

CERTIFICATE IN BIOINFORMATICS

1. Program Title:	CERTIFICATE IN BIOINFORMATICS
2. Nodal Department	CENTRE FOR BIOINFORMATICS
3a. Program Coordinator:	DR. AJIT KUMAR, Centre for Bioinformatics, MDU
3b. Program Co-Coordinator:	DR. MEHAK DANGI, Centre for Bioinformatics, MDU
4. Collaborating Departments within the University:	NIL
5. In partnership: Industry/Institutional/ other Department /s, None	NONE (At present); Planned for industrial partnership in future.
6. Program Description	The course gives an added value to the professionals of biological sciences research both academic level and at industry level. The jobs are available at scientist level in pharma industries, vaccine development, clinical research projects, academic research, etc.
7a. Program Objectives	<ol style="list-style-type: none">1. To introduce the emerging discipline of bioinformatics to students/working professionals of life sciences.2. To make an appreciation of computational and biological sciences, in particular, the terminology employed in both field and is essential for those working at such an interface.3. To cover the commercial and academic perspectives on bioinformatics.4. To learn the impact of bioinformatics on the methodologies used in biological sciences, complex and extensive public and private biological information sources to anticipate a deep change in methods for finding knowledge in the life sciences.5. To provide trained and skilled professionals that are required in this field and in the industry.
7b. Program Specific Outcomes	<ol style="list-style-type: none">1. A good understanding of bioinformatics as an emerging discipline of life sciences.2. Acquisition of commercial and academic perspectives on bioinformatics.3. Understanding the impact of bioinformatics on the methodologies used in biological sciences.4. Skilled life science manpower with an edge of Bioinformatics.5. A special group of manpower serving as bridge between life sciences and IT research.
8. Duration	6 Months

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9. Target Group	The course is designed for graduates pursuing postgraduates or Ph.D. and those working in industry / academics and is scheduled on weekends only.				
10. Eligibility	Any of the following (minimum 50% marks required in qualifying examination): MBBS / B.D.S. / BAMS / B.H.M.S / B.Pharmacy / B.Tech-Biotech / BVSC / B.Sc. (Nursing) / M.Sc./ M.Pharm/ B.Sc. (with minimum one year relevant industry/ academic research work experience). Note: Any candidate pursuing a regular course in M.D. University, Rohtak or any other University of India, may also co-opt for this course along with their regular course.				
11. Timing: Weekend/Evening/ Daytime	Weekend				
12. Online/Offline/Blend of the two/Content sharing and online/Any other (please specify)	Blend of Online Content sharing and weekend Online/Offline classes.				
13. Assessment and Evaluation mode	Students will be evaluated through periodic internal examination, evaluation of assignment and project work. At the end of the course, students will appear for final examination conducted by Centre for Bioinformatics, M.D. University, Rohtak. The students will be awarded as per absolute grading system, detailed in detail at Annexure I.				
14. Fee structure	Rs. 6,000/-				
15. Any other	Intake: 20 Seats				
SEAT METRICS					
	STATE QUOTA				
HOGC	EWS	BC-A	BC-B	SC	PH
07	01	03	02	03	01

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Annexure I

Program objectives:

The course aims to give an added value to the professionals of biological sciences research both at academic level and industry level in the areas like pharma industries, vaccine development, clinical research projects, academic research, etc.

Course syllabus outline & Scheme of examination

S.No.	Course code	Course title	Internal evaluation	End term evaluation	Credits	Total marks
1.	20CPB11C1	Basics of bioinformatics	20	80	4	100
2	20CPB11C2	Genomics & Proteomics	20	80	4	100
3	20CPB11C3	Structural bioinformatics	20	80	4	100
4	20CPB11C4	Project work	--	200	8	200
Total			60	440	20	500

- **Projects:** Each student will select the topic for his/her project within eight weeks of joining the course. Thus the projects can be taken by a group of students (not more than 5). Students will send their proposal to the Course Coordinator/Co-coordinator, who will help to nominate the guides. The project should involve about 10 days of research/field work.

