A Meta-Heuristic Optimization Tool for Simplified Protein Structure Prediction

Dr. Gurpreet Lakha¹

Metaheuristics have been used extensively in last few decades because of their success in solving complex problems in science and engineering. Even though metaheuristics do not guarantee the optimality of the obtained solutions, they are among the most promising and successful techniques which can solve optimization problems with a reasonable accuracy and time. Despite this success, some of the problems are highly complex and still need new/improved metaheuristic techniques to reach at optimal solution. Improvements can be done by careful analysis of the existing algorithms, and/or by adding/removing feature(s) or by hybridization among different algorithms. We have designed a software tool to aid this process of optimizing protein folding in a simplified model. This talk is aimed at demonstrating the tool and its functionality.

¹Department of Computer Science, University of Northern British Columbia, Prince George, BC, V2N4Z9, Canada (lakha@unbc.ca).