

SUMMARY

Title: *Application of Pattern Matching for Sequence Analysis Techniques in Bioinformatics*

Problem under consideration in the proposed research work aims at applying computational pattern matching techniques for some of the most important sequence comparison & analysis problems in the field of bioinformatics. Studied Problems (Sequence Comparison Problems) are from the field of molecular biology; however the solutions employed is purely computational in the form of Newer Algorithms or Computational Model/Strategy.

The following problems have been addressed in the current work:

- Pairwise Sequence Alignment.
- Multiple Sequence Alignment.
- Secondary Structure Prediction of Proteins.
- Pattern Searching (Exact/Approximate) in Sequence Databases.
- Gene Prediction.

Certain upcoming issues are also discussed in the form of reviews and providing theoretical models.

The research methodology for applying computational techniques is in the form of reviews, design and modeling, writing newer algorithms, comparative study followed by their analysis, implementation and validation by incorporating them in a software tool. Computational methods/techniques like neural network, nearest neighbor technique, models based on parallel processing like parallel algorithms and pipelining, object oriented techniques, hashing, suffix trees, concepts of RDBMS, use of efficient sequential algorithms etc. have been employed while providing the solutions to the considered sequence comparison problems. Most of the applied methods and algorithms have been implemented in an integrated tool by the name "Sequence Comparison and Analysis Tool [SCAT]" with a purpose of testing, validation and comparison of the various proposed algorithms along with some standard algorithms.

Presented algorithms are novel and original in their approach that provides a new direction to solve the problems. Few of the presented algorithms provide time complexities comparable to the best existing standard algorithms and others provide the basis for newer dimensions/methodologies towards the solution of the problems.