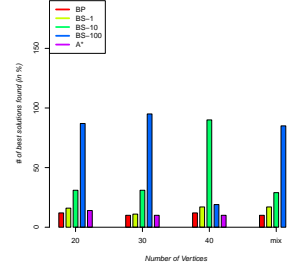
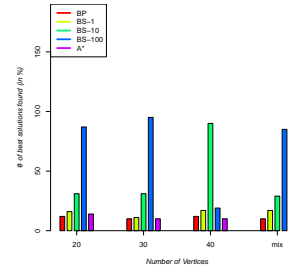


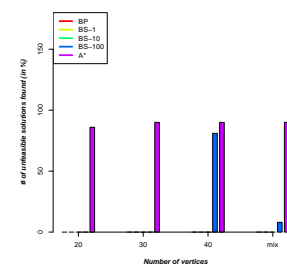
(a) Deviation



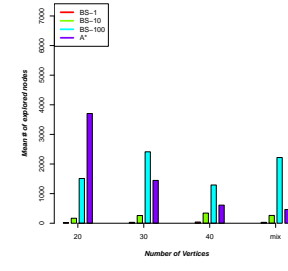
(b) Matching dissimilarity



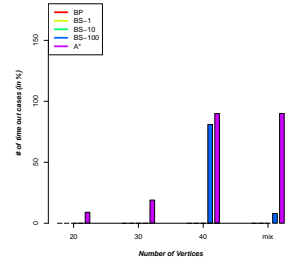
(c) Number of best found distance



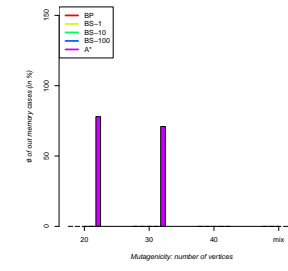
(d) Number of Unfeasible Solutions



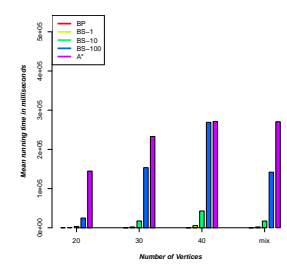
(e) Number of Explored Nodes



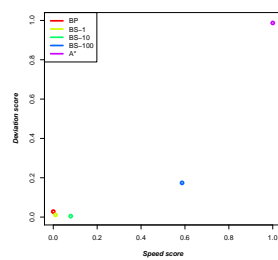
(f) Number of Time-Outs



(g) Number of Out-of-Memory cases



(h) Running Time



(i) Time-Deviation Scores

Fig. 1. Results on Protein and under a reasonable time constraint ($C_T = 300$ seconds).