HAKUBI RESEARCHERS' ACTIVITIES IN ICR

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

Research Topic



Algorithmic Graph Theory with Applications to Bioinformatics

Host Laboratory Laboratory of Mathematical Bioinformatics **Host Professor** AKUTSU, Tatsuya

Program-Specific Assoc Prof JANSSON, Jesper (Ph D)

Outline of Research

This year, my research collaborators and I have continued our work on efficient algorithms for computing different types of consensus trees. Given an input consisting of k phylogenetic trees with n leaves each and with identical leaf label sets, the running times of our algorithms are:

- O(k n) time [majority rule consensus tree],
- O(k n) time [loose consensus tree],
- O(k n²) time [greedy consensus tree],
- min{O(k n²), O(k n (k + log^{2} n))} time [frequency difference consensus tree],
- O(k n log n) [Adams consensus tree],
- $O(n^2)$ [R* consensus tree with k=2],
- O(n² log^{4/3} n) [R* consensus tree with k=3],
- O(n² log^(k+2) n) [R* consensus tree with k>3],
- O(k n³ + 2.733ⁿ) [minimally resolved local consensus tree], and
- O(k n³ + 4ⁿ poly(n)) [minimally rooted-triplet-inducing consensus tree].