

# MAR AUGUSTHINOSE COLLEGE RAMAPURAM



DEPARTMENT OF BIOTECHNOLOGY

SCHEME AND SYLLABUS OF  
ADD ON COURSE

**BASIC AND ADVANCED TOOLS IN  
BIOINFORMATICS**

2020

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## **ACKNOWLEDGEMENT**

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## **GUIDE LINES FOR THE CONDUCT OF ADDON COURSE**

### **Introduction**

The UGC directed introduction of addon courses is a step in the right direction and could dispel widespread disillusionment with theory-intensive college education in India. But the success of the initiative depends on the type of institutional leadership and how innovatively and transparently the programs are implemented. A majority in Indian academia agrees that traditional education has to be supplemented with skill-based education to enhance the employability of graduate and post graduate students. The Addon courses aim to provide additional learner centric graded skill oriented technical training, with the primary objective of improving the employability skills of science and technology students.

In accordance with this concept, we introduced an Addon course in Bioinformatics for the graduate and post graduate students of Biotechnology

### **Aim of the Program**

Understanding various databases and softwares and acquire methodological knowledge in them.

Application of this knowledge in a suitable manner in required fields of research, medicine, agriculture, public health, pharma, food and other similar industries.

### **Eligibility for Admissions**

All UG and PG students of Biotechnology department. The number of intakes to one batch of the course will be limited to 30. Preference will be given to final year students. The course can be offered only if there are at least 5 students opting for it.

**Medium of Instruction:** English.

### **Duration**

Addon course is conducted annually. The duration of addon course is 60 hours in which 30 hrs. for theory and 30 hrs. for practical/experiential learning activities and the course can have a maximum of three hours a day. The addon course will be offered beyond the usual class hours and days of the college. The addon course will be a blend of theory classes / experimental learning / project-based learning / activity-based learning.

# **BASIC AND ADVANCED TOOLS IN BIOINFORMATICS**

## **– SYLLABUS**

**TOTAL HOURS OF INSTRUCTIONS: 60 HOURS**

### **Course Outcomes (CO)**

**CO1.** Students acquire the basic knowledge about the interdisciplinary field of bioinformatics, databases, applications and careers in bioinformatics.

**CO2.** Become able to use the basic applications of various protein structure databases, tools and protein sequence analysis.

**CO3.** Acquire the knowledge of DNA databases and its basic tools and applications.

**CO4.** Acquire the knowledge of sequence alignments, phylogeny construction, modelling, primer designing, drug designing, docking and in the use of various visualization tools.

**CO5.** Become able to use the basic applications of different databases and tools and to conduct the basic analysis of DNA and proteins.

### **Module I: 3Hrs.**

Introduction to bioinformatics, Careers in bioinformatics, Important biological databases, Applications of bioinformatics.

### **Module II: 8 Hrs.**

Protein structure and function prediction, protein sequence databases and analysis, sequence alignment, structural classification, stabilizing residues, protein folding rates, binding free energy and site prediction. Domains in protein sequence.

### **Module III: 5 Hrs.**

DNA sequence analysis, Gene prediction, DNA databases, PAM matrix, BLOSSUM, Global and local alignment, ORF prediction. BLAST and FASTA: features and score.

### **Module IV: 7 Hrs.**

Multiple sequence alignment, UPGMA, Phylogenetic tree, Homology modeling, Molecular modeling, Ligand designing, Conservation score.

### **Module IV: 7 Hrs.**

Computational biology, Computer aided drug design, docking, screening, Primer designing, Development of algorithms, visualization tools, QSAR, ADME toxicity.

