

Model Test Paper-I
B.Sc. Biotechnology Part -III
Fundamentals of bioinformatics and nanotechnology
Paper BT-802

Time Allowed: 3Hours

Max. Marks: 50

Attempt five questions in all, including question no. 1, which is compulsory taking one question from each section.

Q.1 Attempt all questions

- a. Define bioinformatics
- b. Blasta- defination
- c. The primary nuecleotide sequence database are
 - (1) EMBL
 - (2) GenBank
 - (3) DDBJ
 - (4) All of these
- d. The protein sequence database are
 - (1) SWISS-PROT
 - (2) PIR
 - (3) Both (1)& (2)
 - (4) None of these
- e. The dot-plot was discovered by
 - (1) Gibbs and McIntyre
 - (2) M. Dayhoff
 - (3) Senger et al
 - (4) None of these
- f. Each record in a database is called an
 - (1) Entry
 - (2) File
 - (3) Record
 - (4) Ticket
- g. The first bioinformatics database was created by
 - (1) Richard Durbin
 - (2) Dayhoff
 - (3) Durn
 - (4) Pearson
- h. Define- Dendrimer
- i. Define Multiple sequence alignment
- j. Richard Feynman idea of nanotechnology

Section-A

Q.2 Define bioinformatics and its historical prospective. (10)

Q.3 Define Biological databases: primary, secondary and composite along its utility in present time.

Section-B

Q.4 Explain types of alignment tools-with suitable examples. (10)

Q.5 Bioinformatics in India (BTIS network).

Section-C

Q.6 Explain nanotechnology and Richard Feynmen's idea of nanoparticles. (10)

Q.7 Characterization of nanoparticles: structural and chemical methods.

Section-D

Q.8 Explain nanomaterials and application of carbon nanotube, bucky ball, carbon nanotube.(10)

Q.9 Nanotechnology and its impact on environment and medical field.

Model Test Paper-II
B.Sc. Biotechnology Part -III
Fundamentals of bioinformatics and nanotechnology
Paper BT-802

Time Allowed: 3Hours

Max. Marks: 50

Attempt five questions in all, including question no. 1, which is compulsory taking one question from each section.

Q.1 Attempt all questions

- a. The database has sequences deposited normally after verification is
 - (1) Genbank
 - (2) DDBI
 - (3) EST
 - (4) EMBL
- b. Deletions and insertions are collectively known as.....
- c. The database for 3D structures of biological macromolecules determined by X-Ray crystallography and NMR is:
 - (1) PDB
 - (2) SCOP
 - (3) Pfam
 - (4) PAM
- d. Which of the search tools is used to compare submitted amino acid sequences with nucleotide sequence database.
 - (1) BLASTn
 - (2) BLASTx
 - (3) rBLASTx
 - (4) t BLASTx
- e. Define- Dendrimer
- f. define carbon nanotubes.
- g. Richard Feynman's idea of nanotechnology
- h. multiple sequence alignment
- i. DOT-Plot matrix
- j. Environmental factors affected by nanoparticles.

Section-A

- Q.2 Define bioinformatics and nature of biological data (10)
- Q.3 Different types of Biological databases used for storage of information- Explain

Section-B

- Q.4 Explain BLASTA and FASTA- heuristic method of sequence alignment with proper illustration. (10)
- Q.5 Multiple sequence alignment and its superiority over DOT Plot matrix.

Section-C

- Q.6 Introduction to nanotechnology with historical background. (10)
Q.7 Synthesis of nanoparticles: biological and chemical methods.

Section-D

- Q.8 Explain different types of carbon nanomaterials – explain (10)
Q.9 Nanotechnology and its recent development.