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3702

Reg. No. :

Name :

Second Semester M.Sc. (CSS) Degree Examination, June 2009

Branch : Computational Biology

COB 522 : COMPUTATIONAL GENOMICS

Time : 3 Hours

Max. Marks : 60

PART – A

Answer **all** questions. **Each** carries **two** marks.

1. State the central dogma of molecular biology.
2. Give a model of eukaryotic gene structure.
3. What is an open reading frame ?
4. What are the differences between RNA and DNA ?
5. Explain the importance of E-value in BLAST ?
6. Discuss the difference between primary and secondary biological databases ?
7. What is pseudo gene ?
8. Explain the need for DNA amplification ?
9. What is the use of PAM matrices ?
10. Discuss dot plot.

(10×2=20 Marks)

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PART – B

Answer **any eight** questions. **Each** carries **5** marks.

11. Explain the Needleman-Wunch algorithm.
12. Find the optimal local alignment for
Seq 1 : ATCTAT
Seq 2 : TCCTA
with Match +1, Mismatch – 1, Gap – 1
13. Explain genetic linkage map.
14. Write notes on :
a) promoter b) intron c) codon.
15. Explain gel electrophoresis.
16. How a fresh sequence can be submitted to GENBANK ?
17. Explain polymerase chain reaction (PCR).
18. Discuss “FASTA” format with a suitable example.
19. Explain DNA finger printing.
20. Write a note on scoring matrices.

(8×5=40 Marks)