- **Note:** This being a post graduate certificate course, students are expected to gain knowledge through interaction with the faculty, use of library /internet and shared E- course material.

- **Evaluation and Examination**

Students will be evaluated through periodic internal examination, evaluation of assignment and project work. At the end of the course students will appear for final examination conducted by Centre for Bioinformatics, M.D. University, Rohtak.

The students will be awarded as per absolute grading system, detailed below:

Interval of Marks	Grade	Grade Points
> or = 80 but <or =100	O (Outstanding)	10
> or = 70 but <80	A+(Excellent)	9
> or = 65 but <70	A (Very Good)	8
> or = 55 but <60	B+ (Good)	7
> or = 50 but <55	B (Above Average)	6
> or = 45 but <50	C (Average)	5
> or = 40 but <45	P (Pass)	4
Less than 40	F (Fail)	0
	Ab (Absent)	0

Note: A student obtaining Grade F shall be considered failed and will be required to reappear in the examination.

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Program Name	Certificate in Bioinformatics	Program Code	CPB
Course Name	Basics of Bioinformatics	Course Code	20CPB11C1
Credits	4 [2 : 1 : 1 :: L : P : T]	No. of hours/Week	4
Duration of End term examination	3 Hours	Max. marks	100

Note: Nine questions are to be set in all and the candidates are required to attempt five questions including compulsory question. Question no. I is compulsory covering the whole syllabus. Out of remaining eight questions, two questions are to be set from each unit. Candidate is required to attempt four questions, selecting one question from each unit.

Course Objectives:

1. To learn the world of Bioinformatics and its evolution.
2. Assess the, different types of biological data and bioinformatics resources.
3. Assess and explain the tools and techniques of analyzing DNA and protein sequences.
4. Discuss the basic principles and applications of pharmacogenomics.
5. Utilize the different analysis packages available for different computational jobs.

Course Outcomes:

1. Understanding of bioinformatics and data mining concepts.
2. Learning of major bioinformatics resources available.
3. Learning of basic algorithms of sequence alignments of bioinformatics.
4. Learning of bioinformatics tools for sequence alignments.
5. Acquisition of basic bioinformatics skills.

UNIT I

Overview of Bioinformatics and Information Technology

History, Scope and application, Internet and World Wide Web; Generation of computers; Concept of Networking; Introduction to Data Mining; Application of data mining in Bioinformatics.

UNIT II

Bioinformatics Resources

Biological databases, Basic classification – Sequence & Structure; Generalized & Specialized; Primary & Secondary, with example databases (Genbank, EMBL, DDBJ, INSDC, Swiss Prot, PIR, PDB, NDB, BLOCKS, Pfam, ProSITE, etc.); Literature databases.

UNIT III

Bioinformatics techniques

Sequence comparison and alignment; Local and Global Alignment – (Smith Waterman Algorithm; Needleman Wunsch Algorithm); Concept of Gap, Gap Penalty & Scoring Matrices (PAM, BLOSSUM); Dot Plot Analysis.

UNIT IV

Bioinformatics tools

Information retrieval system (Entrez, SRS); Sequence alignment tools (BLAST, FASTA, CLUSTAL-W/X, MUSCLE, TCOFFEE), Variants of BLAST (BLASTn, BLASTp, PSI-BLAST, PHI-BLAST, etc)

Suggested readings:

- Mount, D. W. (2004). Sequence and genome analysis. Bioinformatics: Cold Spring Harbour Laboratory Press: Cold Spring Harbour, 2.
- Selzer, P. M., Marhöfer, R. J., & Rohwer, A. (2008). Applied bioinformatics. An introduction–Springer, Verlag, Berlin, Heidelberg, Germany, 260.

