

KONGUNADU ARTS AND SCIENCE COLLEGE

(AUTONOMOUS)

COIMBATORE – 641 029

PG DIPLOMA IN BIOINFORMATICS

CURRICULUM AND SCHEME OF EXAMINATIONS (CBCS)

(2026 – 2027)



COURSE OFFERED

BY

PG AND RESEARCH DEPARTMENT OF BIOTECHNOLOGY

KONGUNADU ARTS AND SCIENCE COLLEGE (AUTONOMOUS)

COIMBATORE – 641 029

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Vision

Developing the total personality of every student in a holistic way by adhering to the principles of Swami Vivekananda and Mahatma Gandhi.

Mission

- Imparting holistic and man-making education with emphasis on character, culture and value - moral and ethical.
- Designing the curriculum and offering courses that transform its students into value added skilled human resources.
- Constantly updating academic and management practices towards total quality management and promotion of quality in all spheres.
- Extending the best student support services by making them comprehensive and by evolving a curriculum relevant to student community and society at large.
- Taking steps to make education affordable and accessible by extending scholarships to the meritorious and economically disadvantaged students.
- Molding the teachers in such a way that they become the role models in promoting Higher Education

DEPARTMENT OF BIOTECHNOLOGY

Vision

To enable the students to comprehend the tool of Biotechnology so as to attain new vistas in core and applied areas of Biotechnology education and research; such that experiential learning and problem solving attribute shall continuously contribute to the nation building by maintaining high degree of ethical standard and integrity

Mission

- Build comprehensive quest for scientific inquiry provide the basic and advanced courses
- Provide a fundamental knowledge of the various application of Biotechnology and integrate it with cutting edge research in niche areas
- Pursue an integrative interdisciplinary and cross disciplinary approach in teaching, learning and research
- Foster industrial national and international institutional collaboration for promotion of research, innovation and entrepreneurship in Biotechnology

Goal

- Provide a holistic and self-reliant learning environment
- Promote diversity in teaching, learning and research
- Empower stakeholders through ample hands on studies, activity based learning method, Industry oriented case study and project work which shall make learning experience unique
- Enrich the teaching and learning process through adequate industry/local community partnership
- Inculcate high standards of ethic, professionalism and responsibility among the stakeholders

POST GRADUATE DIPLOMA IN BIOINFORMATICS

PROGRAMME OUTCOMES (PO)

- PO1:** To provide a benchmark international platform in the field of bioinformatics to promote initiatives in post-graduate education, and fruitful career.
- PO2:** Attaining new heights in biotechnology research, shaping biotechnology into a premier precision tool for the future
- PO3:** To develop the capacity for leadership in applying modern bioinformatics tools in the field of innovative research for understanding the basics of science.
- PO4:** To develop core competencies, analytical and informatics tools and methodologies for the analysis, interpretation of biological data's generated from genomic and proteomic studies, using high performance computational systems.
- PO5:** To provide personalized training and enhance bioinformatics skills of students in the life sciences.

PROGRAMME SPECIFIC OUTCOMES (PSO)

- PSO1:** Challenge our understanding of bioinformatics fundamentals through integrated approaches
- PSO2:** Cater to the academic and industry requirements in the field of Bioinformatics and NGS - Genomics, and remain up-to-date with current research in the domain of the life sciences applications.
- PSO3:** Realizing full potentials of Bioinformatics as an application tool
- PSO4:** Impart a complete understanding of the principles of bioinformatics algorithms and tools through interactive summaries, polls, discussions.
- PSO5:** Apply the tool of Bioinformatics to solve issues pertaining to various biomolecules in several high end applications

REGULATIONS

Name of the course: The course offered is called **Postgraduate Diploma in Bioinformatics**.

Eligibility: Students who are pursuing their Post graduate courses in any discipline are eligible for admission into the course. The course is operates online in the Online Distant Learning (ODL) mode.

Duration of the Course: Postgraduate Diploma in Bioinformatics is for a period of one year having 2Semesters.

Number of Subjects: The course consists of **Four** Theory Papers and **Three** practical and Project

Number of Credits: The Course will be of 16 credits.

