HAKUBI RESEARCHERS' ACTIVITIES IN ICR

Hakubi Project: Fosterage and Support of Young Researchers, Kyoto University

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Outline of Research

A ''consensus tree'' is a single phylogenetic tree that summarizes the branching structure in a given set of conflicting phylogenetic trees. We developed new deterministic algorithms for constructing several popular types of consensus trees that are faster than all the previously known ones. Given k phylogenetic trees with n leaves each and with identical leaf label sets, our algorithms run in $O(n k)$ time [majority rule consensus tree], $O(n k)$ time [loose consensus tree], $O(n^2 k)$ time [greedy consensus tree], and $\min\{O(k n^2), O(k n (k + \log^2 n))\}$ time [frequency difference consensus tree]. We also implemented our algorithms to make sure that they are practical and applied them to various simulated data sets. These experiments suggested that the running times of our deterministic algorithms are already comparable to (and in many cases, better than) those of the randomized methods found in widely used software packages such as PHYLIP.