

M.Sc. Part-I Semester-II (CBCS Scheme) Examination
BIOINFORMATICS
(Genomics)
Paper—VI

Time : Three Hours]

[Maximum Marks : 80

Note :- (1) **ALL** questions are compulsory and carry equal marks.

(2) Draw suitable diagrams wherever necessary.

1. Describe :

- | | |
|---|---|
| (a) Organization of prokaryotic genome. | 4 |
| (b) Gene prediction in eukaryotes. | 4 |
| (c) Genome maps | 4 |
| (d) Significance of yeast genome. | 4 |

OR

- | | |
|--|---|
| (p) High through put genome sequencing | 4 |
| (q) Applications of computational genomics | 4 |
| (r) Gene prediction tools in prokaryotes | 4 |
| (s) Genome databases. | 4 |

2. Explain :

- | | |
|-------------------------------------|---|
| (a) DNA array database | 4 |
| (b) Applications of DNA micro array | 4 |
| (c) Annotation of genome sequences | 4 |
| (d) Sequence repeats. | 4 |

OR

- (p) DNA array for global expression profile. 4
 - (q) Transposable elements 4
 - (r) Construction of physical maps 4
 - (s) Sequencing of human genome. 4
3. Describe :
- (a) Compositional analysis 4
 - (b) SNP detection 4
 - (c) Epitope prediction 4
 - (d) Prediction of splice site sequence. 4

OR

- (p) Chromosome rearrangement 4
 - (q) Clustering of genes 4
 - (r) SNP databases 4
 - (s) Prediction of promoter sequences. 4
4. Define comparative genomics. Describe in detail any four applications of comparative genomics of eukaryotes.

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OR

Describe in detail the role of comparative genomics in orthologs and paralogs and in vertical and horizontal gene transfer.

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5. Define UPGMA. Describe in detail distance based phylogenetic analysis.

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OR

Define character based phylogenetic analysis. Describe in detail maximum parsimony and maximum likelihood method.

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