Abstract
Phylogenetics is the study of evolutionary relations between different organisms. Phylogenetic trees are the representations of these relations. Researchers have been working on finding fast and systematic approaches to reconstruct phylogenetic trees from observed data for over 40 years. It has been shown that, given a certain criterion to evaluate each tree, finding the best fitted phylogenetic trees among all possible trees is an NP-hard problem. In this study, we focus on the topology searching techniques for the maximum-parsimony and maximum-likelihood phylogeny inference. We proposed two search algorithms based on tabu search and genetic algorithms. We first explore the feasibility of using tabu search for finding the maximum-parsimony trees. Then assess the efficiency and accuracy of the proposed algorithms. The experimental results indicate that the hybrid method of the tabu search and the genetic algorithm can provide maximum-parsimony trees with a good level of accuracy and efficiency. The hybrid method is also implemented for finding maximum-likelihood trees. The experimental results show that the proposed hybrid method produce better maximum-likelihood trees than the default-setting dnaml program in average on the tested data sets. On a much larger data set, the hybrid method outperforms the default-setting dnaml program and has equally good performance as the dnaml program with the selected jumble option.