Theory credits	10
Practical credits	3
Project	3

The proof of this should be submitted during examination (Record Note Book, Project Report) duly signed by the faculty in-charge and HOD

Marks Distributions:

The Maximum 100 marks is awarded per paper

The passing Students should collect totally 16 credits to be eligible for the Postgraduate Diploma in Bioinformatics.

Student will be classified according to the marks scored as:

Marks %	Grade
85-100	O
70-84	D
60-69	A
50-59	B
40-49	C
<40	U (Reappear)

Examination

Examination will be conducted at the completion of each paper. The Controller of Examinations Kongunadu Arts and Science College, Coimbatore will conduct the examination; qualified candidates will be eligible to receive the certificate

Teaching Pedagogy

Smart ClassRoom/Powerpoint presentation/Seminar/Quiz/Discussion/Flipped Classroom/Peer Learning/Experimental Learning/Blended learning
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Syllabus: Detailed syllabus is enclosed.

KONGUNADU ARTS AND SCIENCE COLLEGE (Autonomous)

COIMBATORE-641 029.

PG DIPLOMA IN BIOINFORMATICS

Curriculum & Scheme of Examination under CBCS

(Applicable to Students Admitted from the Academic Year 2026-2027 and onwards)

Subject Code	SUBJECT	Instruction Hours / cycle	Max. Marks			Exam Duration (hrs)	Credit points
			CIA	ESE	Total		
26PDBI101	Core Paper 1 - Essentials of Bioinformatics	15	25	75	100	3	3
26PDBI102	Core Paper 2 - Programming in C	15	25	75	100	3	2
26PDBI1CL	Core Practical I	15	40	60	100	3	1
26PDBI1CM	Core Practical II	15	40	60	100	3	1
	Project & Viva voce	10*	-	-	-	-	-
	Total	70	-	-	400	-	7
26PDBI203	Core Paper 3 - Cheminformatics, Molecular Modeling and Drug Designing	15	25	75	100	3	3
26PDBI204	Core Paper 4 - Python Programming	15	25	75	100	3	2
26PDBI2CN	Core Practical –III	15	40	60	100	3	1
26PDBI2Z1	Project & Viva voce	15*	20	80	100	3	3
	Total	60	-	-	400		9
	Grand Total				800		16

* Not to be included in faculty workload

Note:

CBCS - Choice Based Credit System, **CIA** - Continuous Internal Assessment **ESE** - End of Semester Examinations

COMPONENTS OF CONTINUOUS INTERNAL ASSESSMENT

Components		Marks	Total
Theory			
CIA I	75	(75+75 = 150/10) 15	25
CIA II	75		
Assignment/Seminar*		5	
Attendance		5	
Practical			
CIA Practical		25	40
Observation Notebook		10	
Attendance		5	
Project			
Review		15	20
Regularity		5	

*In courses where group discussions /activities/case studies are given. This may be considered in place of assignments.

BLOOM'S TAXONOMY BASED ASSESSMENT PATTERN

K1-Remember; **K2**-Understanding; **K3**-Apply; **K4**-Analyze; **K5**-Evaluate

1. Theory Examination - Part I, II& III

(i) CIA I & II and ESE: 75 Marks

Knowledge Level	Section	Marks	Description	Total
K1 Q1 to 10	A (Answer all)	10 x 1 = 10	MCQ	75 **
K1 – K5 Q11 to 15	B (Either or pattern)	5 x 5 = 25	Short Answers	
K2 – K5 Q16 to 20	C (Either or pattern)	5 x 8 = 40	Descriptive / Detailed	

**For ESE 75 marks converted to 50 marks.

2. Practical Examination:

Knowledge Level	Section	Marks	Total
K3 ↕ K5	Experiments	50	60
	Record Work	10	

Practical Examination mark breakup:

Knowledge Level	Section
K3 ↑ ↓ K5	Major Experiments:
	Protocol - 5
	Perform - 10
	Result - 5
	Minor Experiments:
	Protocol - 5
	Perform - 5
	Result - 5
	Q&A - 10
	Viva - 5
	Record work 10

3. Project work:

Knowledge Level	Section	Marks	Total
K3 ↑ ↓ K5	Project	60	80
	Viva voce	20	

Project mark breakup

Knowledge Level	Section
K3 ↑ ↓ K5	Project Report:
	Issue identification - 20
	Review - 10
	Analysis - 10
	Recommendation - 10
	Report - 10
	Viva Voce:
	Layout of presentation - 5
	Clarity - 5
	Defense - 10

Programme Code:08	Program name: PG Diploma in Bioinformatics		
Core Paper 1 - ESSENTIALS OF BIOINFORMATICS			
Batch : 2026-2027	Total Hours 15	Credits 3	Employability/ Skill Development

COURSE OBJECTIVES

- To provide a basic understanding on theory and Applications of bioinformatics.
- To decipher the features and use of different databases for DNA, RNA and Proteins.
- To employ alignment tools to understand the complexity of biomolecules.

