

STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI –600 086
(For candidates admitted from the academic year 2015 – 2016)

SUBJECT CODE: 15BI/PC/BI24

M. Sc. DEGREE EXAMINATION, APRIL 2016
BIOINFORMATICS
SECOND SEMESTER

COURSE : MAJOR – CORE
PAPER : BIOINFORMATICS
TIME : 3 HOURS

MAX. MARKS: 100

SECTION – A

ANSWER ALL THE QUESTIONS

(30x1=30)

1. Which of the following is a nucleotide sequence database?
a. EMBL b. SwissProt c. TrEMBL d. PROSITE
2. A database of current sequence map of Human genome is called as
a. OMIM b. HGMD c. Golden path d. GeneCards
3. SWISS PROT is related to
a. Portable data b. Swissbank data c. Sequence data bank d. Sequence data
4. BLOSUM matrices are used for
a. Multiple sequence Alignment b. Pairwise sequence Alignment
c. Phylogenetic Analysis d. All the above
5. Phylogenetic relationship can be shown by
a. Dendrogram b. Gene Bank c. Data retrieving tool d. Data search tool
6. PRINTS are software used for
a. detection of genes from genome sequence b. detection of tRNA genes
c. prediction of function of a new gene d. Identification of functional domains/motifs of proteins
7. The alignment procedure that tries to align the entire sequence is
a. multiple sequence alignment b. pair wise alignment
c. global alignment d. local alignment
8. Sequence alignment helps scientists
a. to trace out evolutionary relationships
b. to infer the functions of newly synthesized genes
c. to predict new members of gene families
d. all of these
9. All are sequence alignment tools except
a. Rasmol b. BLAST c. FASTA d. Clustal W
10. Which of the following is a sequence alignment tool provided by NCBI
a. Chime b. BLAST c. FASTA d. Clustal W
11. Which of the following is a multiple sequence alignment tool?
a. Clustal W b. Chime c. Dismol d. PDB
12. Two sequences are said to be homologous if:
a. they have diverged from a common ancestor.
b. their alignments share 30% identity or more.
c. they belong to the same fold family.
d. they have converged to share similar functional properties.

13. When performing a database search, what is the definition of an E-value?
 - a. The chance that a random sequence could achieve a better score than the query.
 - b. The chance that a homologous sequence could achieve a similar score to the query.
 - c. The chance that a random sequence could achieve a worse score than the query.
 - d. The chance that a homologous sequence could achieve a better score than the query
14. Well-conserved regions in multiple sequence alignments:
 - a. reflect areas of structural importance.
 - b. reflect areas of functional importance.
 - c. reflect areas of both functional and structural importance.
 - d. reflect areas likely to be of functional and/or structural importance.
15. Hydropathy plots are usually used to predict:
 - a. beta secondary structures b. transmembrane domains
 - c. alpha secondary structures d. tertiary structure
16. Databases such as CATH and SCOP are used to identify:
 - a. the structural family to which a protein belongs
 - b. the genic family to which a protein belongs
 - c. homologous proteins
 - d. analogous proteins
17. Coordinates for known protein structures are housed in?
 - a. CATH b. SCOP c. PDBsum d. PDB
18. The software used to construct phylogenetic tree is_____.
 - a. BLAST
 - b. PHYLIP
 - c. Swiss – PDB viewer
 - d. BLOSUM
19. The sequence submission tool is_____.
 - a. Bankit
 - b. Sequim
 - c. Pubmed
 - d. both a & b
20. Bootstrapping repeats the phylogenetic analysis several times, each time reshuffling the columns of the initial alignment, in order to:
 - a. build a consensus tree, where the number of times each branch reforms is counted and used to estimate its probability
 - b. generate a random model from which to benchmark phylogenetic data
 - c. produce a graphical representation of the tree
 - d. assess the probability that the sequences in the alignment are unrelated
21. Which one is correct answer?
 - a. An algorithm is a sequence of instructions that one must perform in order to solve a well-formulated problem.
 - b. An algorithm is a programming language
 - c. An algorithm is a sequence of instructions that one must perform in order to solve solely bioinformatics-related problems
 - d. An algorithm is the same as the ALGOL

SECTION - B

Answer any THREE of the following; each answers not exceeding 500 words.

Draw diagram wherever necessary.

(3 X 10 =30)

21. Write about the sequence retrieval system for database management.
22. Describe about the PSI BLAST algorithm.
23. Short notes on Smith and Waterman algorithm.
24. Briefly explain about the integrated multiple sequence alignment resources.
25. What is Boot strap analysis?

SECTION – C

Answer any TWO of the following, each answer not exceeding 1200 words.

Draw diagram wherever necessary.

(2 X 20 = 40)

26. What is evolutionary tree? How to construct it? What are the tools used for construction of evolutionary tree? Explain in details any one of the tool for tree construction.
27. Describe about the BLAST algorithm with alignment score.
28. Differentiate between PAM and BLOSUM matrix.
29. Illustrate the various biological databases available for DNA.
