| Course | Discipline Specific Elective |
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| Semester | V |
| Paper Number | MBTDS5012T & MBTDS5012P |
| Paper Title | BIOINFORMATICS |
| No. of Credits | 6 |
| Theory/Composite | Composite |
| No. of periods assigned | 4 Theory + 3 Practical |
| Course description/objective | 1. Students will be introduced to the principles of Bioinformatics.<br>. Students will be provided with an essence of the different tools and aspectsof Bioinformatics.<br>. An overview of protein information sources, protein tertiary structure prediction, biological databases, searching of databases andinformation retrieval would be provided.<br>. Students would be introduced to data generating techniques andbioinformatics problems.<br>. Students would be familiarized with techniques in bioinformaticsby means of project/ computer based practicals. |
| Syllabus | **Theory**<br>**Module A: Bioinformatics-I (40marks)**<br><br>**UNIT I:** History of Bioinformatics. The notion of Homology. Sequence Information Sources, EMBL, GENBANK, Entrez, Unigene, Annotated databases; Sequence format; Types of Biological Databases & Information Retrieval. Global & Local alignment: Overview of Needleman–Wunsch & Smith–Waterman methods. Mutation/Substitution Matrices: PAM250 & BLOSUM62, Pairwise Sequence Alignments and Multiple Sequence Alignment, Phylogenetic Analysis.<br>**UNIT II:** Searching Databases: Sequence Retrieval System (SRS), Entrez, Sequence Similarity Searches-BLAST, FASTA, Exposure to the methods of Data Submission. Characteristics of Protein-protein, Protein-DNA and Protein-RNA interaction surfaces. Solvent- Accessible Surface area of Protein: SASA, interactive tool for the exploration of macromolecular interfaces: PISA.<br>**UNIT III:** Protein Information Sources, PDB, SWISSPROT, TREMBL; Protein Structural Classification and Visualization. Protein Tertiary Structure Prediction - Homology Modeling, Threading and Fold Recognition, Overview of MD Simulations and applications. RNA structure prediction; Circular plot. Dot plot analysis of protein and RNA sequences. |

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| | site directed mutagenesis and enzyme engineering, Immobilized enzyme reactors. Application of immobilized and soluble enzyme in health and industry.<br><br>**No. of Classes:** 3 Classes / week<br><br>**Module B: Bioinformatics-II (10 marks)**<br><br>**UNIT V: Introduction of Data Generating Techniques and Bioinformatics problem posed by them:** Restriction Digestion, Blots, PCR and Primer designing; Microarrays; Next-generation sequencing; Genome Annotation: Pattern and repeat finding; Gene identification tools.<br><br>**No. of Classes:** 1 Class / week<br><br>**Practical**<br><br>Bioinformatics project:<br>1. Retrieval of information of a protein of interest,<br>2. Sequence similarity searches, Sequence analysis, Homologymodeling of protein,<br>3. Structure analysis using PyMol, Interactomics<br>4. Gene analysis and primer designing. |
| Readings | 1. Biochemistry – Stryer.<br>2. Structural Bioinformatics and Genome Analysis – D.W. Mount.<br>3. Principles of Gene Manipulation & genomics-Primrose &Twyman.<br>4. Relevant scientific literature. |
| Evaluation | Theory: Continuous Internal Assessment: 10 marksEnd-Semester Theory Examination: 50 marks<br><br>Practical: Continuous Internal Assessment: 32 marksEnd-Semester Examination: 8 marks |
| Paper Structure for End SemTheory | Module A (40 marks)<br>Bioinformatics-I (20 marks)<br>One Compulsory question of 6 marks comprising objective problemsAny two from three questions each carrying 7 marks. No part question will be of more than 4 marks.Structural Enzymology (20 marks)<br>Any two from three questions each carrying 10 marks.No part question will be of more than 5 marks.<br>Module B (10 Marks)<br>1 Compulsory question of 5 marks.<br>Any two out of three questions (2 x 2.5= 5 marks) |