HDQ-003-006505   Seat No. _____

B. Sc. (Bioinformatics) (Sem. V) Examination

November / December – 2017

BI-503 : Transcriptomics & Gene Expression Analysis

Faculty Code : 003

Subject Code : 006505

Time : $2\frac{1}{2}$ Hours]   [Total Marks : **70**

Instructions : (1) All questions are compulsory.

(2) The right side figure indicate total marks of the question.

PART - A

(20 Marks)

1   Name any 2 methods for Quantification of individual transcripts.

2   Which method of EST is used if the sequence similarity is 96%?

3   Name the EST database which is a division of GenBank.

4   _____ was efficient to determine the gene content of an organism without sequencing the entire genome.

5   What was the drawback of Quantification techniques?

6   ESTs may be used to identify gene transcripts, and are instrumental in _____ and in gene sequence determination.

7   The identification of ESTs has proceeded rapidly, with approximately _____ ESTs now available in public databases.

8   Transcriptomes may also be used to infer _____ among individuals.

9   The plant EST database has recently passed the _____ sequence landmark.

10 MicroRNAs are about _____ and usually have a post-transcriptional regulatory role by directing cleavage of a specific transcript.

11 Are biological models beneficial? Either yes or no justify.

12 How many signaling proteins can be synthesized from 2,000 signaling genes?

13 Biological Modeling is a combination of _____and _____.

14 Relation between Asynchronicity and Boolean network.

15 Simulations are generally _____in there development.

16 Name any two general purpose simulators that predict the behavior of metabolic pathways.

17 What is the aim of Bio-simulations?

18 When are the "Multistate Molecules" used in an algorithm?

19 Gene regulation pattern differs from _____

20 What are the challenges of the model?

PART - B

1 (a) Explain any **three** :   6

     (1) Name few Quantification techniques and give their common drawback.

     (2) Rank the Transcriptomics techniques.

     (3) Explain cluster analysis of model networks

     (4) State the advantages and disadvantages of ESTs and its databases.

     (5) Northern Blot

     (6) UniGene cluster

(b) Explain any **three** :   9

    (1) Transcriptomics Data Analysis

    (2) Diagrammatically represent the construction of EST.

    (3) Name any 3 tools for EST clustering.

    (4) What is the need of development of organism specific EST databases?

    (5) Limitations of SAGE.

    (6) Sequencing based method for mRNA quantification.

(c) Attempt any **two** :   10

    (1) Summarize the technique used for Transcriptomics.

    (2) Give the steps to construct EST.

    (3) Briefly explain the tools used in Gene Expression analysis

    (4) Discuss in details about SAGE expression mapping

    (5) Explain one of the clustering techniques used in microarray data analysis?

2 (a) Explain any **three** :   6

    (1) What is computational biology?

    (2) Boolean model

    (3) What are the important factors to be considered during evaluation of a model?

    (4) Stochastic model

    (5) Monte Carlo Simulation

    (6) Which are the two methods in Intermediate or Hybrid models

(b) Explain any **three** : 9

    (1) Discuss few challenges of biological modeling.

    (2) Brief out 6 advantages of biological models.

    (3) Stochastic simulation

    (4) Monte Carlo Simulation

    (5) Bio-simulation

    (6) Give difference between model and simulation

(c) Attempt any **two** : 10

    (1) Discuss in detail the advantages and disadvantages of biological modeling.

    (2) Benefits and shortcomings of biological modeling over experimental biology.

    (3) Explain in detail any two simulation software used in Transcriptomics

    (4) Mention the points that are needed for modeling the systems.

    (5) How can you analyze Microarray Image?

    (6) Write notes on databases used in Gene Expression analysis.

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