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- Rastogi S. C. (2014) Bioinformatics: Methods and Applications - Genomics, Proteomics and Drug Discovery: PHI Learning.
- Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press.
- Miller, W. (2006). An Introduction to Bioinformatics Algorithms.

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Program Name	Certificate in Bioinformatics	Program Code	CPB
Course Name	Genomics and Proteomics	Course Code	20CPB11C2
Credits	4 [2 : 1 : 1 :: L : P : T]	No. of hours/Week	4
Duration of End term examination	3 Hours	Max. marks	100
<p>Note: Nine questions are to be set in all and the candidates are required to attempt five questions including compulsory question. Question no. I is compulsory covering the whole syllabus. Out of remaining eight questions, two questions are to be set from each unit. Candidate is required to attempt four questions, selecting one question from each unit.</p>			
<p>Course Objectives:</p> <ol style="list-style-type: none"> 1. To learn the world of genomics and tools of genome analysis. 2. To learn different genome projects and Metagenomics. 3. To understand and explain the tools and techniques of proteomics. 4. Discuss the basic principles and applications of functional genomics. 5. Discuss the basic principles and applications of functional proteomics. 			
<p>Course Outcomes:</p> <ol style="list-style-type: none"> 1. Understanding the science of genomics, its tools and applications. 2. Learning of major genome sequencing projects. 3. Learning of protein science and proteomics. 4. Learning of bioinformatics tools for functional analysis of genome. 5. Learning of bioinformatics tools for functional analysis of proteomes. 			
<p>UNIT I Introduction to Genomics Introduction to the concept of genome, gene networks: basic concepts, Prediction of genes, promoters, splice sites, regulatory regions: basic principles, application of methods genome projects. Tools for genome analysis-RFLP, DNA fingerprinting, RAPD, PCR, Linkage and Pedigree analysis-physical and genetic mapping.</p>			
<p>UNIT II Genome sequencing projects Microbes, plants and animals; Accessing and retrieving genome project information from web; Comparative genomics, Identification and classification using molecular markers-16S rRNA typing/sequencing, ESTs and SNPs. Human Genome Project. Large scale genome sequencing strategies, Genome assembly and annotation. Genome databases of Plants, animals and pathogens, Metagenomics: Concept and applications.</p>			
<p>UNIT III Proteomics Concept of proteome, Protein analysis (includes measurement of concentration, amino-acid composition, N-terminal sequencing); 2-D electrophoresis of proteins; Microscale solution isoelectric focusing; Peptide fingerprinting; LC/MS-MS for identification of proteins and modified proteins; MALDI-TOF; SAGE and Differential display proteomics, Protein-protein interactions, Yeast two hybrid system.</p>			
<p>UNIT IV Functional genomics and proteomics Analysis of microarray data; Protein and peptide microarray-based technology; PCR-directed protein in situ arrays; Structural proteomics. Deriving function from sequence, Proteomics in drug discovery and toxicology.</p>			

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Suggested readings:

- Selzer, P. M., Marhöfer, R. J., & Rohwer, A. (2008). Applied bioinformatics. An introduction–Springer, Verlag, Berlin, Heidelberg, Germany, 260.
- Mount, D. W. (2004). Sequence and genome analysis. Bioinformatics: Cold Spring Harbour Laboratory Press: Cold Spring Harbour, 2.
- Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press

