

Exam Date & Time: 30-Sep-2020 (02:00 PM - 05:45 PM)



PSG COLLEGE OF ARTS AND SCIENCE

Note: Writing 3hrs: Checking & Inserting Image : 30mins+ Grace Time : 15mins

MSc DEGREE EXAMINATION MAY 2020
(Fourth Semester)

Branch - APPLIED MICROBIOLOGY

DISCIPLINE SPECIFIC ELECTIVE - II - INTRODUCTION TO BIOINFORMATICS [19MBP23A]

Marks: 75

Duration: 225 mins.

SECTION - A

Answer all the questions.

- 1) Each record in a database is called an _____.
 (i) Entry
 (ii) File
 (iii) Record
 (iv) Ticket (1)
- 2) All of the following are protein sequence databases except _____.
 (i) PIR
 (ii) PSD
 (iii) SWISS PROT
 (iv) EMBL (1)
- 3) Which of the following is a sequence alignment tool?
 (i) BLAST
 (ii) PRINT
 (iii) PROSITE
 (iv) PIR (1)
- 4) The procedure of aligning many sequences simultaneously is called _____.
 (i) Multiple sequence alignment
 (ii) Pairwise alignment
 (iii) Global alignment
 (iv) Local alignment (1)
- 5) When a phylogenetic tree consider as rooted one?
 (i) extends back to origin
 (ii) base is located the common ancestor
 (iii) illustrate the rampant gene swap
 (iv) with very few branch points (1)
- 6) Species that are not closely related and that do not share many anatomical similarities can still be placed together on the same phylogenetic tree by comparing their _____.
 (i) Plasmid
 (ii) Mitochondrial genome (1)

- (iii) Homologous genes
- (iv) Chloroplast genome

- 7) Which of the following is incorrect regarding gene annotation?
 (i) Human genome employs a combination of theoretical prediction and experimental verification
 (ii) First predicted by abinitio exon prediction programs (1)
 (iii) Compared with cDNA and EST sequences
 (iv) Pairwise alignment program are not involved
- 8) DNA sequencing followed by genome annotation are steps of _____
 (i) comparative genomics
 (ii) structural genomics (1)
 (iii) functional genomics
 (iv) transcriptomics
- 9) Which of the following are known as helix breakers?
 (i) Proline and Glycine
 (ii) Isoleucine and leucine (1)
 (iii) Valine
 (iv) Threomine
- 10) Abinitio approach makes structural prediction based on _____
 (i) Single RNA sequence
 (ii) Comparing RNA sequences (1)
 (iii) Evolutionary basis
 (iv) Pure Phylogneetics

SECTION - B

Answer all the questions.

- 11) Analyze briefly about different modes of database search. (5)
 a)
 [OR] Apply your knowledge about the importance of PDB. (5)
 b)
- 12) Determine the basic concepts of local sequence alignment. (5)
 a)
 [OR] Illustrate in brief about substitution matrices. (5)
 b)
- 13) Explain about uprooted phylogenetic tree. (5)
 a)
 [OR] State out any one pathway analysis in Bioinformatics. (5)
 b)
- 14) Justify wet experiments provide better results in biological research. (5)

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- a)
[OR] Discuss in short about protein coding genes. (5)
- b) (5)
- 15) Sketch out base covariance models. (5)
- a)
- [OR] Organize your views on transcriptomics. (5)
- b) (5)

SECTION - C

Answer all the questions.

- 16) Categorize different database tables with examples. (8)
- a)
- [OR] Evaluate the advantages and applications of DDBJ. (8)
- b) (8)
- 17) Analyze the needs of pairwise sequence alignment. (8)
- a)
- [OR] Enumerate on suitable method for scoring an alignment. (8)
- b) (8)
- 18) Give critical comment on UPGMA. (8)
- a)
- [OR] Classify different types of phylogenetic tree. (8)
- b) (8)
- 19) Compare prediction and simulation with suitable examples. (8)
- a)
- [OR] Design functional annotations of EST cluster. (8)
- b) (8)
- 20) Elucidate in brief about Abinitio prediction. (8)
- a)
- [OR] Differentiate synthetic biology with systematic biology. (8)
- b) (8)

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