[Total Marks: 60]

N.B. (1) All questions are compulsory.

(2) Draw diagram where necessary.

(3) Answer to every new question must be written on a new page.

Q.1. **One marks questions:**

(1*12= 12 M)

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- a) Write full form of CATH and SCOP.
- b) Give detail of any one tool used for protein classification?
- c) Is Mathews correlation coefficient a protein prediction tool? If not then why it is used?
- d) Explain applications of SWISSPDB VIEWER.
- e) Dali or vast Which tool is better and why?
- f) What is temperature factor in PDB file format explain.

g) Explain Z score output in protein comparison.

- h) Write formula for Q3 prediction.
- i) Explain term Synteny.
- j) Describe segment overlap.
- k) Rosetta is used for.....
- 1) Draw HMM for prokaryotic gene prediction.
- Q.2. (a) Give details of Q3 accuracy method. Enlist its advantages and 6 applications.
 (b) Explain Chou- Fasman method for protein secondary structure 6
 - (b) Explain Chou- Fasman method for protein secondary structure prediction in detail.

OR

- (c) Explain third generation method for secondary structure prediction with example of one tool.
- (d) Describe GOR method for protein secondary structure prediction. 6
- Q.3.
- (a) Enlist and describe in short all 3 methods for protein tertiary structure prediction.
 - (b) Write all comparison between the two protein structure classification databases.

OR

(c) Give details about HSSP and FSSP database in brief. 6

(d) Write a note on *Ab initio* and threading method for protein tertiary 6 structure prediction.

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(b) Describe OMIM database.

OR

(c) Give details of any one strategy for disease gene identification.

- (d) Draw and explain schematic representation of elements involved in bacterial transcription initiation. Describe working of one tool by which prokaryotic gene can be predicted.
- Q.5.

(a) What are Markov model and its various orders? Explain with example construction of HMM.

(b) Describe gene prediction in prokaryotes using HMM.

OR

(c) What are markov models? Explain HMM and IMM with duration 6 and their differences.

(d) Explain generalized pair HMM used for gene prediction.

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