Exam. Code : 206601 Subject Code : 4598

M.Sc. Bio-Informatics Semester—I BI-515 : INTRODUCTION TO BIOINFORMATICS AND BIOLOGICAL DATABASES

Time Allowed—3 Hours] [Maximum Marks—75

Note :— Section-A is compulsory. Each part is of 1.5 marks. Attempt *one* question from each unit of Section-B. Each question is of 12 marks.

SECTION-A

This section is compulsory.

- 1. Answer the following (at least in 4 lines) :
 - (a) A charge is placed through the gel and the DNA moves towards the positive end, explain why this happens ?
 - (b) Explain similarity, identity, and homology in context of protein sequences.
 - (c) Give difference between codon and anticodon.
 - (d) Explain why restriction enzymes that produce sticky ends are more desirable when trying to insert a new DNA sequence into a genome ?
 - (e) Why curated database is supposed to be more useful than non-curated one ?

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- (f) Difference and similarity between bankit and sequin.
- (g) What role EST played in genomic research ?
- (h) Explain the use of LinkOut.
- (i) If you had 1,500 base pair pieces of random DNA and you wanted to know how many of them had homology to known genes, what would you do to determine that ?
- (j) Describe the difference between pattern and motif. $10 \times 1.5 = 15$

SECTION-B

Answer one question from each unit.

UNIT-I

- 2. (a) Explain central dogma. Explain its importance in bioinformatics.
 - (b) Describe ORFs and their significance in genes in genome. What do you understand by six frame translation ? 6+6=12
- 3. (a) Illuminate the concept of gene. Explain the different information that can be retrieved from genes.
 - (b) What are different notations used in homology. Describe significance of homology.
 - (c) The presence of splice variants makes proteomics more complex. Do you agree or disagree with the statement? Why ? $3 \times 4=12$

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2

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UNIT—II

- 4. (a) Describe the steps required to prepare gel DNA samples for performing gel electrophoresis.
 - (b) What are different areas bioinformatics deal with ? Explain the role bioinformatics played in these areas. 6+6=12
- 5. Write an essay entitled *Bioinformatics* and *DNA analysis*. 12

UNIT-III

- 6. (a) Compare and contrast EMBL, DDBJ and GenBank.
 - (b) Give an account on metadata and its application. 6+6=12
- 7. (a) Mention different protein databases and their importance.
 - (b) Write a note on different database retrieval and deposition systems. 6+6=12

UNIT-IV

- 8. (a) Explain the species diversity and genetic diversity. Aren't the two term are synonyms as both actually deals with diversity in genome. Explain whether you agree or disagree with the previous statement and why ?
 - (b) Write a note on Ensemble Genome Project. 9+3=12

3

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- 9. (a) Illustrate different tools used for EST analysis and explain the issue faced during the result interpretation of EST analysis.
 - (b) Write a note on EcoGene. 8+4=12

UNIT-V

- (a) Compare and contrast between motif, blocks, fingerprints, and profiles in context of protein databases.
 - (b) Mention the significance of RNA databases.

8+4=12

100

- 11. (a) Mention the highly annotated protein sequence databases and describe their features.
 - (b) Describe the practical utility of SCOR, miRBase and LIPIDAT. 6+6=12

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