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Total Number of Pages:2

B.TECH
PCBT4304

6th Semester Regular / Back Examination 2016-17

BIOINFORMATICS

BRANCH: BIOTECHNOLOGY

Time: 3 Hours

Max Marks: 70

Q.CODE: Z525

**Answer Question No.1 which is compulsory and any five from the rest.
The figures in the right hand margin indicate marks.**

- Q1 Answer the following: (2 x 10)**
- a) What are database retrieval tools and what are its uses?
 - b) Write the advantages of SWISS PORT database?
 - c) To identify a weak but biologically relevant sequence similarities one should perform _____.
 - d) In bioinformatics a methods for solving particular computational problem is known as _____.
 - e) In how many ways two sequences can be aligned and compared?
 - f) Write the full form of EMBL and KEGG? Write its uses?
 - g) How will you differentiate between directed and random sequencing?
 - h) What is PIR? Write any two of its data bases?
 - i) What is the tool used for identification of motifs?
 - j) What does abbreviation for NCBI stands for and why is this site important in bioinformatics?
- Q2 Write short notes on**
- a) Basic algorithms for prediction of ORF. (5)
 - b) Docking methods. (5)
- Q3 Classify and explain major databases in bioinformatics giving examples of each database. (10)**
- Q4 What is structure visualization? Explain the various rendering tools in structure visualization. (2+8)**

- Q5** (a) What is Homology Modeling? Explain its use in protein structure prediction? (5)
(b) Justify BLAST is tool for homology searching? (5)
- Q6** (a) Explain the drug design process for a known and unknown target. (5)
(b) Distinguish global and local alignment with reference to alignment algorithm? (5)
- Q7** (a) Write a notes on retrieving microbial and viral genome information (5)
(b) Describe protein classification based on SCOP database? (5)
- Q8** Write short notes on (*any two*) (5 x 2)
(a) UTRs Sequence variation and molecular evolution
(b) FASTA tool
(c) CATH
(d) QSAR analysis