓	✓	✓	✓	✓		✓	✓	✓	
CO3			✓	✓	✓	✓	✓	✓	✓	✓
CO4				✓	✓	✓	✓	✓	✓	✓
CO5	✓	✓			✓	✓	✓	✓	✓	✓
Number of Matches = 35, Relationship : High										

Prepared by:
1. Dr. K.Gobalan

Checked by:
1.Dr. T. Nargis Begum.

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
I	**20PDBI1CC5P**	**Core - V**	**C PROGRAMMING AND WEB PUBLISHING - PRACTICAL**	**6**	**4**	**100**	**20**	**80**

Course Outcomes

At the end of the course, students will be able to:

1. Describe the C programming concepts like Structures, Pointers and Command line arguments and data structures
2. Identify the application of some basic programs in C and Web based application.
3. Acquire the knowledge Practice the use of conditional and looping statements.
4. Illustrate the structure; implement arrays, functions and pointers.
5. Improve the new skills to handle strings and files.

List of Practicals:

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

Books for Reference:

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. Steve Wright., Instant HTML Programmer's Reference — WROX Press Ltd. 2011.

Web Source

1. https://www.youtube.com/watch?v=c program/k1pp
2. https://www.youtube.com/watch?v=html /k1O9jBHgsxs

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	Code	Title of the Paper	Hours	Credits
I	20PDBI1CC5P	C PROGRAMMING AND WEB PUBLISHING - PRACTICAL	6	4

Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)				
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
CO2	✓	✓	✓	✓			✓	✓	✓	✓
CO3	✓	✓	✓			✓	✓	✓	✓	✓
CO4	✓	✓	✓					✓	✓	✓
CO5	✓	✓	✓	✓	✓			✓	✓	✓
Number of Matches = 40, Relationship : High										

Prepared by:
1. Dr. K. Gobalan

Checked by:
1.Dr.Y. Arsia Tarnam.

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
II	**20PDBI 2CC6**	**Core - V I**	**DATABASE MANAGEMENT SYSTEMS**	**6**	**4**	**100**	**25**	**75**

Course Outcomes

At the end of the course, students will be able to:

1. Acquire the basics, concepts, objectives of Database.
2. Describe the fundamental elements of data models and database management systems.
3. Apply and use data manipulation language to query update and manage a data base.
4. Analyze the physical and logic database designs and addressing techniques: indexing methods and Hashing.
5. Construct a simple database system with the understanding of essential DBMS concepts such as Database security.

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 – File Database – Tree 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**

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

Books for Reference:

1.C.J. Date, An Introduction to Database systems, 3rd edition, Narosa Publishing House, 2004

2.James Martin, Principles of Database Management, Prentice Hall of India, 2012

Web Source

1. https://nptel.ac.in/courses/106105175/

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	**Code**		**Title of the Paper**			**Hours**		**Credits**	
II	**20PDBI 2CC6**		**DATABASE MANAGEMENT SYSTEMS**			**6**		**4**	
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)			
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓		✓	✓	✓		✓	✓	✓	✓
CO2	✓		✓	✓	✓			✓	✓	✓
CO3	✓		✓	✓	✓			✓	✓	✓
CO4	✓		✓	✓	✓			✓	✓	✓
CO5	✓	✓	✓	✓	✓	✓		✓	✓	✓
Number of Matches = 38, Relationship : High										

Prepared by:
1. Dr. T. Nargis Begum

-

Checked by:
1.Dr. J. Sebastin Raj

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
II	**20PDBI 2CC7**	**Core - VII**	**GENOMICS AND PROTEOMICS**	**6**	**4**	**100**	**25**	**75**

Course Outcomes

At the end of the course, students will be able to:

1. Apply the basic concepts of genomics, transcriptomics and proteomics.
2. Discuss the use of genomics and proteomics in human health.
3. Demonstrate outline solution to theoretical and experimental Problems in Genomics and proteomics fields.
4. Evaluate the work in core facilities and commercial biological and medical laboratories as well as in their postgraduate studies.
5. Improve the new skills databases that store various data about genes, proteins, genomes and proteomes.

