

International Institute of Health Management Research
Term End Examination
Bioinformatics

Max. Mark: 70

Max Time: 02:00 Hrs

Section A

Multiple Choice Questions

2 x 25 = 50 marks

1. Conversion of RNA to Protein is called as
 - a. Translation
 - b. Replication
 - c. Transcription
 - d. Conjugation
2. The stop codons are
 - a. UAA, UGA, UGG
 - b. UAA, UGA, UAG
 - c. UAG, UAC, UGG
 - d. UAA, UGG, UAG
3. Which of the following statement is not true about Open reading frame
 - a. Does not contain a stop codon
 - b. Is a stretch of DNA that always starts with start codon
 - c. Can be two segments of DNA stretch joined together
 - d. Can start in one reading frame and continue in the next
4. The human genome contains approximately _____.
 - a. 6 billion base pairs
 - b. 5 billion base pairs
 - c. 3 billion base pairs
 - d. 4 billion base pairs
5. Which of the following are not the application of bioinformatics?
 - a. Drug designing
 - b. Data storage and management
 - c. Understand the relationships between organisms
 - d. None of the above
6. The laboratory work using computers and associated with web-based analysis generally online is referred to as _____.
 - a. In silico
 - b. Dry lab
 - c. Wet lab
 - d. All of the above
7. The first protein database is called

- a. Swiss-Prot
- b. PDB
- c. Atlas of Proteins
- d. Protein Sequence Databank

8. Each record in a database is called

- a. Entry
- b. File
- c. Record
- d. Ticket

9. Literature databases include

- a. Medline and PDB
- b. Medline and PDS
- c. Medline and Pubmed
- d. Pubmed and PDB

10. Format of sequence file does not include

- a. Fasta
- b. NBRF
- c. Excel
- d. MSF

11. The _____ database is not a primary database

- a. PIR
- b. DDBJ
- c. TrEMBL
- d. MIPS

12. Which of the following is a protein database

- a. PIR
- b. DDBJ
- c. EMBL
- d. GenBank

13. GenBank is maintained by

- a. Brookhaven Laboratory
- b. DNA databank of Japan
- c. European Molecular Biology Laboratory
- d. National Centre for Biotechnology Information

14. The _____ database is not a primary database

- a. PIR
- b. DDBJ
- c. TrEMBL
- d. MIPS

15. The stepwise method for solving problems in computer science is called _____.
a. Flowchart
b. Algorithm
c. Procedure
d. Sequential design
16. Characterizing molecular component is
a. Genomics
b. Cheminformatics
c. Proteomics
d. Bioinformatics
17. Analysing or comparing entire genome of species
a. Bioinformatics
b. Genomics
c. Proteomics
d. Pharmacogenomics
18. The identification of drugs through genomic study
a. Genomics
b. Cheminformatics
c. Pharmacogenomics
d. Phrmacogenetics
19. Submission to GenBank is done through
a. Entrez and Sequin
b. Sequin and BankIt
c. Entrz
d. BankIt and BankIn
20. Which of the following is incorrect about evolution?
a. The macromolecules can be considered molecular fossils that encode the history of millions of years of evolution
b. The building blocks of these biological macromolecules, nucleotide bases, and amino acids form linear sequences that determine the primary structure of the molecules
c. DNA and proteins are products of evolution
d. The molecular sequences barely undergo change
21. The presence of evolutionary traces is because some of the residues that perform key functional and structural roles tend to be preserved by natural selection; other residues that may be less crucial for structure and function tend to mutate more frequently.
a. True
b. False

22. If the two sequences share significant similarity, it is extremely _____ that the extensive similarity between the two sequences has been acquired randomly, meaning that the two sequences must have derived from a common evolutionary origin.

- a. Unlikely
- b. Possible
- c. Likely
- d. relevant

23. Genes that are similar in origin but have distinct functions are known as

- a. Orthologous
- b. Paralogous
- c. Xenologous
- d. Morphologous

24. Which of the following is incorrect regarding sequence homology?

- a. Two sequences can homologous relationship even if have do not have common origin
- b. It is an important concept in sequence analysis
- c. When two sequences are descended from a common evolutionary origin, they are said to have a homologous relationship
- d. When two sequences are descended from a common evolutionary origin, they are said to share homology

25. Flybase is a _____ database

- a. biodiversity
- b. model organism
- c. literature
- d. biomolecular

Section B

Both questions to be uploaded

10 x 2 = 20 marks

1. Explain central dogma of biology in detail
2. Given the following table develop Apriori Algorithm at Support threshold=50%, Confidence= 60%

Transaction	List of Items
T1	1,2,3
T2	2,3,4
T3	4,5
T4	1,2,4
T5	1,2,3,5
T6	1,2,3,4