

4. Write a note on the follow points :—
  - (a) Sequence alignment based on evolutionary model.
  - (b) Reliability of phylogenetic predictions.
5. Write a note on promoter prediction in eukaryotes.
6. Describe any two software packages for gene prediction in prokaryotes.
7. Write a note on the following :—
  - (a) Domains in the protein structure
  - (b) Beta sheet in protein structure.
8. Write a note on the tools and techniques for the B cell epitope prediction using protein sequences.

**Exam. Code : 206602**  
**Subject Code : 4788**

**M.Sc. Bioinformatics 2<sup>nd</sup> Semester**

**COMPUTATIONAL METHODS FOR SEQUENCE  
ANALYSIS**

**Paper—BI-524**

Time Allowed—2 Hours] [Maximum Marks—75

**Note :—** There are *eight* questions of equal marks.  
Candidates are required to attempt any  
*four* questions.

1. Write the difference between the following :—
  - (a) PSI-BLAST and PHI-BLAST
  - (b) BLAST and FASTA.
2. Describe the following with proper explanations :—
  - (a) CLUSTALW and PILEUP
  - (b) Iterative methods of MSA, and scoring MSA.
3. Describe the following with proper explanations :—
  - (a) Distance methods of phylogenetic trees
  - (b) Maximum Parsimony method for phylogenetic trees.