E 1220 (Pages : 2) Reg. No.....

Name.....

B.Sc. DEGREE (C.B.C.S.S.) EXAMINATION, MARCH 2018

Sixth Semester

Choice Based Core Course – BIOINFORMATICS

(For B.Sc. Biotechnology)

[2013 Admission onwards]

Time : Three Hours Maximum Marks : 80

Part A

Answer **all** *the following questions.*

1 *mark each.*

1. What is PHYLIP?
2. Name a database for literature search.
3. Define Sequence alignment.
4. What is the number of base pairs in the human genome?
5. Define Pharmacogenomics.
6. Name the scientist who developed BLAST.
7. State the use of Needleman-Wansch algorithm.
8. Name a protein sequence database.
9. What is a DNA chip?
10. Expand PERL.

(10 × 1 = 10)

Part B

Answer any **eight** *of the following.*

2 *marks each.*

11. What is multiple sequence alignment?
12. What are the different levels of protein structure?
13. How would you recognise highly similar sequence in a dot matrix?
14. What is gap penalty?
15. Give any *two* advantages of PERL programming in bioinformatics.
16. What are ORF?

Turn over

17. Define Transcriptomics.
18. Expand BLAST. What is its use?
19. Give the use of PDB in drug designing.
20. What is a database? Cite an example.
21. How can you submit a new sequence to a database?
22. What are secondary databases? Give an example.

(8 × 2 = 16)

Part C

Answer any **six** *of the following.*

4 *marks each.*

23. What are the features of a molecular visualization tool? Cite an example.
24. Write the principle of a DNA microarray hybridization with the help of a labelled diagram.
25. What is the difference between local and global sequence alignment?
26. Give the major differences between Structural genomics and Functional genomics.
27. What are the career opportunities in bioinformatics?
28. What is the use of dot matrix analysis?
29. Give the significance of personalised medicine.
30. How is NCBI so important in Bioinformatics?
31. Differentiate between Metabolomics and Transciptomics. Why is proteome always larger than the genome?

(6 × 4 = 24)

Part D

Answer any **two** *of the following*

15 *marks each.*

32. What are biological databases? Explain their uses and importance with examples.
33. What is meant by molecular phylogeny? List the tools used for it.
34. Define Sequence Alignment. Explain in detail on the various approaches and tools for sequence alignment.
35. What are the strategies adopted to identify structural genes in a DNA sequence?

(2 × 15 = 30)