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**

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#.

Unit III **18 hours**

Genomics Whole genome analysis – Physical methods of sequencing – automated sequencing – genome expression and analysis – serial analysis. #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 toxicology#, microbial drug,tumour immunology, vaccine discovery, drug design.

Unit V **18 hours**

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:

T.B. 1.Doolittle RF Molecular evolution, Computer Analysis of Protein and Nucleic acid Sequences, Methods in Enzymology, Academic Press, New York. 1990.

T.B. 2.Baxevanis AD and B.F.F. Ouellette, Wiley Bioinformatics – A practical guide to the analysis of genes and proteins. (ed) – Interscience, New York, 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-2

Books for Reference:

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

Web Source

1. https://courses.lumenlearning.com/boundless-biology/chapter/genomics-and-proteomics/
2. https://www.ncbi.nlm.nih.gov/books/NBK19861/

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	**Code**		**Title of the Paper**			**Hours**			**Credits**	
II	**20PDBI 2CC7**		**GENOMICS AND PROTEOMICS**			**6**			**4**	
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)				
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓		✓	✓		✓		✓	✓	
CO2	✓		✓	✓	✓	✓		✓	✓	✓
CO3	✓	✓	✓		✓	✓	✓	✓		✓
CO4	✓	✓				✓	✓			
CO5	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Number of Matches = 36, Relationship : High										

Prepared by:
1.H.F. Seyed Mafiya Haniff

Checked by:
1.Dr.S. Benazir Begum

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
II	**20PDBI 2CC8**	**Core - VIII**	**COMPUTATIONAL BIOLOGY**	**6**	**4**	**100**	**25**	**75**

Course Outcomes

At the end of the course, students will be able to:

1. Describe different types of biological database and sequence submission tools.
2. Summarize the basics of sequence alignment and various approaches in phylogenetic analysis.
3. Assess the structure, properties and interactions of protein and its databases.
4. Explain the structure and various approaches in 3D structure prediction.
5. Classify and explain the tools and algorithms used for genome sequencing assembly.

Unit I **18 hours**

Structure of DNA & Protein – Sequence analysis – pairwise 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:

T.B-1 StephenMisener& Stephen A. Krawetz, Bioinformatics: Methods and Protocols HumanaPress, New Jersey, 2000.

T.B-2A.D.Baxevanis, B.F.F. Ouellette Bioinformatics: A practical guide to the analysis of genes and proteins– Wiley Interscience – New York, 2001.

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.

Web Source

1. https://nptel.ac.in/courses/102/106/102106068/

2. https://onlinecourses-archive.nptel.ac.in/noc18_bt22/preview

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	**Code**			**Title of the Paper**			**Hours**			**Credits**
II	**20PDBI 2CC8**			**COMPUTATIONAL BIOLOGY**			**6**			**4**
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)				
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓	✓	✓	✓		✓		✓	✓	✓
CO2	✓	✓	✓	✓		✓		✓	✓	✓
CO3	✓	✓	✓	✓		✓		✓	✓	✓
CO4	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
CO5	✓	✓	✓	✓	✓	✓		✓	✓	✓
Number of Matches = 43, Relationship : High										

Prepared by:

1.Dr. Y. ArsiaTarnam

Checked by:

1. Dr. J. Sebastin Raj

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
II	**20PDBI 2CC9**	**Core - IX**	**MOLECULAR MODELING AND DRUG DESIGN**	**6**	**4**	**100**	**25**	**75**

Course Outcomes

At the end of the course, students will be able to:

1. Discuss various techniques and concepts used in structure-based drug design.
2. Describe the algorithms used in drug analysis.
3. Analyze the principles involved in molecular modeling and drug design.
4. Demonstrate the various tools employed in drug discovery and its applications.
5. Systematize about genomics and proteomics in disease analysis at molecular level

Unit I **18 hours**

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

Unit II **18 hours**

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#.

