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

SUBJECT CODE: BI/PC/RB44

M. Sc. DEGREE EXAMINATION, APRIL 2012
BIOINFORMATICS
FOURTH SEMESTER

COURSE : CORE
PAPER : RECENT ADVANCES IN BIOINFORMATICS
TIME : 3 HOURS **MAX. MARKS: 100**

SECTION – A

ANSWER ALL QUESTIONS **(20 X 1=20)**

1. SNP density can be predicted by the
A) RFLP B) AFLP C) Gene sequencing D) Micro-satellite

2. A SNP in which both alleles produce the same polypeptide sequence is called
A) synonymous polymorphism B) replacement polymorphism
C) missense mutation D) nonsense mutation

3. Alzheimer's disease is characterised by loss of neurons and synapses in the
A) Ganglia B) Central Nervous system C) spinal cord D) cerebral cortex

4. Find out the sequence in order
A) Excretion-Absorption-Distribution-Metabolism
B) Distribution – Absorption-Metabolism-Excretion
C) Absorption-Distribution-Metabolism-Excretion
D) Metabolism-Excretion-Absorption-Distribution

5. The CHUCKLES language was developed to express chemical structure at
A) The "Monomer" level rather then at the atomic level
B) The "Atomic "level rather than at the molecular level
C) The '' Molecular" level rather than at the atomic level
D) All of the above

6. Cheminformatics is the combination of
A) Chemical synthesis B) Biological synthesis
C) Physical synthesis D) All the above

7. The QSAR model is based on a biophore consisting of a six-membered aromatic ring containing two _____nitrogen atom.
A) SP_2-hybridized B) SP_3-hybridized
C)SP-hybridized D) None of the above

8. Scanner type programs are more or less used for
A) Aluminium compound screening B) Lead compound screening
C) Carbon compound screening D) Iron compound screening

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9. The major histocompatibility complex proteins function to
A) degrade T4 and T8 polypeptides B) bind antibody for lymphokine production
C) bind complement for cell lysis D) bind antigen fragments for presentation to T-cells

10. BCG is used to protect against:
A) Tuberculosis B) Rabies C) Hepatitis B D) Influenza

11. A epitope present in
A) Antibody B) Vaccine C) Drugs D) none of the above

12. The DNA microarrays technology that tracks deletions and amplifications of specific DNA sequences is called _____.
A) DNA variation screening B) gene expression profiling
C) microarray comparative genomic hybridization D) antisense

13. DNA microarrays are used for _____.
A) DNA variation screening B) gene expression profiling
C) microarray comparative genomic hybridization D) All of the above.

14. A single microarray may have a surface area of less than three square inches, yet may contain unique spots of tens of thousands of gene sequences.
A) True B) False

15. Multiple sequence alignment is used to
A) Predict nucleotide similarity B) Predict bacterial identity
C) Predict protein sequence D) None of the above

16. The identification of the function of a gene in a genome can be accomplished using
A) functional genomics. B) gene micro arrays.
C) gel electrophoresis. E) proteomics

17. Labeling a stretch of DNA according to its function is called
A) recombinant DNA technology. B) functional analysis.
C) annotation. D) screening.

18. R. programming was developed by
A) Bil Gates B) Steve Jobs
C) Chambers D) Ihaka and Gentleman

19. R is an implementation of the programming language _____
A) C B)C++ C) S D) Java

20. R Programming is applied in the field of
A) Statistics B) Graphics
C) both A and B D) none of the above

SECTION – B

ANSWER ANY FOUR QUESTIONS. EACH ANSWER SHOULD NOT EXCEED 500 WORDS. All ANSWERS CARRY EQUAL MARKS. DRAW DIAGRAMS WHEREVER NECESSARY (4 X 10 = 40)

21. What is toxicogenomics? Explain briefly about the Comparative Toxicogenomics Database (CTD).

22. Describe the prospects of cheminformatics tool SMILES

23. What is epitope mapping? What are the methods available for epitope mapping?

24. How to find out drug molecules for specific disease? What are the tools and database used for this purpose ?

25. Briefly explain about tools for vaccine development.

26. Describe the basic steps involved in gene sequencing with DNA microarray.

27. How to create the objects and value assignment in R programming?

SECTION – C

ANSWER ANY TWO QUESTIONS. EACH ANSWER SHOULD NOT EXCEED1200 WORDS. All ANSWERS CARRY EQUAL MARKS. DRAW DIAGRAMS WHEREVER NECESSARY (2 X 20 = 40)

28. Give a brief account on characteristic feature of pharmacogenomics of Alzheimer disease and its gene - drug interactions.

29. What are the 3-D QSAR active site models? Explain and give their application.

30. Describe in brief about the strategy of development of personalized medicine based on Immunoinformatics.

31. What is microarray data? How to visualize the data? Describe in detail about microarray data Analysis.

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