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Total Number of Pages:2

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**M.TECH
P2BTBCO2**

2nd Semester Regular Examination – 2016-17

APPLIED BIOINFORMATICS

BRANCH: BIOTECHNOLOGY

Time: 3 Hours

Max Marks: 100

Q.CODE:Z475

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

- Q1 **Answer the following:** (2 x 10)
- a) What are the various parameters used *in-silico* gene finding approach?
 - b) If you obtain a novel sequence, which database searches would you perform first and why?
 - c) Boot-strap analysis?
 - d) What does NCBI stands for? Within NCBI the SNP is_____.
 - e)
 - f) What is a Dot matrix? When is it used?
 - g)
 - h) Name two protein databases. What is cross-referencing in database.
 - i) What is ReadSeq?
 - j) What is T-COFFEE ? Mention its important function?
- Q2 (a) Write in detail on RNA secondary structure prediction methods. (10)
- b) How to predict secondary structure of trans-membrane proteins. (10)
- Q3 (a) Which database deals with structural and functional annotation of protein sequences? Elaborate briefly on this database. (10)
- b) (10)
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- Q4 (a) Explain briefly about the primary sequence databases of nucleic acids. (10)
- b) (10)
- Phylogenetic tree
- construction and analysis?

- Q5 (a) What is progressive alignment? Describe multiple sequence alignment giving emphasis on CLUSTAL-W. (10)
- b) algorithm (10)
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- Q6 (a) What do you understand by BLAST family search tool? Explain briefly about PSI-BLAST and PHI-BLAST. (10)
- b) What are derived databases of patterns? Write notes on Prints-S and Pfam. (10)
- Q7 (a) Write notes on different steps involved drug discovery. Describe about SRS and QSAR technique in drug design. (10)
- b) Write notes dendrogram and its application. (10)