## **PRACTICALS 30 Hrs.**

1. Making search for the scientific literature and sequences.
2. Characterization of a Known Gene.
3. Finding out open reading frames (ORF) through NCBI ORF finder.
4. Translating an unknown DNA Sequence.
5. Identifying a gene using BLAST program.
6. Finding Domains in Protein Sequences.
7. Nucleotide BLAST (BLASTn).
8. Protein BLAST (Blastp).
9. Translated BLAST (Blastx).
10. PSI-BLAST (position specific interacted BLAST).
11. Sequence alignment through FASTA.
12. Editing and analysing multiple sequence alignment using Jalview.
13. Making multiple alignment with T-coffee.
14. Performing Online Mendelian Inheritance in Man (OMIM).
15. Bioinformatics Databases (KEGG DRUG, Protein Data Bank (PDB), NCBI, SWISSPROT, EMBL, DDBJ)
16. Tools for the prediction of Secondary Structure of Protein (GOR)
17. Tools for Primer Designing (Primer-BLAST)
18. Phylogenetic Analysis Tools (JaL View, Clustal W)
19. Gene Prediction tools (GenScan, ORF Finder).
20. Tools for the prediction of Motif using profiles and patterns (MOTIFS SCAN, PROSITE, INTERPROSCAN)
21. Tools for ligand designing (Chem Sketch, OpenBabel)
22. Tools for chemical structure representation (ChemDoodle, PyMOL, RasMol)
23. Tools for Homology Modelling (Modeller, I-TASSER, SWISS-MODEL)
24. Tools for binding site prediction (CastP, Pymol)
25. Tools for the prediction of specialized structure of protein (PROTSKALE)
26. Tools for the prediction of physical and chemical properties of protein (Protein Data Bank).
27. Protein Optimization & Energy Minimization (SwissPDBViewer)
28. Tools for Docking (AutoDock, Glide)
29. Tools for screening. (Pharmer, REDUCE, Balloon, PUMA, AURamol, Blaster, SimDOCK)
30. Tools target prediction. (PatchSearch, HURAKAN, MolScore-Antibiotics, SEA, PASSonline, PPB)
31. Tools for Binding free energy estimation. (included in docking)
32. Docking Visualization (UCSF Chimera)
33. Tools for QSAR. (3-D QSAR)
34. Tools for ADME toxicity. (swiss admet, molinspiration)

## **Evaluation**

1. The add-on course shall be evaluated through an examination, comprising theory and practical, at the end of the course.
2. The duration of examination is two hours.

3.The total marks of the examination shall be 100

4.A committee consisting of the Head of the Department, the course coordinator and a faculty member nominated by the Head of the department shall monitor the evaluation process.

5.The list of students along with the marks and the grades earned may be forwarded to the Principal/Chief Superintendent of Examinations.

6.The Coordinator of the course is responsible for maintaining and processing the records with regard to the course, assessment marks and results.

7.Course certificates will be issued to those students with 75% attendance, timely submission of assignment and a minimum of 50% marks in the qualifying examination.

<b>Pattern of theory question paper</b>				
<b>Part</b>	<b>Total questions</b>	<b>To be answered</b>	<b>Mark of each question</b>	<b>Total</b>
A	8	5	2	<b>10</b>
B	5	2	5	<b>10</b>
C	4	2	10	<b>20</b>
Total	17	9		<b>40</b>

<b>Course Evaluation Scheme</b>			
<b>Sl. No.</b>		<b>Max. mark</b>	<b>Min. for pass</b>
1	Theory examination	40	20
2	Practical	50	25
3	Assignment	10	5
	<b>Total</b>	<b>100</b>	<b>50</b>

<b>Grading system</b>	
<b>Percentage of mark</b>	<b>Grade</b>
90% to 100%	A
80% to 90%	B
70% to 80%	C
60% to 70%	D
50% to 60%	E
<50%	Failed

### Sample Mark list of Addon Course

Sl. No.	Class No.	Name of Student	Theory exam	Practical exam	Assignment	Total	%	Grade
1								
2								
3								
4								
5								
6								
7								
8								
9								
10								
11								
12								
13								
14								
15								

<b>Course Outcome Evaluation</b>		
Course outcome attainments are evaluated by giving practical assignments based on course outcomes, to the students and evaluating the assignments.		
Course outcome	Questions	Evaluation at 4-point scale
Course outcome I		1 – 4
Course outcome II		1 – 4
Course outcome II		1 – 4
Course outcome IV		1 – 4
Course outcome V		1 – 4
<b>Total</b>		000
<b>GPA</b>		Total/5
<b>Grade</b>		