

SARDAR PATEL UNIVERSITY

M.Sc. IVth semester Biochemistry Examination

Monday, 11<sup>th</sup> April, 2016

Time: 2.30 p.m. to 5.30 p.m.

PS 04 EBIC09 Bioinformatics

[105]

*Note: Numbers in parenthesis indicate marks*

Max marks: 70

(08)

Q.1 Choose the correct options for the following questions.

1. GenBank, the nucleic acid databank is maintained by
  - (a) Brookhaven Laboratory
  - (b) DNA Database of Japan (DDBJ)
  - (c) European Molecular Biology Laboratory (EMBL)
  - (d) National Centre for Biotechnology Information (NCBI)
  
2. Clustal W is
  - (a) Multiple sequences alignment tool
  - (b) Protein secondary structure predicting tool
  - (c) Data retrieving tool
  - (d) Nucleic acid sequence analysis tool
  
3. Each node in a phylogenetic tree is called
  - (a) a taxonomic unit
  - (b) a cladogram
  - (c) a dendrogram
  - (d) a common ancestor
  
4. An example of homology and similarity tool is
 

(a) EMBOSS	(b) Pfam	(c) BLAST	(d) None of the above
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5. The information retrieval tool of NCBI is
 

(a) ENTREZ	(b) TAG	(c) Sequin	(d) Text search
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6. Which of the following are secondary databases?
 

(a) Pfam	(b) CATH	(c) KEGG	(d) all of the above
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7. Which of these is not a homolog
 

(a) Ortholog	(b) Analog	(c) Paralog	(d) All are homologs
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8. Which of the following is a nucleotide sequence database
 

(a) EMBL	(b) SWISS PROT	(c) TREMBL	(d) None of the above
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Q.2 Answer **any seven** of the following questions in brief:

(14 marks)

1. Define Bioinformatics.
2. Which is the most common file format used for BLAST?
3. Name any database of structural classification of proteins.
4. Why is it necessary to use bioinformatics to store, organize, retrieve and analyze biological data?
5. How can we find whether any two genes share common evolutionary history or not?
6. Differentiate between eukaryotic and prokaryotic gene structure.
7. Differentiate between rooted and unrooted phylogenetic tree.
8. What is an accession number of a sequence?
9. Name any two software tools useful for multiple sequence alignment.

Q3 A. Explain any six applications of Bioinformatics. (06)

B. List various file formats and explain any two of them. (06)

OR

Q3 B. What is NCBI? Write a note on data and various resources made available by NCBI. (06)

Q4 A. What is sequence alignment? Give an account on pair wise sequence alignment. (06)

B. Explain Primary and Secondary databases. (06)

OR

Q4 B. Explain the concept of Gaps in alignment and 'Gap Penalty' in sequence alignment. (06)

Q5 A Explain the prokaryotic gene prediction. (06)

B. (i) Why different scoring matrices are used for nucleotide and protein sequence alignment? (03)

(ii) Differentiate between local alignment and global alignment. (03)

OR

B. What is gene annotation? What are the various approaches for gene annotation? (06)

Q6 A What is phylogenetic tree? Name the software/s to construct phylogenetic tree and explain the importance of phylogenetic tree construction. (06)

B What is comparative genomics? Explain the problem of scale and complexity of genome. (06)

OR

B What is proteomics? Explain how large scale screenings of proteins of a cell are carried out. (06)