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**

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#.

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:

T.B-1 Andrew Leach, Molecular Modelling: Principles and Applications, 5nd Edition, Addison Wesley Longman, Essex, England, 2015.

T.B-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 7.1-79.T.B.1
Unit V	Chapters I	Sections 1.1-1.10.T.B-1

Books for Reference:

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

Web Source

1. https://nptel.ac.in/courses/102/106/102106070/
2. https://onlinecourses.nptel.ac.in/noc19_bt22/preview

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	**Code**			**Title of the Paper**			**Hours**		**Credits**	
II	**20PDBI 2CC9**			**MOLECULAR MODELING AND DRUG DESIGN**			**6**		**5**	
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)				
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
CO2	✓	✓	✓	✓		✓	✓	✓	✓	✓
CO3	✓	✓	✓	✓		✓		✓	✓	✓
CO4	✓	✓	✓	✓		✓		✓	✓	✓
CO5	✓	✓	✓	✓	✓	✓		✓	✓	✓
Number of Matches = 44, Relationship : High										

Prepared by:

1. Dr. Y. Arsia Tarnam

Checked by:

1. Dr. J. Sebastin Raj

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

Semester	Code	Course	Title of the Course	Hours	Credits	Max. Marks	Internal Marks	External Marks
II	**20PDBI2CC10P**	**Core - X**	**BIOINFORMATICS – PRACTICAL**	**6**	**4**	**100**	**20**	**80**

Course Outcomes

At the end of the course, students will be able to:

1. Describe about sequencing alignment and similar search tool.
2. Provide hands on training on various tools and techniques employed in biological sequence analysis.
3. Explain about protein structural analysis using Bioinformatics tools.
4. Expose to several DNA and protein databases.
5. Practice methods and tools used for phylogenetic analysis.

List of Practicals:

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

Text Books:

1. A. Baxevanis and B.F. Ouellette, Bioinformatics: A practical Guide to the Analysis of Genes and Proteins, Wiley-Inter science, Hoboken, NJ, 1998.

2. D. Andreas, B.F. Baxevanis, Francis Ouellette, Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins, Wiley-Interscience, 3rd edition, 2006.

Books for Reference:

1. K. Teresa, Attwood and J. David, Parry Smith, Introduction to Bioinformatics, Pearson Education, 1999.

2. S.C. Rastogi, NamitaMendiratta Parag Rastogi. Bioinformatics Concepts, Skills & Applications, CBS Publishers & Distributors, First edition, 2003.

Web Source

1. https://nptel.ac.in/courses/102/106/102106065/
2. https://nptel.ac.in/content/storage2/courses/102103044/pdf/mod6.pdf

Relationship Matrix for Course Outcomes, Programme Outcomes and Programme Specific Outcomes:

Semester	Code			Title of the Paper				Hours		Credits
II	20PDBI2CC10P			BIOINFORMATICS – PRACTICAL				6		5
Course Outcomes (COs)	Programme Outcomes (POs)					Programme Specific Outcomes (PSOs)				
	PO1	PO2	PO3	PO4	PO5	PSO1	PSO2	PSO3	PSO4	PSO5
CO1	✓	✓	✓	✓		✓		✓	✓	✓
CO2	✓	✓	✓	✓		✓		✓	✓	✓
CO3	✓	✓	✓	✓		✓		✓	✓	✓
CO4	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
CO5	✓	✓	✓	✓	✓	✓		✓	✓	✓
Number of Matches = 43, Relationship : High										

Prepared by:

1.Dr. Y. ArsiaTarnam

Checked by:

1. Dr. J. Sebastin Raj

Note:

Mapping	1-29%	30-59%	60-69%	70-89%	90-100%
Matches	1-14	15-29	30-34	35-44	45-50
Relationship	Very poor	Poor	Moderate	High	Very high

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