SUBJECT CODE: 15BI/PC/GP34

M. Sc. DEGREE EXAMINATION, NOVEMBER 2018
BIOINFORMATICS
THIRD SEMESTER

COURSE   : CORE
PAPER   : GENOMICS AND PROTEOMICS
TIME   : 90 MINUTES   MAX. MARKS: 50

SECTION – A

ANSWER ALL THE QUESTIONS: **(20x1=20)**

1. Which of the following is incorrect regarding the advantages of Molecular data for phylogenetics study?
    a.   They are more numerous than fossil records.
    b.   They are easier to obtain as compared to fossil recors.
    c.   Sampling bias is involved
    d.   More clear-cut & robust phylogenetic trees can be constructed with the molecular data

2. The molecular clock is based on the finding that.
    a.   all mutations are either advantageous of disadvantageous to the organism.
    b.   new species have evolved at a kuniform rate throughout evolutionary time
    c.   genetic differences accumulate at a fairly constant rate.
    d.   all mutations are neutral to selection

3. Divergence is necessary for all of the following EXCEPT
    a.   speciation
    b.   the accumulation of different random mutations in the genes of two species
    c.   the use of the molecular clock.
    d.   the accumulation of random mutations in the DNA.

4. To use molecular data to reconstruct evolutionary history requires making a number of reasonable assumptions. Which of the following is incorrect about it?
    a.   The molecular sequences used in phylogenetic construction are homologous
    b.   The molecular sequences used in phylogenetic construction share a common origin
    c.   Phylogenetic divergence cannot be bifurcationg
    d.   Parent branch splits into two daughter branches at any given point

5. International Human Genome project was initiated by
    a.   National Institute of Health (NIH)
    b.   Celera genomics
    c.   US Deparament of Energy(D0E)
    d.   NOH and US D0E

6. DNA sequencing followed by genome annotation are steps of
    a.   Comparative genomics   b.   Structural genomics
    c.   Functional genomics   d.   transcriptomics

7. All are genome sequencing strategies except
    a.   Edman degradation method   b.   short gun library
    c.   Whole genome short gun sequencing d.   Directed gene sequencing

8. Small cDNA sequence that represents a unique segment of an active gene is called
    a.   SNPs   b.   SnRNAs   c.   ESTs   d.   contigs

9. The technique of subtractive hybridization allows identification of genes that are selectively activated under a certain set of conditions.
    a.   True   b.   False

10. Which of these might be an advantage to genetic testing of individuals via microarrays?
    a.   Many different potential mutations in a single gene could be tested at once.
    b.   Expression patterns of many different genes can be analyzed simultaneously.
    c.   Microarray analysis can provide relative levels of expression of particular genes
    d.   All of these

11. Which of these would not be a valid reason that use of microarray technology to differentiate between closely related bacterial species and subspecies is important?
    a.   Certain strains of bacteria are more pathogenic than other related strains
    b.   Some strains of bacteria are more active in bioremediation than other related strains.
    c.   Infection by different strains of bacteria may require different therapeutic approaches
    d.   In many cases, critical information about characteristics of a bacterium causing an infection needs to be immediately available.

12. The two most common processes that lead to production of multiple functional proteins from the same DNA sequence are:
    a.   RNA editing and alternative splicing.
    b.   Protein folding and posttranslational covalent modifications
    c.   Alternative splicing and posttranslational covalent modifications
    d.   Posttranslational covalent modification and transcriptional regulation.

13. Which of these conclusions might be drawn from the results of a 2D gel electrophoresis experiment?
    a.   Levels of mRNA expression for two different genes are lower under one set of conditions than another
    b.   In a mutant cell, the lack of protein expression is due to production of unstable mRNA, which is rapidly degraded.
    c.   A mutation prevents proper posttranslational modification of a protein
    d.   None of All of these are reasonable conclusions

14. Which of these concerns would apply to functional protein microarrays but not antibody microarray?

15. How many potential open reading frames are present in a DNA sequence?

16. Why might you want to search a database for a protein motif?

17. What is a 'proteotypic' peptide?

18. Isobaric tags are:

19. If your quantitative proteomics experiment contains a large number of samples, which of these would be a good method to chose?

20. Which of these is the most important aspect of planning and designing a good proteomics experiment?

SECTION – B

ANSWER ANY THREE QUESTIONS (Draw Diagrams wherever necessary)(3x10=30)

21. Describe the salient features of Human genome and compare it with chimpanzee genome.
22. Give brief account on computer mediated analysis for gene function.
23. Explain in details about the pathway regulatory networks with its importance.
24. Elaborate the mapping of protein modification with suitable example.
25. Write brief account on protein-protein interactions with Y2B method.

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