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C 28214 (Pages 2) Name

Reg. No.....................

# FOURTH SEMESTER M.Sc. DEGREE EXAMINATION, JULY 2012

(CSS)

Microbiology

## MB 4C 11—BIOSTATISTICS AND BIOINFORMATICS

(2010 Admissions)

Time : Three Hours

Maximum : 36 Weightage

### Part A

*Answer* all *questions.*
*Each question carries 1 weightage.*

1. $x^2$-*test* is mainly based on :
   (a) Permutation.
   (b) Frequency.
   (c) Independent variable.
   (d) Degrees of freedom.
2. The measure of average relationship between two or more variables in terms of original units of data is known as :
   (a) Correlation.
   (b) Regression.
   (c) Covariance.
   (d) Permutation.
3. The programming language used to create relational database is called :
   (a) C".
   (b) SQL.
   (c) PERL.
   (d) Oracle.
4. Which of the following one is highly curated and annotated database ?
   (a) GenBank.
   (b) PFam.
   (c) DDBJ.
   (d) Uniprot.
5. The structural database available in NCBI
   (a) PPB.
   (b) MMDB.
   (c) CATH.
   (d) SCOP.
6. The term optimal alignment mean :
   (a) Global alignment.
   (b) Local alignment.
   (c) Both (a) and (b).
   (d) Progressive alignment.
7. RCSB stands for ————————————
8. NCBI databases are maintained by ————————————
9. Which of the following programme is NOT a multiple sequence alignment tool ?
   (a) CLUSTAL X.
   (b) CINEMA.
   (c) PHYLIP.
   (d) T-COFFEE.

Turn over

10. Which of the following tool is used for the prediction of secondary structure of proteins ?
    - (a) GRAIL.
    - (b) SOPMA.
    - (c) PROTPARAM.
    - (d) GENSCAN.

11. A group of organism descended from a single common ancestor in a phylogenetic tree is called :
    - (a) Taxa.
    - (b) Cladi.
    - (c) Lineage.
    - (d) Root.

12. The computational biology tool that builds a phylogenetic tree by a sequential clustering approach is called :
    - (a) FM.
    - (b) NJ.
    - (c) UPGMA.
    - (d) ME.

13. Which of the following database is a pattern database ?
    - (a) GENSCAN.
    - (b) KEGG.
    - (c) PROSITE.
    - (d) OMIM.

14. An example of a UNIX program for molecular dynamics simulation in structural bioinformatics :
    - (a) ANOLEA.
    - (b) ERRAT.
    - (c) PROCHECK.
    - (d) GROMOS.

(14 x 1 = 14 marks)

## Part B

*Answer* any seven *questions.*
*Each question carries* 2 *weightage.*

15. Bibliographic databases.
16. Null hypothesis.
17. Progressive alignment.
18. Structural superposition.
19. Molecular clock hypothesis.
20. Dynamic programming.
21. DBMS.
22. -test.
23. PSI-BLAST.

(7 x 2 = 14 mark

## Part C

*Answer any* two *questions.*
*Each question carries* 4 *weightage.*

24. Describe students T-test with an example.
25. Briefly discuss the salient features of PDB flat file.
26. What do you mean by pairwise alignment ? Discuss various tools for pairwise alignment.

(2 x 4 = 8 marks,