

STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086
(For candidates admitted from the academic year 2010 – 11)

SUBJECT CODE: BI/PC/GP34

M. Sc. DEGREE EXAMINATION, NOVEMBER 2011
BIOINFORMATICS
THIRD SEMESTER

COURSE : CORE
PAPER : GENOMICS AND PROTEOMICS
TIME : 1½ HOURS

MAX. MARKS: 50

SECTION – A

ANSWER ALL THE QUESTIONS:

(20x1=20)

CHOOSE THE CORRECT ANSWER:

- How are the following symbol represented in the bioinformatics - W
a. strong hydrogen bonds b. any c. weak hydrogen bond d. keto group
- Who is credited with coining the term genomics?
a. H. Winkler b. Patrick Brown c. Francis Collins d. T. H. Roderick
- Which of the following genomes is richest in interspersed repeat sequences?
a. Human genome b. Maize genome c. *Drosophila* genome d. *E. coli* genome
- What is metagenomics?
a. genomic analysis of a specific family of micro-organisms
b. genomic analysis of a environmental sample
c. genomic analysis of a complete population of micro-organism
d. genomic analysis of a unknown sample
- Which of these would be considered the simplest organism with a nucleus?
a. *Saccharomyces cerevisiae* b. *Caenorhabditis elegans*
c. *Drosophila melanogaster* d. *Physcomitrella patens*
- . Expressed sequence tags (ESTs) allow researchers to identify:
a. Genes that encode proteins b. Microsatellites
c. Ribosomal RNA genes d. Introns
- Sequencing shows that humans share the genomic similarities with which of these?
a. Yeast b. Fruit fly c. Chimpanzee d. rat
- Researchers used _____ to orient and overlap sequence data to create complete sequence maps of entire chromosomes.
a. DNA micro array b. Fluorescent single-molecule detection
c. TIGR d. Sequence tagged sites (STSs)

9. Functional genomics studies only protein encoding DNA sequences.
a. True b. False
10. As the complexity of an organism increases, all of the following characteristics emerge except _____.
a. the gene density decreases b. the number of introns increases
c. the gene size increases d. an increase in the number of chromosomes
e. repetitive sequences are present
11. How are so many different antibodies produced from fewer than 300 major genes?
a. gene duplication b. alternative splicing mechanisms
c. the formation of polyproteins
d. recombination, deletions, and random assortment of DNA segments
12. What would be a likely explanation for the existence of pseudogenes?
a. gene duplication b. gene duplication and mutation events
c. mutation events d. unequal crossing over
13. CpG islands and codon bias are tools used in eukaryotic genomics to _____
a. identify open reading frames b. find regulatory sequences
c. differentiate between eukaryotic and prokaryotic DNA sequences
d. look for DNA-binding domains
14. Molecular clocks allow us to estimate _____.
a. How long our species has lived on earth
b. how long a particular population is expected to survive under specific environmental conditions
c. when a set of closely related species diverged from a common relative
d. the life span of a particular species
15. Proteins with the same or similar function do not always show significant sequence similarity
a. Yes b. No
16. _____ was the first organism to have its entire genome sequenced.
a. The fruit fly b. *E. Coli* c. *Homo sapiens* d. *Haemophilus influenzae*
17. If you were using a proteomics approach to find the cause of a muscle disorder, which of the following techniques might you be using?
a. creating a genomic library b. sequencing the gene responsible for the disorder
c. developing physical maps from genomic clones
d. determining which environmental factors influence the expression of gene of interest
18. Knowing the complete human genome sequence will have practical applications in:
a. Health care b. Anthropology c. Comparative genomics d. all of these

19. Who was the first director of the human genome project?
a. James Watson b. Francis Crick c. Jacques Monod d. Craig Ventner
20. Which genome has the fewest introns?
a. *Drosophila* genome b. Human genome
b. Maize genome d. *Saccharomyces* genome

SECTION – B

ANSWER ANY THREE QUESTIONS IN 300 WORDS EACH. ALL QUESTIONS CARRY EQUAL MARKS : (Draw Diagrams wherever necessary) (3x10=30)

21. Describe in detail about 2D gel electrophoresis and its application on proteomics.
22. Describe various tools to achieve phylogeny with the help of Distance methods.
23. Explain briefly about SAGE. How will the study of gene expression prove useful for medicine.
24. Correlate between molecular clocks with evolution.
25. Define Protein – protein interactions. Explain detail about tools which are used to find out protein –protein interactions.
