### **Course Number and Name** BBM054 - Bio Informatics **Credits and Contact Hours** 3 and 45 **Course Coordinator's Name** Dr T.Jayalakshmi **Text Books and References** Text book: 1. R.D.Lele "Computer in Medicine" Tata McGraw Hill, Newyork, 1999. References: 1. S.K.Chauhan "PC Organisation", S.K.Kataria and Sons, Delhi 2000. 2. Harold Sackamn "Bio Medical Information Technology", Academic Press, New York. 3.https://www.lehigh.edu/~inbios21/PDF/Fall2008/Lopresti\_11142008.pdf **Course Description** To introduce Bioinformatics-Elementary commands and Protocols, ftp, telnet, http. Primer on information theory **Prerequisites Co-requisites** Biology for Engineers. NII required, elective, or selected elective (as per Table 5-1) Selected elective **Course Outcomes (COs)** CO1: To learn bioinformatics and the protocols. CO2: To learn Strings-Edit distances two strings-string similarity local alignment gapsparametric sequence alignments. CO3: To have a clear view on Amino acid substitution matrices PAM and BLOSSUM. CO4: To learn Ultrasonic trees-parsimony-Ultrametric problem-perfect phylogenyphylogenetic alignment. CO5: To DNA Mapping and sequencing-Map alignment-Large scale sequencing. CO6: DNA Mapping and sequencing-Map alignment-Large scale sequencing and alignment. Student Outcomes (SOs) from Criterion 3 covered by this Course COs/SOs i а h k q CO<sub>1</sub> Η CO<sub>2</sub> Н Н M CO3 Н Н M CO<sub>4</sub> Н Н Μ CO<sub>5</sub> Н Η

CO6

# **List of Topics Covered**

#### UNIT – I BIOINFORMATICS

9

Scope of Bioinformatics-Elementary commands and Protocols, ftp, telnet, http.Primer on information theory.

#### UNIT – II SEQUENCING ALIGNMENT AND DYNAMIC PROGRAMMING

9

Introduction-Strings-Edit distance two strings-string similarity local alignment gaps-parametric sequence alignments-suboptimal alignments-multiple alignment-common multiple alignment methods.

#### UNIT – III SEQUENCE DATABASE AND THEIR USE

9

Introduction to databases-database search-Algorithms issues in database search-sequence database searchFASTA-BLAST-Amino acid substitution matrices PAM and BLOSSUM.

#### **UNIT - IV EVOLUTIONARY TREES AND PHYLOGENY**

9

Ultrasonic trees-parsimony-Ultrametric problem-perfect phylogeny-phylogenetic alignment-connection between multiple alignment and tree construction.

## **UNIT - V SPECIAL TOPICS IN BIOINFORMATICS**

9

DNA Mapping and sequencing-Map alignment-Large scale sequencing and alignment-Shotgun-DNA sequencing-Sequence assembly-Gene predictions-Molecular predictions with DNA strings.