COURSE OUTCOMES

On successful completion of the course, the students will be able to:

↑ ↓	K1	CO1	Capable to identify the existing biological problem and to apply the relevant omics Concept
		CO2	Able to explore the biological data to solve several issues in healthcare Domains
		CO3	Accomplish the different level of protein structure and the respective database
		CO4	Potential to recognize the similar function and structure for sequences
K5		CO5	Perform MSA to infer conserved regions and domains of biological molecules

SYLLABUS

Unit 1

(3 Hours)

Bioinformatics: Definition, Basics of Bioinformatics, Applications and Opportunities of Bioinformatics. Biological Databases- Introduction, Types, Uses and importance of Biological Databases. Multi-Omics concepts of Bioinformatics- Proteomics, Genomics, Transcriptomics, Metagenomics, Pharmacogenomics.

Unit 2

(3 Hours)

Primary Nucleotide Databases: National Center for Bioinformatics Institute (NCBI), GenBank, European Bioinformatics Institute (EBI), European Molecular Biology Laboratory (EMBL), DNA Data Bank of Japan (DDBJ), Online Mendelian Inheritance in Man(OMIM), Sequence submission tools (Sequin, BankIT), Sequence Retrieval System (Entrez)

Unit 3**(3 Hours)**

Primary Protein sequence Databases: UniProt- Swiss-Prot, Tr-EMBL, Protein Information Resource (PIR), Secondary Protein sequence Databases: Protein Family database (PFam), PROSITE, PRODOM , Protein tertiary Structure Databases: Protein Data Bank (PDB)

Unit 4**(3 Hours)**

Protein sequence Alignment, Homology, Similarity, Identity, Gaps, Alignment types, Pairwise alignments: Dot Plots, Scoring Matrix-PAM, BLOSUM, Gap Penalty, Dynamics programming - Alignment Algorithms: Global Sequence Alignment: Needleman-Wunsch Algorithm. Local Sequence Alignment: Smith –Waterman Algorithm

Unit 5**(3 Hours)**

Multiple Sequence Alignment (MSA):Definition, Types, Tools for MSA, ClustalW, MEGA, Databases of Multiple Sequence Alignment Programs- BLOCKS, PRINTS, Integrated ***Multiple Sequence Alignment Resources: Inter Pro, iPro Class**

****Denotes self-study*****Text books**

1. Introduction to Bioinformatics- TK Attwood and DJ Parry-Smith, Pearson PLC, 2003
2. Essentials of Bioinformatics- JinXiong, Texas A & M University, Cambridge University Press, 2006.
3. Bioinformatics Concepts Skills and Application-S.C. Rastogi, New Delhi: PHI Learning, 2008.
4. Bioinformatics- B G Curran; R J Walker and S C Bhatia, CBS Pub, New Delhi, 2010
5. Structural Bioinformatics – Jenny Gu, Philip E. Bourne, Wiley-Blackwell (2nd ed), 2011.
6. Principles of Proteomics-Richard Twyman, Garland Science, 2013

Reference

1. Bioinformatics Sequence and Genome Analysis-David W.Mount.: CBS Publishers, 2003.
2. Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins-
Baxevanis, Andreas, D. and Francis B.F. Ouellette, NewYork: John Wiley, 2004.