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Program Name	Certificate in Bioinformatics	Program Code	CPB
Course Name	Structural Bioinformatics	Course Code	20CPB11C3
Credits	4 [2 : 1 : 1 :: L : P : T]	No. of hours/Week	4
Duration of End term examination	3 Hours	Max. marks	100
<p>Note: Nine questions are to be set in all and the candidates are required to attempt five questions including compulsory question. Question no. I is compulsory covering the whole syllabus. Out of remaining eight questions, two questions are to be set from each unit. Candidate is required to attempt four questions, selecting one question from each unit.</p>			
<p>Course Objectives:</p> <ol style="list-style-type: none"> 1. To learn the structural features of biomolecules. 2. To learn computational tools used in structural biology. 3. To learn different molecular visualization tools. 4. To learn secondary structure prediction methods of proteins. 5. To understand homology modeling tools and methods. 			
<p>Course Outcomes:</p> <ol style="list-style-type: none"> 1. Understanding of bioinformatics and data mining concepts. 2. Learning of major bioinformatics resources available. 3. Learning of basic algorithms of sequence alignments of bioinformatics. 4. Learning of bioinformatics tools for sequence alignments. 5. Acquiring protein modeling skills. 			
<p>UNIT I Macromolecular Structure Conformational Analysis of protein, Forces that determine protein structure, polypeptide chain geometries, Ramachandran Map, potential energy calculations, observed values for rotation angles, structure comparison and alignment. Conformational analysis of nucleic acids and carbohydrates, general characteristics of nucleic acid structure – geometries, glycosidic bond, rotational isomers and ribose puckering - forces stabilizing ordered forms – base pairing, base stacking.</p>			
<p>UNIT II Computational structural biology Overview of molecular modelling - Introduction and challenges; Molecular modelling methods; Conformational searching, Potential energy maps, Ramachandran maps, Ab-initio methods, Semi-empirical methods; Empirical methods, Conformational analysis-Introduction and Methods: Molecular fitting, Energy Minimisation. Molecular dynamics simulations of Bio-macromolecules.</p>			
<p>UNIT III Molecular visualization tools Visualization of tertiary structures, quaternary structures, architectures and topologies of proteins and DNA using molecular visualization softwares such as RasMol, Cn3D, SPDBV, Chime, Mol4D, etc.</p>			
<p>UNIT IV Structure prediction tools and homology modelling Prediction of secondary structures of proteins using at least 5 different methods with analysis and interpretation of the results. Comparison of the performance of the different methods for various classes of proteins. Internet based modeling tools. Prediction of tertiary structures of proteins using Homology Modeling approach: SWISSMODEL, SWISS-PDB Viewer Prediction of tertiary structures of proteins using at least 3 methods for fold recognition along with analysis and interpretation of results. Structure Databases – PDB, NDB, CCD - Structural Classification – SCOP, CATH, FSSP.</p>			

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Suggested readings:

- Gu, J., & Bourne, P. E. (Eds.). (2009). Structural bioinformatics (Vol. 44). John Wiley & Sons.
- Brown, J. B. (Ed.). (2018). Computational Chemogenomics. Humana Press.
- Wei, D., Xu, Q., Zhao, T., & Dai, H. (Eds.). (2015). Advance in structural bioinformatics. Springer.
- Claverie, J. M., & Notredame, C. (2006). Bioinformatics for dummies. John Wiley & Sons.
- Selzer, P. M., Marhöfer, R. J., & Rohwer, A. (2008). Applied bioinformatics. An introduction–Springer, Verlag, Berlin, Heidelberg, Germany, 260.
- Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press

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Program Name	Certificate in Bioinformatics	Program Code	CPB
Course Name	Project Work	Course Code	20CPB11C1
Credits	8 [0 : 8 : 0 : : L : P : T]	No. of hours/Week	4
Duration of End term examination	3 Hours	Max. marks	200
Course Objectives: <ol style="list-style-type: none">1. To conceptualize a small project on a relevant topic.2. To plan and execute the project in a time bound manner.3. To learn scientific report writing skills.			
Course Outcomes: <ol style="list-style-type: none">1. The course will help to understand the relevance of bioinformatics in biological research.2. The course will help to learn and apply different bioinformatics tools in solving biological problems.			
<p>Each student will select the topic for his/her project within eight weeks of joining the course. Thus the projects can be taken by a group of students (not more than 5). Students will send their proposal to the Course Coordinator/Co-coordinator, who will help to nominate/select the project guides. The project should involve about 10 days of research/field work and will be evaluated by external examiner(s).</p>			