

M. Sc. DEGREE EXAMINATION, NOVEMBER 2017
BIOINFORMATICS
THIRD SEMESTER

COURSE : CORE
PAPER : GENOMICS AND PROTEOMICS
TIME : 90 MINUTES

MAX. MARKS: 50

SECTION – A

ANSWER ALL THE QUESTIONS: (20x1=20)

1. When examining the evidence provided by a molecular clock, such as cytochrome c, more changes in the nucleotide sequences between two organisms means they are less closely related.
A) true B) false
2. Molecular clocks measure
A) differences in nucleotide sequences between different species.
B) the age of fossils more than 150 million years old.
C) Similarities in nucleotide sequences between different species.
D) the half-life of potassium-16.
3. Molecular clock dating approaches assign age estimates to nodes of a cladogram. Which of the following statements is correct?
A) Divergence age estimation and tree (topology) estimation are always separate, consecutive steps in all presently available relaxed molecular clock tools.
B) Empirical evidence shows that a strict molecular clock can be assumed in most cases.
C) Using fossils with a known age is the typical way to calibrate a chronogram. Current algorithms can only handle one fossil calibration point per tree.
D) Substitution rates (changes per site per time) can differ among lineages, and this should be taken into account
4. The main difference between the directed mutation theory and the random mutation theory is:
A) The chemical nature of the mutagens.
B) The effect of the mutation on the phenotype.
C) The cause of the mutation.
D) The heritability of the trait.
5. In which situation would you expect the mutation frequency to increase over time?
A) The deleterious effect of the mutation is balanced with the mutation rate.
B) A lethal allele is created at a high mutation rate.
C) A neutral allele is created at low mutation rate.
D) All of the above.

6. The term genomics was coined by
A) Thomas Cech B) T.H Morgan C) Tom Roderick D) Craig Venter
7. The first completed genome sequencing project is of
A) *E.coli* B) *Haemophilus influenzae* C) ϕ X174 D) *Drosophila melanogaster*
8. If, someday, an archaean cell is discovered whose SSU-rRNA sequence is more similar to that of humans than the sequence of mouse SSU-rRNA is to that of humans, the best explanation for this apparent discrepancy would be.
A) homology. B) homoplasy. C) Common ancestry. D) retro-evolution by humans
9. Which of the following statements on maximum likelihood as framework for phylogenetic inference is incorrect?
A) secondary structure can be incorporated into the analysis by means of a doublet model.
B) Codon models are rarely used for tree topology inference due to the computational burden.
C) Maximum likelihood employs substitution models, usually expressed as intensity matrices.
D) Confidence in nodes of trees computed via maximum likelihood cannot be evaluated With resampling plans like bootstrapping or jackknifing; instead, topological tests are used.
10. In phylogenetics, following is not a Bayesian MCMC approaches
A) ...are used with the aim to approximate the prior distribution of parameters.
B) ...can be used for computing Bayes factors for hypothesis testing.
C)...come up with clade credibility estimates as integral part of the tree inference procedure.
D)....do not usually invoke superimposed bootstrapping of the data to get more precise confidence intervals for estimated parameters.
11. Finding that genes associated with an internalizing disorder will associate with other internalized disorders and genes associated with an externalizing disorder will be associated with other externalizing disorders suggests that the genetic effects in psychopathology.
A) are broad, and like cognitive ability, controlled by “generalist genes”.
B) are highly heritable, and like cognitive ability, controlled by a small number of genes.
C) are narrow in their specific effects, and like cognitive ability, qualitative in nature.
D) are broad, indicating that there should be no clinical distinctions between sychopathology types.

12. In terms of understanding the pathways between genes and behaviour, it is fairly safe to say that
- A) we know more about the environment than the genes
 - B) we know more about the genes than the environment
 - C) the new field of molecular genetics is the best way to gain a full understanding of the gene/environment interactions in the pathways
 - D) QTL analysis has actually hindered the understanding of these pathways by suggesting so many separate gene contributions to basic behaviour processes
13. When you scan the microarray in the scanner, the data show some black spots. What do these represent?
- A) The DNA that has been replicated in healthy cells.
 - B) The mRNA that was washed away in the washing solution.
 - C) The DNA that was not transcribed and expressed in healthy cells.
 - D) The mRNA that was not bound by Oligo-d-tails in the beads.
14. How is a microarray constructed? In each spot, there are:
- A) Copies of all the genes for an organism.
 - B) Multiple copies of one gene; each spot has copies for a different gene.
 - C) Multiple copies of intergenetic sequences, which bind to genes in the samples.
 - D) Copies of intergenetic sequences, which promote the replication of DNA in a sample.
15. Scientists call hybridization the key to microarrays. Hybridization occurs when:
- A) Two complimentary strands of DNA from different sources bind to each other.
 - B) Poly-A tails bind to Poly-Ts.
 - C) Different species interbreed and create new DNA base pairings.
 - D) Two strands of identical DNA bind without using the traditional nucleotide pairs
16. A cDNA library:
- A) Can also be called an expressed sequence tag (EST) library.
 - B) Consists of coding sequences from genes that are expressed.
 - C) Is specific to the set of conditions under which the original mRNA was generated.
 - D) All of these.
17. 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.
18. Which of the following statements regarding the proteome is the most correct?
- A) A large proportion of the proteome is expressed by each cell of a species.
 - B) Levels of gene expression at the mRNA level generally correlate highly with levels of functional protein.
 - C) The proteins produced by a specific cell depend on cell type and environmental conditions.
 - D) All of the above.
19. In two dimensional gel electrophoresis:
- A) Different forms of the same protein will tend to migrate at the same position.
 - B) Up to about a hundred different proteins can be distinguished from each other.
 - C) Proteins with similar functions will be located near each other.
 - D) None of these.

20. 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) By random chance, a second reading frame within the gene also has an open reading frame.
 - B) This gene includes introns which are not multiples of three.
 - C) This is a mutant allele that has had several small insertions.
 - D) All of these.

SECTION – B

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

- 21. Describe the experimental techniques used for finding the gene location and its function
- 22. How to identify the human disease with Human Genome sequence.
- 23. Explain in details about the gene expression analysis with Microarray experiments
- 24. Write the Mass spectroscopy technique for protein analysis.
- 25. Write brief account on Protein – Protein interactions in the cell