Web sources Link

1. <https://www.ebi.ac.uk/services/data-resources-and-tools/>
2. <https://www.uoanbar.edu.iq/eStoreImages/Bank/15853.pdf>
3. <https://mccollegeonline.co.in/attendance/classnotes/files/1586267644.pdf>
4. <https://www.ebi.ac.uk/jdispatcher/msa/clustalo>
5. <https://bioinformaticshome.com/tools/msa/msa.html#gsc.tab=0>

MAPPING

PSO CO	PSO1	PSO 2	PSO 3	PSO 4	PSO 5
CO1	H	S	M	M	H
CO2	M	H	H	M	M
CO3	H	H	S	M	M
CO4	M	S	H	M	H
CO5	M	M	M	M	H

S – Strong

H – High

M – Medium

L – Low

Content prepared by (Based on Inputs) Signature of the Course in-charge (Dr. R.Sathish kumar)	Signature of the HOD (Dr. R.Sathish kumar)
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Programme Code:08		Program name: PG Diploma in Bioinformatics	
Core Paper 2 - PROGRAMMING IN C			
Batch : 2026-2027	Total Hours 15	Credits 2	Employability/ Skill Development

COURSE OBJECTIVES

- To familiarize students with the programming language
- To gain knowledge of C programming language
- To enable the application of C program in real time programs

COURSE OUTCOMES

On successful completion of the course, the students will be able to:

K1 ↑ ↓ K5	CO1	Able to write syntax and code using C program
	CO2	Relate the importance of programming in biology
	CO3	Apply in developing tools for computational analysis of biological molecules
	CO4	Illustrate the process of data file manipulations using C
	CO5	Design programs using variety of data structures

SYLLABUS**Unit 1 (3 Hours)**

Overview of C: History of C -Importance of C - Sample C Programs- Basic structure of C programs- Programming style - Executing a C Program. Constants, Variables and Data types: Character set – C tokens – Keywords and identifiers – Constants – Variables – Data types – Declaration of variables – Assigning values to variables – Defining symbolic constants.

Unit 2 (3 Hours)

Operators: Arithmetic Operators – Relational Operators – Logical Operators – Assignment Operators - Increment and Decrement Operators – Conditional Operator – Bitwise Operators- Special Operators. Expression: Arithmetic expressions – Evaluation of expressions – Precedence of arithmetic operators – Some computational problems – Type conversions in expressions – Operator precedence and associativity – Mathematical functions.

Unit 3 (3 Hours)

Managing Input and Output Operations: Reading a character – Writing a character
Formatted Input – Formatted Output.

Unit 4 (3 Hours)

Decision Making and Branching: Decision making with IF statement – Simple IF statement – The IF ... ELSE statement – Nesting of IF ... ELSE statements – The ELSE IF ladder – The Switch statement – The? *operator- The GOTO statement.

Unit 5**(3 Hours)**

Decision Making and Looping: The WHILE statement – The DO statement – The FOR statement
– Jumps in loops.

denotes self-study*Text Books**

1. E. Balagurusamy, Programming in ANSI C , 7th edition, Tata McGraw- Hill Publishing Company Ltd., New Delhi, 2017.

Web sources Link

1. <https://www.wscubetech.com/resources/c-programming/structure>
2. <https://www.wscubetech.com/resources/c-programming/operators>
3. <https://www.studocu.com/in/document/bharathidasan-university/bca-computer-application/formatted-input-and-output-functions/21706224>
4. <https://www.projectmanager.com/blog/decision-making-tools-techniques>
5. <https://www.studocu.com/in/document/davangere-university/bachelor-of-computer-application/decision-making-and-looping-statements/35295492>

MAPPING

CO \ PSO	PSO1	PSO 2	PSO 3	PSO 4	PSO 5
CO1	M	S	H	M	M
CO2	H	H	M	H	M
CO3	H	S	H	M	H
CO4	M	S	H	H	H
CO5	H	H	H	M	M

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Subject Code: 08010201			
Programme Code:08	Program name: PG Diploma in Bioinformatics		
Core Practical I			
Batch : 2026-2027	Total Hours 15	Credits 1	Employability/ Skill Development

COURSE OBJECTIVES

- i. To understand the basic feature of different biological databases
- ii. To retrieve information of scientific interest from the specific database
- iii. To utilize the tools existing for nucleic acid and protein analysis

COURSE OUTCOMES

On successful completion of the course, the students will be able to:

K3 ↑ ↓ K5	CO1	Relate the biological sequence databases for computational analysis
	CO2	Annotate the biological sequences to attain scientifically significant information
	CO3	Implement the sequence similarity tools to acquire significant information
	CO4	Apply the knowledge of computational tools to address the clinical problems
	CO5	Analyze the data of gene and protein for evolutionary studies

