

STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086
(For candidates admitted from the academic year 2019 - 2020)

SUBJECT CODE: 19BI/PC/EB14

M. Sc. DEGREE EXAMINATION, NOVEMBER 2019

BIOINFORMATICS

FIRST SEMESTER

COURSE : CORE

PAPER : ESSENTIALS OF BIOINFORMATICS

TIME : 1½ HOURS

MAX. MARKS: 50

SECTION – A

ANSWER ALL THE QUESTIONS:

(20x1=20)

1. Expand CMBI.
2. Expand SRS
3. Name the yeast genome database.
4. What is the literature database?
5. Which of the following is not a software for dot plot analysis?
a) SIMMI, b) DOTLET, c) DOTMATCHER, d) LALIGN
6. For palindromic sequence, what is the structure of the dot plot?
a) 2 intersecting diagonal lines at the midpoint, b) One diagonal
c) Two parallel diagonals, d) No diagonal
7. Global alignment
8. Sakura
9. The BLAST tool is developed based on _____ algorithm.
10. A recent improvement in the implementation of BLAST is the ability to provide gapped alignment, True or False.
11. Which of the following is not a variant of BLAST?
a) BLASTN, b) BLASTP, c) BLASTX, d) TBLASTNX
12. Define E-value.
13. The alignment procedure that tries to align regions with high level of matches without considering the alignment of rest of the sequences is
a) Multiple sequence alignment; b) Pair wise alignment
c) Global alignment; d) Local alignment
14. Which of the following is a multiple sequence alignment tool?
a) ClustalW, b) Chime, c) Dismol, d) PDB.

15. 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
16. Alignment method suitable for aligning closely related sequence is
- a) Multiple sequence alignment
 - b) Pair wise alignment
 - c) Global alignment
 - d) Local alignment
17. Parsimony can give _____ information when rates of sequence change ____ in the different branches of a tree that are represented by the sequence data.
- a) misleading, vary
 - b) useful, change
 - c) misleading, are constant
 - d) sometimes contradicting, are constant
18. Which of the following is untrue regarding the maximum parsimony method?
- a) The analysis steps are continued for every position in the sequence alignment
 - b) This method is used for large numbers of sequences
 - c) Those trees that produce the smallest number of changes overall for all sequence positions are identified
 - d) This method is used for sequences that are quite similar
19. Which of the following is incorrect regarding the terminologies of phylogenetics?
- a) The branching pattern in a tree is called tree topology
 - b) When all branches bifurcate on a phylogenetic tree, it is referred to as dichotomy
 - c) In case of dichotomy, each ancestor divides and gives rise to multiple descendants
 - d) An unrooted phylogenetic tree does not assume knowledge of a common ancestor
20. Building phylogenetic tree involves bifurcation and multifurcation. True or False.

SECTION – B

ANSWER ANY TWO QUESTIONS:

(2x15=30)

21. Comment on primary nucleotide sequence databases in detail.
22. Note on the following: a) PAM; b) BLOSUM; c) Global and Local alignment.
23. Write about Advanced BLAST at specialized sites.
24. Explain in detail about multiple sequence alignment programs.
