

M. Sc. DEGREE EXAMINATION, NOVEMBER 2019
BIOINFORMATICS
THIRD SEMESTER

COURSE : CORE

PAPER : GENOMICS AND PROTEOMICS

TIME : 90 MINUTES

MAX. MARKS: 50

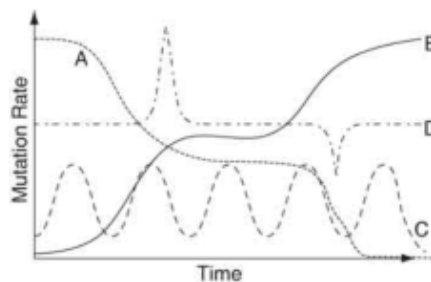
SECTION – A

ANSWER ALL THE QUESTIONS:

(20x1=20)

1. What, approximately, is the fraction of genetic variation in the nuclear genome is that is expected to have a harmful effect on gene function?
a) 50%. b) 25%. c) 10%. d) 1%.
2. How many open reading frames are present in a double stranded DNA sequence?
a) One. b) Three. c) Six. d) More than six.
3. Two more recent uses of phylogenetic analysis are to analyze _____ and to trace the evolutionary history of specific genes. Which of the following could not be the correct blank?
a) gene families b) genomes
c) proteomes d) physical separation methods
4. If organisms A, B, and C belong to the same class but to different orders and if organisms D, E, and F belong to the same order but to different families, which of the following pairs of organisms would be expected to show the greatest degree of structural homology?
a) A and B b) A and C c) B and D d) D and F
5. Phylogenetic hypotheses are strongest when
a) they are based on amino acid sequences from homologous proteins, as long as the genes that code for such proteins contain no introns.
b) each clade is defined by a single derived character.
c) they are supported by more than one kind of evidence, such as when fossil evidence corroborates molecular evidence.
d) they are accepted by the foremost authorities in the field, especially if they have won Nobel Prizes.
6. Three living species X, Y, and Z share a common ancestor T, as do extinct species U and V. A grouping that includes species T, X, Y, and Z makes up
a) a valid taxon. b) a monophyletic clade.
c) an ingroup, with species U as the outgroup. d) a paraphyletic grouping.
7. In an analysis of eukaryotic gene, you identify several non-overlapping open reading frames, but they are not all in the same frame. Which explanation makes the most sense?
a) This is a mutant allele that has had several small insertions.
b) This gene includes introns which are not multiples of three.
c) By random chance, a second reading frame within the gene also has an open reading frame.
d) All of these

8. To apply parsimony to constructing a phylogenetic tree,
- choose the tree that assumes all evolutionary changes are equally probable.
 - choose the tree in which the branch points are based on as many shared derived characters as possible.
 - base phylogenetic trees only on the fossil record, as this provides the simplest explanation for evolution.
 - choose the tree that represents the fewest evolutionary changes, either in DNA sequences or morphology.
9. If a person has the C/G genotype for an SNP on one chromosome, and the A/T genotype for the SNP on the other chromosome, then they are considered for this SNP.
- homozygous
 - heterozygous
 - a mixture
 - a combination
10. If a certain section of a resequencing microarray is used to sequence a 100 base pair section of DNA, how many total probes would be needed to figure it out?
- 25
 - 100
 - 200
 - 400
11. How long is a typical probe used for microarray analysis?
- 8 base pairs
 - 25 base pairs
 - 100 base pairs
 - there is no set length to the probes
12. In the color microarray image, which colors represent that a lot of the RNA has hybridized with the probes in the feature (and thus the gene is highly expressed)?
- black and blue
 - light blue and green
 - red and white
 - the color does not indicate how much has hybridized
13. Which curve in the graph below best depicts the way that mutation rate varies over time in a gene that can serve as a reliable molecular clock? .



14. The human nuclear genome includes hundreds of genes that are orthologs of bacterial genes, and hundreds of other genes that are orthologs of archaean genes. This finding can be explained by proposing that
- neither archaea nor bacteria contain paralogous genes.
 - the eukaryotic lineage leading to humans involved at least one fusion of an ancient bacterium with an ancient archaean.
 - the infection of humans by bacteriophage introduced prokaryotic genes into the human genome.
 - horizontal gene transfer did not occur to any significant extent among the prokaryotic ancestors of humans.
15. Which of these four gene parts should allow the construction of the most accurate phylogenetic tree, assuming that this is the only part of the gene that has acted as a reliable molecular clock?
- Intron I
 - Exon I
 - Intron VI
 - Exon V

16. Sets of proteins that are part of stable complexes and sets of proteins involved in transient interactions _____ in terms of the similarity in gene expression among the set of proteins.
a) are similar b) differ c) are same d) show similar function
17. Protein-protein interactions can be identified by
a) Phage display b) Microarrays
c) Hierarchical clustering d) Mass spectrometry
18. Protein A is an α -keratin while Protein B is a transport protein. Which characteristic could be shared by Protein A and Protein B?
a) Both could be fibrous proteins containing multiple polypeptide chains.
b) Both could be globular proteins with similar primary structures.
c) Both could contain disulfide bridges linking methionine residues.
d) Both could contain hydrogen bonds between peptide bond atoms.
19. Which one of the following is a group of proteolytic enzymes?
a) Bromelain and Papain b) Cellulase and myrosinase
c) Maltase and Diastase d) Phosphatase and Chlorophyllase
20. Which of the following is a wrong statement?
a) To assume biological activity, many nascent polypeptides have to be covalently modified before or after the folding process
b) In eukaryotic cells most modifications take place in the endoplasmic reticulum and the Golgi apparatus
c) The modifications in eukaryotic cells include proteolytic cleavage; formation of disulfide bonds; addition of phosphoryl, methyl, acetyl, or other groups onto certain amino acid residues
d) The modifications in eukaryotic cells doesn't include attachment of oligosaccharides or prosthetic groups to create mature proteins

SECTION – B

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

21. Explain the techniques used for Gene Location and how to determining the functions of individual genes
22. Compare the Genomes of Chimpanzees and Humans and write the application of genome Analysis for Human Diseases
23. Describe the strategies used for Generating ESTs and applications of Microarrays in Medicine
24. Write the techniques adopted for Mapping of Protein Modifications
25. Explain MALDI – TOF techniques for protein analysis