EXPERIMENTS

1. Access and retrieve information from primary nucleotide sequence databases: NCBI, EMBL, DDBJ
2. Access and retrieve information from primary protein sequence databases : Swiss-Prot
3. Access and retrieve literature information using PubMed
4. Perform similarity search for nucleotide sequences using BLASTn against different databases
5. Perform similarity search for protein sequence using Basic Local Alignment Search Tool (BLAST)
6. Access and retrieve protein classification information from PFAM
7. Access and retrieve 3D structure information from PDB
8. Perform protein structure visualization using Pymol
9. Protein structure analysis using SPDB Viewer
10. Perform pairwise sequence alignment using DOTPLOT method

11. Analyze the homology, identity and gap in sequence alignment.
12. Perform MSA using ClustalW
13. Analyze the conserved, partial conserved regions in the MSA files.
14. Phylogenetic Tree Construction Tool: MEGA
15. Design primer from sequence information

COMPONENTS OF CONTINUOUS INTERNAL ASSESSMENT

Practical		
CIA Practical	25	40
Observation Notebook	10	
Attendance	5	

ESE Practical Examination:

Knowledge Level	Section	Marks	Total
K3 ↕ K5	Experiments	50	60
	Record Work	10	

Practical Examination mark breakup:

Knowledge Level	Section
K3 ↑ ↓ K5	Major Experiments:
	Protocol - 5
	Perform - 10
	Result - 5
	Minor Experiments:
	Protocol - 5
	Perform - 5
	Result - 5
	Q&A - 10
	Viva - 5
	Record work 10

MAPPING

PSO CO	PSO1	PSO 2	PSO 3	PSO 4	PSO 5
CO1	H	H	S	M	H
CO2	M	S	H	H	H
CO3	M	S	S	H	M
CO4	H	H	H	M	M
CO5	H	H	S	M	M

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(Dr. R.Sathish kumar)

Programme Code:08		Program name: PG Diploma in Bioinformatics	
Core Practical II			
Batch : 2026-2027	Total Hours 15	Credits 1	Employability/ Skill Development

COURSE OBJECTIVES

- To familiarize with coding and syntax for writing a program
- To understand and rectify the errors
- To relate computational programming knowledge and biological problems

COURSE OUTCOMES

On successful completion of the course, the students will be able to: able to

K3 ↑ ↓ K5	CO1	Identify the appropriate data structure for solving real world problems
	CO2	Implement various kinds of searching and sorting techniques
	CO3	Debug the coding/syntax errors
	CO4	Apply the concepts of object-oriented programming
	CO5	Illustrate the process of functions and classes using C++

EXPERIMENTS

1. Program to identify Prime numbers.
2. Program to find Simple Interest.
3. Program to find the Solution of the quadratic equation.
4. Program to find the Factorial of a number.
5. Program to frame Fibonacci series.
6. Program to find the sum of digits of a number.
7. Program to find the arithmetic mean of n numbers.
8. Program to find the median of n numbers.
9. Program to find the sum and difference of two matrices.
10. Program to find the multiplication of two matrices.
11. Program to find the inverse of trigonometric functions.
12. Program to find whether a given word is a palindrome or not.

COMPONENTS OF CONTINUOUS INTERNAL ASSESSMENT

Practical		
CIA Practical	25	40
Observation Notebook	10	
Attendance	5	

ESE Practical Examination:

Knowledge Level	Section	Marks	Total
K3 ↕ K5	Experiments	50	60
	Record Work	10	

Practical Examination mark breakup:

Knowledge Level	Section
K3 ↑ ↓ K5	Major Experiments: Protocol - 5 Perform - 10 Result - 5 Minor Experiments: Protocol - 5 Perform - 5 Result - 5 Q&A - 10 Viva - 5 Record work 10

MAPPING

PSO CO	PSO1	PSO 2	PSO 3	PSO 4	PSO 5
CO1	H	S	S	M	H
CO2	M	M	S	H	H
CO3	H	H	H	H	M
CO4	H	H	S	M	M
CO5	H	S	H	H	M

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Programme Code:08	Program name: PG Diploma in Bioinformatics		
Core Paper 3 –CHEMINFORMATICS, MOLECULAR MODELING AND DRUG DESIGNING			
Batch : 2026-2027	Total Hours 15	Credits 3	Employability/ Skill Development

