(Following Paper ID and Roll No. to be filled in your Answer Books)

Paper ID : 2012353 Roll No.

B.TECH

Regular Theory Examination (Odd Sem-V), 2016-17

BIOINFORMATICS - I

Time : 3 Hours *Max. Marks : 100*

SECTION - A

Note : Attempt all the questions. (10×2=20)

1. a) Define Orthologus.

b) What is Pubmed?

c) What is SEQUIN?

d) Define EMBL.

e) What do you know about Global alignment?

f) What is Bootstrap Value?

g) What is difference between homologus and paralogus?

h) What are motifs?

i) What is Empherical significance testing?

j) What is CDS?

SECTION - B

Note : Attempt any three questions. (3×10=30)

1. List out the procedures and the softwares you would need to use to get a protein tertiary structure, if a nucleotide sequence is given to you.

2. Discuss the role of bioinformatics in drug discovery and drug designing.

3. List out the differences between distance based, maximum parsimony and maximum likelihood methods.

4. Write a note on methods available for detecting functional sites in the DNA.

5. Describe structure file formats and explain PDB flat files in details?

SECTION - C

Note : Attempt all questions (5×10=50)

1. What are the purposes of performing a similarity search? What are the difference between FASTA and BLAST programme?

2. What is Phylogenetic analysis? Discuss different methods of phylogenetic tree construction.

3. Discuss multiple sequence alignment with an example. Give its applications.

4. What are the basic assumptions in molecular phylogeny? List out all the advantages of using molecular data to infer evolutionary relationship.

5. Discuss the applications and challenges in Bioinformatics in Agriculture.

OR

What are the major steps involved in drug discovery process follow identification of the biological target? Explain.