Register Number……

B.TECH. DEGREE EXAMINATIONS: NOV/DEC 2012

Seventh Semester

BIO TECHNOLOGY

BTY211: Genomics and Proteomics

Time: Three Hours **Maximum Marks: 100**

Answer All Questions:-

PART A (10 x 1 = 10 Marks)

1. C value paradox is Lack of correlation between

   A. DNA content and complexity B. mRNA content and complexity

   C. Protein content and complexity D. Total RNA content and complexity

2. Which of the following model genome study helps in understanding developmental biology …….

   A. *C.elegans* B. *E.coli* C. *Arabidapsis thaliana* D. Yeast

3. Major limitation of using restriction mapping method for preparing genome map of higher organisms is

   A. large genomes cannot be restricted by RE

   B. Large fragments cannot be separated by electrophoresis technique.

   C. Complex technique

   D. Error rate is high

4. FISH mapping is …… method

   A. high resolution physical mapping B. low resolution genetic mapping

   C. High resolution genetic mapping D. Low resolution physical mapping

5. Physical gaps detected in the genome sequence assembly can be closed by .....

   A. Resequencing of already available library clones

   B. Sequencing of new library clones

   C. Paired end sequencing of overlapping clones

   D. Paired end sequencing of non-overlapping clones

6. Draft genome sequence is characterized by …….

   A. presence of gaps with unambiguous data B. absence of gaps with ambiguous data

   C. Presence of gaps with ambiguous data D. Absence of gaps with unambiguous data

7. ……..analysis of the genome sequence helps in developing personalized medicine

A. SNP profiling B. Comparative genome C. Microarray D. SAGE

8. Which of the following is not a transcriptomics techniques

A. SAGE B. SNP typing C. RDA D. Subtractive hybridization

9. Yeast two hybrid systems helps in indentifying .....

A. DNA – protein interaction B. Protein- Protein interaction

C. Protein-mRNA interaction D. RNA –RNA interaction

10. Spots in the 2D gels are cauterized by their.....

A. pI and Mr B. pH and Mr C. Relative molecular weight only D. Accurate pI value

PART B (10x2=20 Marks)

11. When human genome project was started in 1990, model organism's genomes were sequenced instead of sequencing human genome -Why?
12. List out the model organism's genomes that were sequenced alongside HGP.
13. What is radiation hybrid panel?
14. Define genome map and add a note on its importance in genome sequencing.
15. What are BAC libraries?
16. What are the characteristic features of finished genome sequence data?
17. What is genome annotation?
18. Differentiate orthologous and paralogous genes.
19. Why is proteolytic cleavage of proteins done before MS analysis?
20. How will you enrich phosphoproteins using affinity chromatography?

PART C (5x14=70 Marks)

21. a) Trace the history of Human Genome Project and add a note on goals and achievements of HGP.

(OR)

b) Discuss the ethical social and legal issues (ELSI) related to HGP.

22. a) Explain the following cytogenetic mapping methods

(i) FISH

(ii) Fibre FISH

(OR)

b) Explain the following restriction mapping methods with suitable illustrations

(i) PFGE

(ii) Optical mapping

23. a) (i) What are the two commonly followed strategies for genome sequencing? (2)

(ii) Elaborate on whole genome shotgun method of genome sequence with its advantages and disadvantages associated with this method. (12)

(OR)

b) Write short notes on the following

(i) Physical gaps (4)

(ii) Sequence gaps (3)

(iii) Draft gnome sequence assembly (3)

(iv) Finished genome sequence assembly (4)

24. a) What is the principle of Serial Analysis of Gene expression (SAGE) and elaborate the steps for transcript identification and quantification using SAGE.

(OR)

b) (i) Elaborate on fabrication of microarray using photolithography. (6)

(ii) How will you identify gene expression in two different tissues using microarray hybridization. (8)

25. a) Write the principle of MALDI-ToF Mass Spectrometry and how will you identify the proteins using mass spectrometry?

(OR)

b) How will you exploit iso- electric point and molecular weight of proteins using two dimensional gel electrophoresis?

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