COURSE OBJECTIVES

- To introduce the basic concepts of drug designing and modeling
- To Provide impacts on various resources available for biological molecules
- To Understand the interactions between molecules using various Computational tools

COURSE OUTCOMES

On successful completion of the course, the students will be able to:

K1 ↑ ↕ ↓ K5	CO1	Classify small molecules and interpret results from chemoinformatics analysis
	CO2	Interpret the significance of computationally modeled biomolecules
	CO3	Depict the importance of natural small molecules in pharmaceutical applications
	CO4	Apply the concepts for modern drug discovery process
	CO5	Demonstrate the key features to notice in target-ligand interactions

SYLLABUS

Unit 1

(3 Hours)

Cheminformatics: Definition, Basics of Cheminformatics, Databases: Chemical Structure Databases (PubChem, Drug bank), Structure databases; Reaction Databases; Literature Databases; Medline, Databases of Small Molecules (ZINC).

Unit 2

(3 Hours)

Different Types of Notations, SMILES Coding, Structure of Mol files and Sdfiles (Molecular converter, SMILES Translator), Drawing the Chemical Structure: 2D and 3D Drawing Tools (ACD Chems sketch), Structure Optimization, Absorption, Distribution, Metabolism, Elimination and Toxicity- ADMET Prediction

Unit 3

(3 Hours)

Protein secondary structure analysis tools - Expasy, Garneier-Osguthorpe-Robson (GOR), Chou- Fasman Method, Protein tertiary structure: Homology model programs (SwissProt, Modeller), ab- initio method (I-tasser), Protein Visualization tools: Rasmol, PyMol, SPDBV, Cn3D, VMD

Unit 4**(3 Hours)**

Definition of drugs, Types of drug designing: Structure-Based Drug Design, Ligand-based Design, De Novo Drug Design Virtual Screening / Docking of Ligands, ***Protein structure-Fragment-Based Drug Design**

Unit 5**(3 Hours)**

Drug Development Process Overview - The Changing Landscape of drugs development, FDA regulations on Drug Development, Target Identification and Discovery, Structure Validation, Active Site Prediction, Molecule docking study.

**denotes self-study*

Text Books:

1. Molecular Modelling Principles and Application-A.R. Leach, Longman, 2001.
2. Molecular Dynamics Simulation Elementary Methods-J.M. Haile, John Wiley and Sons, 1997.
3. Chemoinformatics: A Textbook -Johann Gasteiger and Thomas Engel ,Wiley-VCH,2003
4. Introduction to Cheminformatics- Andrew R. Leach, Valerie J. Gillet, Cluwer, Academic Publisher, Netherlands, 2003.

References:

1. Proteomics - S.R. Pennigton and M.J. Dunn. Viva Books Private Limited. New Delhi.2002.
2. Molecular Modeling: Principles and Applications -Andrew R. Leach. USA: PrenticeHall, 2007.
3. Bioinformatics – Concepts, Skills, Applications (2nded.,) S.C. Rastogi, Namita Mendiratta, Parag Rastogi. CBS Publishers & Distributors Pvt. Ltd. 2014
4. Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins -Baxevanis, Andreas, D. and Francis B.F. Ouellette, NewYork: John Wiley, 2004.

Web sources link

1. <https://chemoinfo.ipmc.cnrs.fr>
2. http://www.structuralchemistry.org/pcsb/capp_cdf.php
3. <https://www.rcsb.org/search/chemical>
4. <https://pubchem.ncbi.nlm.nih.gov/edit3/index.html>
5. <https://bio.tools/psipred>
6. <https://www.drugdesign.org>
7. <https://www.appsilon.com/post/drug-development-process>

MAPPING

PSO CO	PSO1	PSO 2	PSO 3	PSO 4	PSO 5
CO1	M	H	H	M	H
CO2	M	H	S	H	H
CO3	H	S	S	M	H
CO4	M	S	H	M	M
CO5	H	S	H	H	M

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Programme Code:08	Program name: PG Diploma in Bioinformatics		
Core Paper 4–PYTHON PROGRAMMING			
Batch : 2026-2027	Total Hours 15	Credits 2	Employability/ Skill Development

