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学位： Ph.D. (Computer Science, Lund University, 2003)
専門分野： Efficient Graph Algorithms with Applications to Bioinformatics
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◆研究キーワード / Keywords

Graph theory / Combinatorial pattern matching / Phylogenetics / Dynamic programming / NP-hardness

◆主要業績

総数 (10) 件

- [Academic book] J. Jansson and K. Sadakane. "Succinct Representation of Bit Vectors Supporting Efficient rank and select Queries". Expert Commentary in Software Engineering and Development, pp. 3-12, Nova Science Publishers, Inc., New York, 2009. ISBN: 97
- [Research paper] A. Czumaj, J. Czyzowicz, L. Gasieniec, J. Jansson, A. Lingas, and P. Zylinski. "Approximation Algorithms for Buy-at-Bulk Geometric Network Design". Proceedings of the Eleventh International Symposium on Algorithms and Data Structures (WAD
- [Research paper] J. C. Clemente, J. Jansson, and G. Valiente. "Accurate Taxonomic Assignment of Short Pyrosequencing Reads". Proceedings of the Fifteenth Pacific Symposium on Biocomputing (PSB 2010), PSB Online Proceedings, pp. 3-9, 2010.
- [Research paper] T. Shibuya, J. Jansson, and K. Sadakane. "Linear-Time Protein 3-D Structure Searching with Insertions and Deletions". Algorithms for Molecular Biology, Vol. 5, Article 7, BioMed Central Ltd., 2010 (special issue containing selected papers
- [Research paper] J. Byrka, S. Guillemot, and J. Jansson. "New Results on Optimizing Rooted Triplets Consistency". Discrete Applied Mathematics, Vol. 158, Number 11, pp. 1136-1147, Elsevier B.V., 2010.

◆研究内容 / Research Pursuits

My research is about graph algorithms and bioinformatics. More specifically, I worked on the following topics during AC 2009: 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, inferring a chemical structure from a path frequency vector, accurate taxonomic assignment of ambiguous pyrosequencing reads, and fast computation of the Robinson-Foulds distance between phylogenetic networks. I attended the following international refereed conferences to present my research: SIROCCO 2009 in Piran (Slovenia), WADS 2009 in Banff (Canada), WABI 2009 in Philadelphia (U.S.A.), and ISAAC 2009 in Honolulu (U.S.A.). During AC 2009, I also wrote three article summaries for American Mathematical Society (AMS)'s Mathematical Reviews (MR), refereed several papers for various international conferences and journals, and worked as a member of the editorial board of an international journal named "Algorithms", ISSN 1999-4893, Molecular Diversity Preservation International (MDPI). Finally, I was one of the three speakers at Ochanomizu University's Tutorial Workshop on Discrete Algorithms and Machine Learning on 2009-07-01, and my talk was entitled "Discrete Algorithms for Inferring Phylogenetic Trees".

◆教育内容 / Educational Pursuits

Guest lecturer at Ochanomizu University in the following courses: "General Bioinformatics" (2009-11-25), "Rigaku Souron" (2009-11-30), and "Bioinformatics/Data Mining" (2010-01-28).

◆研究計画

Research plan:

1) My next two projects will consider the complexity of inferring a minimally resolved phylogenetic supertree and how to compute the so-called R^* distance between two trees in subcubic time. 2) I expect to publish many good papers in international conferences and reputable journals. 3) During AC 2010, 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).

◆メッセージ

Please contact me if you are interested in finding elegant solutions to combinatorial problems which have important applications to Bioinformatics.