## Faculty of Engineering & Technology

# M.E. (Digital Electronics) (Part Time/Full Time) Semester-II (C.G.S.-New) Examination **BIO-INFORMATICS**

#### Elective-II

### Paper-2 UMEF 5

#### Sections-A & B

| Time—Three Hours] |
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[Maximum Marks-80

### INSTRUCTIONS TO CANDIDATES

- (1) All questions carry marks as indicated.
- (2) Answer THREE questions from Section A and THREE questions from Section B.
- (3) Assume suitable data wherever necessary. (4) Illustrate your answers wherever necessary with the help of neat sketches.
- (5) Mobile/Cell Phone prohibited in exam. hall.
- (6) Use pen of Blue/Black ink/refill only for writing the answer book.

#### SECTION-A

- 7 (a) Explain the categories of research in informatics. 1. 6 (b) Explain the characteristics of Bioinformatics database. 6
- (a) Describe applications of bioinformatics. 2. 7 (b) Explain scope of bioinformatics in detail.
- (a) Explain three databases exchange and update data on a daily basis with neat schematic 3.
  - diagram. 6 (b) Explain protein sequence data bases.

#### OR

- (a) Describe the methods for searching from protein sequence databases. 7 4.
  - 6 (b) Explain Gene expressing database in brief.

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| 5.  | (a)         | Explain the main classification level of CATH.   | 5          |
|-----|-------------|--|------------|
| v   | <b>(b</b> ) | Briefly give reason why MMDB would yield different structural neighbour                  | s from the |
|     |             | other classification methods.  | 7          |
|     |             | or or  | ·          |
| 6.  | (a)         | Describe the enzyme, pathway databases.  | 7          |
|     | <b>(b)</b>  | Explain the information retrieval system to obtain data from databases.                  | 7          |
|     |             | SECTION—B  |            |
| 7.  | (a)         | Which are the two tools available for data submission in Gene Bank? Explain              | n any one. |
|     |             |  | 7          |
|     | (b)         | What is the basis for selecting a tool for submission? What condition will               | you check  |
|     |             | for while selecting any of these tools?  | 7          |
|     |             | OR   |            |
| 8.  | (a)         | Explain phylogenetic tree with neat sketch.  | 6          |
|     | (b)         | Explain similarities and differences between BLAST and FASTA tools for alignment.        | sequence   |
| 9.  | (a)         |  | 8          |
| ٠,  | (b)         | Explain the bioinformatics software for bioinformatics tasks.                            | 5          |
|     | (0)         | Explain the classification of Algorithm.   | 8          |
| 10  | (-)         | OR   |            |
| 10. |             | Explain the bioinformatics tasks and corresponding algorithms.                           | 7          |
|     | (b)         | Explain the biological Algorithm.  | 6          |
| 11. | (a)         | Explain similarity based approach to Gene prediction algorithm.                          | 7          |
|     | (b)         | What do you mean by protein function prediction? How is it done? Explaisuitable example. |            |
|     |             | -  | 6          |
| 12. | (a)         | OR   |            |
| 12, |             | Explain in brief phylogenetic prediction algorithm.                                      | 5          |
|     | <b>(b)</b>  | Explain sequence alignment optimal algorithms.   | 8          |