COURSE OBJECTIVES

- Demonstrate the methodology to locate and download files for data analysis involving DNA and Protein structures
- Select datasets, open files and pre-process data using Python
- Develop python scripts to replace missing values, normalize data, discretize data, and sample data

COURSE OUTCOMES

On successful completion of the course, the students will be able to: able to:

K1 ↑ K5	CO1	Relate the necessity for programming in biology
	CO2	Handle biological data with Python scripts
	CO3	Develop codes/scripts for resolving the biological data queries
	CO4	Access online resources for R and import new function packages into the Python workspace
	CO5	Interpret the statistical significance of genomic data in a particular disease condition

SYLLABUS

Unit 1

(3 Hours)

Computer Hardware Architecture - Overview of Programming Languages - Introduction to Python - Python Overview – Comments in Python - Python Identifiers - Reserved Keywords – Variables - Standard Data Types - Python Casting.

Unit 2

(3 Hours)

Python Operators – Types of Operators - Statement and Expressions - String Operations: Creating String in Python - Strings indexing and splitting - Reassigning Strings- Deleting the String - String Operators -Multiline Strings- Built-in String Methods-Boolean Expressions –Python List – Various List Operation – Loop List - List Methods.

Unit 3

(3 Hours)

Python Tuples – Various Tuples Operations – Loop Tuples -Tuple Methods – Python Set – Various Set Operations – Loop Set – Set Methods – Python Dictionaries – Various Dictionaries Operations – Nested Dictionaries – Dictionary Methods - Python Dates- Python Conditions and Python IF Statement- Python IF ELIFELSE Statements - Python nested IF statements- The pass Statement.

Unit 4**(3 Hours)**

Python Loops - Python while Loop Statements-Infinite Loop- for Loop Statements- Iterating by Sequence Index - Python nested loops- Python Numbers- Mathematical Functions- Random Number Functions- Python Functions - Calling a Function - Pass by reference vs value - Function Arguments - The return Statement -Python Lambda functions.

Unit 5**(3 Hours)**

Scope of Variables - Local Scope- Global Scope- Python Exceptions Handling - Assertions in Python - Handling an exception - Python String Formatting - Python User Input- Python Files I/O - File Handling- File Open- Read Only Parts of the File- Read Lines- Close Files- Python File Write- Createa New File -Delete File- ***Delete Folder- Python Matplotlib.**

**denotes self-study*

Text Book:

1. Problem Solving and Python Programming -E. Balagurusamy, McGraw-Hill, First Edition, 2017.

Reference Books:

1. Python for Complete Beginners -Martin Jones ,Createspace Independent Publisher, First Edition,2015
2. Programming And Problem Solving With Python -Ashok Namdev Kamthane, Amit Ashok Kamthane , McGraw-Hill, First Edition. 2017
3. Mark Lutz, Programming Python, O`Reilly, 4th Edition, 2010

Web sources link

1. <https://www.geeksforgeeks.org/computer-science-fundamentals/introduction-to-programming-languages/>
2. <https://openresources.co.uk/tools/string-functions/>
3. <https://www.wscubetech.com/resources/python/tuples>
4. <https://www.wscubetech.com/resources/python/nested-loops>
5. <https://docs.python.org/3/library/io.html>
6. <https://www.sevenmentor.com/exception-handling-in-python>

MAPPING

CO \ PSO	PSO1	PSO 2	PSO 3	PSO 4	PSO 5
CO1	H	H	M	H	H
CO2	S	M	H	H	H
CO3	M	S	S	M	M
CO4	M	S	S	M	M
CO5	M	H	H	H	M
S – Strong		H – High	M – Medium		L – Low

Content prepared by (Based on Inputs)	
Signature of the Course in-charge (Dr. L. kathirvel Kumaran)	Signature of the HOD (Dr. R.Sathish kumar)

Programme Code:08	Program name: PG Diploma in Bioinformatics		
	Core Practical III		
Batch : 2026-2027	Total Hours 15	Credits 1	Employability/ Skill Development

COURSE OBJECTIVES

- To explain basic concepts of chemoinformatics
- To understand the most appropriate method (or methods) to use for a particular problem
- To develop or strengthen skills in working with computational chemistry and bioinformatics applications and databases.

