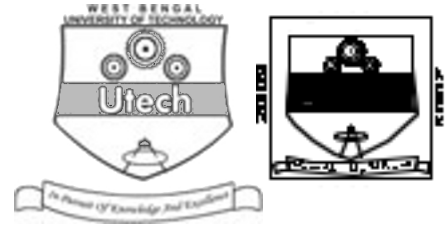


# BIO-INFORMATICS ( SEMESTER - 8 )

**CS/B.Tech(BME)/SEM-8/BME-803C/09**



1. ....  
Signature of Invigilator

2. ....  
Signature of the Officer-in-Charge

**Reg. No.**

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**Roll No. of the Candidate**

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**CS/B.Tech(BME)/SEM-8/BME-803C/09  
ENGINEERING & MANAGEMENT EXAMINATIONS, APRIL – 2009  
BIO-INFORMATICS ( SEMESTER - 8 )**

Time : 3 Hours ]

[ Full Marks : 70

**INSTRUCTIONS TO THE CANDIDATES :**

1. This Booklet is a Question-cum-Answer Booklet. The Booklet consists of **32 pages**. The questions of this concerned subject commence from Page No. 3.
2. a) In **Group – A**, Questions are of Multiple Choice type. You have to write the correct choice in the box provided **against each question**.  
b) For **Groups – B & C** you have to answer the questions in the space provided marked 'Answer Sheet'. Questions of **Group – B** are Short answer type. Questions of **Group – C** are Long answer type. Write on both sides of the paper.
3. **Fill in your Roll No. in the box** provided as in your Admit Card before answering the questions.
4. Read the instructions given inside carefully before answering.
5. You should not forget to write the corresponding question numbers while answering.
6. Do not write your name or put any special mark in the booklet that may disclose your identity, which will render you liable to disqualification. Any candidate found copying will be subject to Disciplinary Action under the relevant rules.
7. **Use of Mobile Phone and Programmable Calculator is totally prohibited in the examination hall.**
8. You should return the booklet to the invigilator at the end of the examination and should not take any page of this booklet with you outside the examination hall, **which will lead to disqualification**.
9. Rough work, if necessary is to be done in this booklet only and cross it through.

**No additional sheets are to be used and no loose paper will be provided**

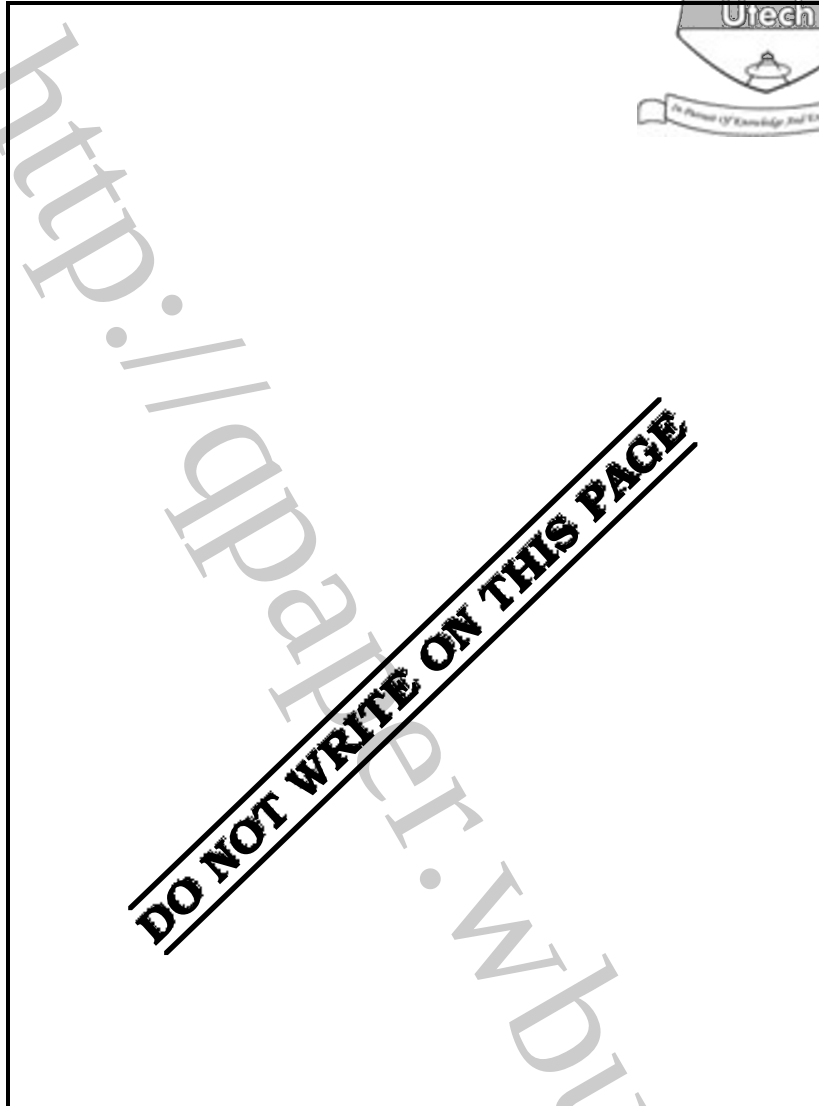
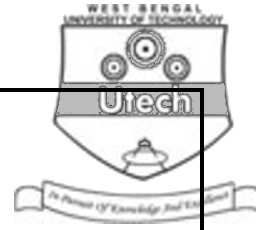
**FOR OFFICE USE / EVALUATION ONLY**

