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専門分野： Efficient Graph Algorithms with Applications to Bioinformatics
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◆研究キーワード / Keywords

Algorithms / Phylogenetics / Combinatorial pattern matching / Graph theory / Computational complexity

◆主要業績

総数 (7) 件

- [Academic book] J. Jansson. "Directed Perfect Phylogeny (Binary Characters) -- 1991; Gusfield". Invited chapter in Springer's Encyclopedia of Algorithms, pp. 246-248, Springer Science+Business Media, LLC.,2008. ISBN: 978-0-387-36061-4.
- [Academic book] J. Jansson. "Perfect Phylogeny (Bounded Number of States) -- 1997; Kannan, Warnow". Invited chapter in Springer's Encyclopedia of Algorithms, pp. 644-647, Springer Science+Business Media, LLC.,2008. ISBN: 978-0-387-36061-4.
- [Academic book] J. Jansson. "Phylogenetic Tree Construction from a Distance Matrix -- 1989; Hein". Invited chapter in Springer's Encyclopedia of Algorithms, pp. 651-653, Springer Science+Business Media, LLC.,2008. ISBN: 978-0-387-36061-4.
- [Academic book] J. Jansson and W.-K. Sung. "The Maximum Agreement of Two Nested Phylogenetic Networks". Chapter 4 of New Topics in Theoretical Computer Science, pp. 119-141, Nova Science Publishers, Inc., New York, 2008. ISBN: 978-1-60456-100-5.
- [Research paper] J. Byrka, S. Guillemot, and J. Jansson. "New Results on Optimizing Rooted Triplets Consistency". Proceedings of the Nineteenth Annual International Symposium on Algorithms and Computation (ISAAC 2008), Lecture Notes in Computer Science Vol. 5369, pp. 484-495, Springer-Verlag Berlin Heidelberg, 2008.

◆研究内容 / Research Pursuits

My research is focused on Graph Algorithms and Bioinformatics. During AC 2008, I worked on the following topics: Combining a given set of rooted triplets into a phylogenetic supertree which keeps as much branching information as possible, graph edge orientation to maximize the minimum weighted outdegree, periodic graph traversal by an oblivious agent, geometric network design, approximate pattern matching in node-labeled trees, succinct representation of bit vectors supporting efficient rank and select queries, algorithms for computing a smallest multi-labeled phylogenetic tree, faster methods for searching in 3D-structure databases of proteins, and inferring a chemical structure from a path frequency vector. During AC 2008, I also finished writing three entries for Springer-Verlag's "Encyclopedia of Algorithms" entitled "Phylogenetic Tree Construction from a Distance Matrix", "Directed Perfect Phylogeny (Binary Characters)", and "Perfect Phylogeny (Bounded Number of States)", served as a member of the Journées Ouvertes Biologie Informatique Mathématiques (JOBIM 2008) organizing committee in Lille (France), served as a program committee member of the Second International Conference on Theories and Applications of Computer Science (ICTACS'09) in Nha Trang (Vietnam), reviewed several papers for various international conferences and journals, wrote four article summaries for American Mathematical Society (AMS)'s Mathematical Reviews (MR), and joined the editorial board of a new international journal named "Algorithms", ISSN 1999-4893, Molecular Diversity Preservation International (MDPI).

◆教育内容 / Educational Pursuits

I did not have any opportunities to participate in any teaching activities during AC 2008.

◆研究計画

- 1) During AC 2009, I will continue my collaboration with scientists from some of the most famous universities and research institutes in Japan (University of Tokyo, Kyoto University, Kyushu University, National Institute of Informatics, and JAIST) and other countries (U.K., France, Sweden, Slovakia, Switzerland, Poland, Canada, Singapore, and China).
- 2) I expect to publish many good papers in international conferences and reputable journals.
- 3) In case my grant applications for inviting guests to Japan are successful, I plan to start one new research project related to phylogenetic networks with researchers in Spain and one new research project related to graph pattern matching with a researcher from Russia.

◆メッセージ

I believe that the main objective of all science is to explain complicated things in simple ways. This provides us with concepts to handle the massive amounts of information in nature, and also allows us to develop efficient tools that help us to further understand and manipulate the underlying patterns and mathematical structures. If you would like to study abstract, combinatorial problems with elegant solutions which have important applications to Bioinformatics, please join our lab!