K1 ↑ ↓ K5	CO1	Analyze and validate the structure stability of computationally processed protein model
	CO2	Handle the different file formats of biomolecules
	CO3	Investigate the importance of therapeutic target specificity for particular diseases
	CO4	Design the biological targets and properties of the small molecule under investigation
	CO5	Interpret the lead compound- target interactions

EXPERIMENTS

1. Access and retrieve structure information of small molecules from PubChem
2. Access and retrieve drug information from Drug Bank
3. Perform Structure drawing of small molecules using Chem sketch
4. Predict the ADMET properties of small molecules
5. Predict the biological activity importance for small molecules using Pass prediction
6. Observe the file formats of small molecules (mol and sdf)
7. Convert the file formats using Open Babel
8. Explore Expasy Tools to predict the secondary structure of protein using GOR and Chou-Fasman method.
9. Perform homology based molecule modeling using Swiss-Model
10. Perform ab-initio based molecule modeling using I-Tasser
11. Perform Structure validation- Ramachandran Plot
12. Predict the Active Site for protein models
13. Perform Molecule Docking analysis using Auto Dock
14. Perform Docking analysis using Argus Lab
15. Perform Drug-Target interaction analysis using Pymol

COMPONENTS OF CONTINUOUS INTERNAL ASSESSMENT

Practical		
CIA Practical	25	40
Observation Notebook	10	
Attendance	5	

ESE Practical Examination:

Knowledge Level	Section	Marks	Total
K3 $\updownarrow$ K5	Experiments	50	60
	Record Work	10	

Practical Examination mark breakup:

Knowledge Level	Section
K3 $\updownarrow$ K5	Major Experiments:
	Protocol - 5
	Perform - 10
	Result - 5
	Minor Experiments:
	Protocol - 5
	Perform - 5
	Result - 5
	Q&A - 10
	Viva - 5
	Record work 10

MAPPING

PSO CO	PSO1	PSO 2	PSO 3	PSO 4	PSO 5
CO1	S	H	S	M	S
CO2	H	H	M	H	H
CO3	M	S	H	M	H
CO4	M	S	H	H	M
CO5	H	S	M	S	M

S – Strong

H – High

M – Medium

L – Low

Content prepared by
(Based on Inputs)

Signature of the Course in-charge
(Dr. R.Sathish kumar)

Signature of the HOD
(Dr. R.Sathish kumar)

Programme code: 08		Programme name: B. Sc. Biotechnology	
Project & Viva voce			
Batch: 2026-2027	Total Hours 25	Credits 3	Employability/ Skill Development

Course objectives

1. To understand and differentiate between the wet-lab experimentation and data generation by using computational applications of biological data.
2. To create opportunity to interact with algorithms, tools and data in current scenario.
3. To comprehend the student with a strong emphasis in exploration and navigation of various biological databases to perform the research analysis in bioinformatics tools.
4. To know the concept and types of biological networks in biology to solve real world biological problems.
5. To understand various methods of molecular modeling and their advantages, disadvantages and applications in biology.

Work Instructions

- Each student will be allotted to the teaching faculty in a Department based on random lot
- The topic of the project work will be finalized by the respective guide
- Monitoring of the progression of the project work will be done by the respective guides on a continuous basis
- Every student will subject himself or herself to a mid-review on project work progression on a date fixed by the Department
- The student shall submit the consolidated project work report in the format prescribed by the Department by the end of the End semester or a date intimated by the authorities
- The guide and the student shall ensure maximum integrity and shall not go astray in any form
- The project work report will be subjected to the end semester examination and will be jointly evaluated by internal examiner and External examiner
- Plagiarism in any form shall not be entertained in the dissertation and if found shall invite necessary disciplinary action on grounds of mal practice

COMPONENTS OF CONTINUOUS INTERNAL ASSESSMENT

Project		
Review	15	20
Regularity	5	

Project work:

Knowledge Level	Section	Marks	Total
K3 ↑ ↓ K5	Project	60	80
	Viva voce	20	

Project mark breakup

Knowledge Level	Section
K3 ↑ ↓ K5	Project Report: Issue identification - 20 Review - 10 Analysis - 10 Recommendation - 10 Report - 10
	Viva Voce: Layout of presentation - 5 Clarity - 5 Defense - 10

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