Marks Obtained

	Group – A				Group – B				Group – C					
<b>Question Number</b>													<b>Total Marks</b>	<b>Examiner's Signature</b>
<b>Marks Obtained</b>														

.....  
**Head-Examiner/Co-Ordinator/Scrutineer**

**8888 C/D ( 27/04 )**





ENGINEERING & MANAGEMENT EXAMINATIONS, APRIL - 2009

**BIO-INFORMATICS**

**SEMESTER - 8**



Time : 3 Hours ]

[ Full Marks : 70

**GROUP - A**

**( Multiple Choice Type Questions )**

1. Choose the correct alternatives for the following : 10 × 1 = 10

i) Which one is very powerful tool, as mentioned below, allowing users to formulate queries across a range of different data types via a single interface, without having to worry about underlying data structures, query languages and so on ?

- |                   |                     |                          |
|-------------------|---------------------|--------------------------|
| a) SRS            | b) RFLP             |                          |
| c) Microsatellite | d) Electrophoresis. | <input type="checkbox"/> |

ii) Gene Bank is one of the principal database relevant to

- |             |                   |                          |
|-------------|-------------------|--------------------------|
| a) DNA      | b) <i>m</i> -RNA  |                          |
| c) proteins | d) <i>c</i> -DNA. | <input type="checkbox"/> |

iii) PDB is one of the principal database concerned to

- |             |                   |                          |
|-------------|-------------------|--------------------------|
| a) DNA      | b) RNA            |                          |
| c) proteins | d) <i>r</i> -RNA. | <input type="checkbox"/> |

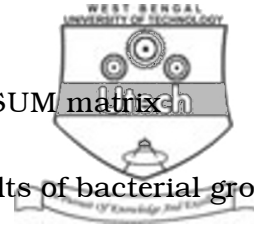
iv) Which one of the following is the sequence similarity search tool ?

- |           |          |                          |
|-----------|----------|--------------------------|
| a) BLASTX | b) FASTA |                          |
| c) Contig | d) EST.  | <input type="checkbox"/> |



v) 'Dayhoff Mutation Data Matrix' is concerned to

- |                    |                                 |                          |
|--------------------|---------------------------------|--------------------------|
| a) PAM matrix      | b) BLOSUM matrix                |                          |
| c) DOT Plot matrix | d) Results of bacterial growth. | <input type="checkbox"/> |



vi) The Needleman and Wunch algorithm is widely used for

- |                    |                     |                          |
|--------------------|---------------------|--------------------------|
| a) local alignment | b) global alignment |                          |
| c) both of these   | d) none of these.   | <input type="checkbox"/> |

vii) In multiple sequence alignment, which one of the following tools is widely used ?

- |          |                |                          |
|----------|----------------|--------------------------|
| a) BLAST | b) CLASTALW    |                          |
| c) EST   | d) SWISS-PROT. | <input type="checkbox"/> |

viii) Maximum Parsimony and UPGMA methods are relevant to

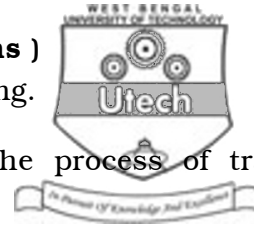
- |                             |                             |                          |
|-----------------------------|-----------------------------|--------------------------|
| a) Phylogenetic analysis    | b) Hierarchical analysis    |                          |
| c) Gene expression analysis | d) Molecular data analysis. | <input type="checkbox"/> |

ix) PAM and BLOSUM are involved in

- |                        |                            |                          |
|------------------------|----------------------------|--------------------------|
| a) dynamic programming | b) stand alone programming |                          |
| c) both of these       | d) none of these.          | <input type="checkbox"/> |

x) In FASTA format of sequence presentation, all presentable characters should be in

- |                |                   |                          |
|----------------|-------------------|--------------------------|
| a) lower case  | b) upper case     |                          |
| c) binary form | d) none of these. | <input type="checkbox"/> |

**GROUP – B****( Short Answer Type Questions )**Answer any *three* of the following.

3 × 5 = 15

2. What is plasmid ? Discuss briefly the steps of the process of transcription in prokaryotes. 1 + 4
3. What is an allosteric enzyme ? Give a brief note on the process of glycolysis. 1 + 4
4. What is gene mutation ? Mention few points paying regards to repair mechanisms of DNA against mutation. 1 + 4
5. Write about the regulation of gene expression. Draw your attention to note some significance in favour of that regulatory effect. 2 + 3
6. What is Genetic Code ? Give a brief note on the process of translation in prokaryotes. 1 + 4

**GROUP – C****( Long Answer Type Questions )**Answer any *three* of the following.

3 × 15 = 45

7. Discuss about the main features of PAM and BLOSUM matrices along with their practical implications. 15
8. Discuss about the different methods of phylogenetic analysis. Among all of the methods which one appears as much suitable to you and why ? 12 + 3
9. Give an account on general architecture of both prokaryotic and eukaryotic genes. 15
10. Discuss briefly about A, B and Z-DNA along with their occurrence. What are positive and negative supercoilings ? 10 + 5
11. What is the linking number of DNA ? Give an account on the structure of nucleosome. 4 + 11
12. Discuss briefly on primary, secondary and tertiary structures of proteins. What is 'domain' in a protein structure ? 10 + 5

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 END