

[A-88]

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Sardar Patel University  
BSc Examination -Semester 6  
US06CGEN04: Bioinformatics  
Monday 4<sup>th</sup> April, 2016  
2:30 pm to 5:30 pm

Note:

Total Marks: 70

1. Figures to the right indicate marks.
2. Draw neat and labelled diagram, wherever necessary.

**Q.1 Multiple choice questions**

[10]

- 1 The main circuit board in a computer is called the \_\_\_\_\_.  
a. RAM                      b. dongle                      c. motherboard                      d. power supply unit
- 2 If a Windows program has become unresponsive, which keys do you press to open the Task Manager?  
a. Shift, Tab, Enter                      b. Home, Control, Shift  
c. Space bar, F1, Tab                      d. Control, Alt, Delete
- 3 GenBank and SWISSPORT are example of \_\_\_\_\_.  
a. primary database                      b. secondary database  
c. composite database                      d. none of these
- 4 PDB is \_\_\_\_\_.  
a. Primary database for macromolecules  
b. can be determined by gel electrophoresis  
c. composite database  
d. database for three dimensional structure of biological macromolecule
- 5 Uppermost bar showing the name of the application is called \_\_\_\_\_.  
a. status bar                      b. menu bar                      c. task bar                      d. title bar
- 6 Continuous set of spaces in the sequence is \_\_\_\_\_.  
a. Match                      b. Gaps                      c. Mismatch                      d. None of these
- 7 Alignment method suitable for aligning closely related sequence is \_\_\_\_\_.  
a. multiple sequence alignment                      b. pair wise alignment  
c. global alignment                      d. local alignment
- 8 BLAST X program is used for \_\_\_\_\_.  
a. translate protein sequence                      b. translate DNA database  
c. translate input sequence                      d. none of these
- 9 Sequence of amino acids in the polypeptide chains is known as the \_\_\_\_\_ structure of a protein.  
a. Primary                      b. Secondary                      c. Tertiary                      d. Quaternary
- 10 A series of codons from a single strand of DNA sequence which can be "read" in three different ways, depending on whether one starts at the first nucleotide position, the second or third \_\_\_\_\_.  
a. Reading Frame (RF)                      b. Alternative Splicing  
c. Open Reading Frame (ORF)                      d. mRNA Processing

**Q.2 Attempt any Ten**

[20]

- 1 Difference between RAM and ROM.
- 2 Briefly explain the ways to copy past text in word processor.
- 3 Why Unix is safer to virus threats than windows?
- 4 What is Bioinformatics?

- 5 Briefly explain the role of internet in growth of bioinformatics.
- 6 Differentiate primary and secondary database.
- 7 Briefly describe applications of FASTA software package.
- 8 What is gap penalty?
- 9 What is ORF?
- 10 What is promoter?
- 11 Enlist and briefly explain protein tertiary structure prediction methods.
- 12 What is alpha helix and beta sheet?

**Q.3** Briefly explain the generations of computers. Draw a labelled diagram of computer with peripherals. [10]

OR

A What is OS? Give a comparative account of Windows and Unix. [05]

B Write a short note on the applications of MS office. [05]

**Q.4** What is database? What are biological database and their types? Narrate the NCBI model (architecture) in maintenance of biological data. [10]

OR

A Narrate the goal, scope and enlist the applications of bioinformatics. [06]

B Write short note on Genbank. [04]

**Q.5** A Write a detail note on BLAST. [05]

B Compare freeware and open source software. [05]

OR

A Write a detailed note on multiple sequence alignment and their applications. [06]

B Differentiate local alignment and global alignment with example. [04]

**Q.6** What is gene? Compare gene organization in prokaryotes and eukaryotes. [10]  
Narrate the methods used for gene prediction in prokaryotes.

OR

Briefly describe the level of organization in proteins. Enlist the algorithms used in secondary structure prediction and explain any one in detail. [10]

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