THE TAMIL NADU DR. M.G.R. MEDICAL UNIVERSITY

[LP 967] NOVEMBER 2019 **Sub. Code: 2967**

M.PHARM. DEGREE EXAMINATION
(PCI New regulations 2016)
SEMESTER-II
BRANCH-IV – PHARMACEUTICAL BIOTECHNOLOGY – MPB
PAPER III – BIOINFORMATICS AND COMPUTER TECHNOLOGY

Q.P. Code : 262967

Time : Three hours **Maximum : 75 Marks**

I. Elaborate on: **(2 x 20 = 40)**

1. Explain various formats of protein and nucleic acid databases with its applications. Explain the role of National Center for Biotechnology Information in bioinformatics.

2. Explain the methods involved in pairwise sequence analysis and multiple sequence analysis with few diagrams.

II. Write notes on: **(7 x 5 = 35)**

1. Brief note on Data mining.
2. Write briefly on eukaryotic genome structure organisation.
3. Write use of PHYLIP in phylogenetic tree construction.
4. Write brief note on gene mapping and its applications.
5. Write a note on target discovery.
6. Explain the terms in brief:
   a) Algorithm b) DDBJ and PDB c) BLAST and FASTA
7. Explain the brief history of bioinformatics with a note on its application in biotechnology.

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THE TAMIL NADU DR. M.G.R. MEDICAL UNIVERSITY

[MPHARM 0921] SEPTEMBER 2021 Sub. Code: 2967
(OCTOBER 2020 EXAM SESSION)

M.PHARMACY DEGREE EXAMINATION
SEMESTER-II (PCI New regulations 2016)
PHARMACEUTICAL BIOTECHNOLOGY - MPB
PAPER III – BIOINFORMATICS AND COMPUTER TECHNOLOGY
Q.P. Code : 262967

Time : Three hours **Answer ALL Questions** **Maximum : 75 Marks**

I. Elaborate on: **(2 x 20 = 40)**

1. Elaborate in detail about the Construction of Phylogenetic Tree.

2. a) What is structural database?
   b) Explain briefly about the sequence of database management and storage.

II. Write notes on: **(7 x 5 = 35)**

1. Explain about the Homology modeling.
2. How to interpret docking results?
3. Explain in detail about Sequence assembly.
4. Give a note on significance of proteome.
5. Explain the role of ligand libraries for high throughput screening.
6. Write a note on Topology fingerprint approach for prediction of protein.
7. Illustrate about the Surface mapping of proteins.

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