氏名	**Jesper Jansson**
	JESPER JANSSON
所属	お茶大アカデミック・プロダクション
職名	特任助教
学位	Ph.D. in Computer Science, Lund University, Sweden, 2003.
専門分野	Efficient graph algorithms with applications to Bioinformatics.
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■ 研究者キーワード / Keywords

Graph theory
Combinatorial pattern matching
Phylogenetics
Dynamic programming
NP-hardness

■ 主要業績

[Research paper] J. Jansson and Z. Peng. "Algorithms for Finding a Most Similar Subforest". Theory of Computing Systems, Vol. 48, Number 4, pp. 865-887, Springer-Verlag New York, 2011.

[Research paper] J. C. Clemente, J. Jansson, and G. Valiente. "Flexible taxonomic assignment of ambiguous sequencing reads". BMC Bioinformatics, Vol. 12, Article 8, BioMed Central Ltd., 2011.

[Research paper] Y. Asahiro, J. Jansson, E. Miyano, H. Ono, and K. Zenmyo. "Approximation Algorithms for the Graph Orientation Minimizing the Maximum Weighted Outdegree". Journal of Combinatorial Optimization, Vol. 22, Number 1, pp. 78-96, Springer Science+Business Media, LLC., 2011.

[Research paper] J. Jansson and W.-K. Sung. "Constructing the R* Consensus Tree of Two Trees in Subcubic Time". Proceedings of the Eighteenth Annual European Symposium on Algorithms (ESA 2010), Lecture Notes in Computer Science Vol. 6346, pp. 573-584, Springer-Verlag Berlin Heidelberg, 2010.

[Research paper] J. Jansson, R. S. Lemence, and A. Lingas. "The Complexity of Inferring a Minimally Resolved Phylogenetic Supertree". Proceedings of the Tenth International Workshop on Algorithms in Bioinformatics (WABI 2010), Lecture Notes in Computer Science Vol. 6293, pp. 262-273, Springer-Verlag Berlin Heidelberg, 2010.

■ 研究内容 / Research Pursuits

My research is about graph algorithms. In short, I develop new mathematical theories and computational techniques for solving practically important problems that can be expressed elegantly using graphs and tree structures. The goal is to design simple, efficient, and flexible methods that may be useful in many different situations. I am especially interested in computational/combinatorial problems originating from the biological sciences, and I believe that this line of research will continue to grow in importance in the 21st century. I worked on the following research topics during AC 2010: Combining a given set of rooted triplets into a phylogenetic supertree which keeps as much branching information as possible, the polynomial-time inapproximability of inferring a minimally resolved supertree and its connection to the chromatic number of a graph, how to construct the R* consensus tree of two given (rooted) trees efficiently, edge orientation to minimize the maximum weighted outdegree of an input undirected graph, periodic graph traversal by an oblivious agent, geometric network design, approximate pattern matching in node-labeled trees, algorithms for computing a smallest multi-labeled phylogenetic tree, 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. This resulted in several published papers together with researchers from famous universities in Japan and elsewhere.

I attended the following international refereed conferences to present my research: CPM 2010 in New York (U.S.A.) and ESA 2010 in Liverpool (U.K.). Furthermore, I was one of six invited plenary speakers at the 2010 MSP Annual Convention in Cebu City in May 2010, organized by the Mathematical Society of the Philippines (MSP), with about 350 mathematicians, university students, and high school teachers attending my talk. During AC 2010, I also wrote three article summaries for American Mathematical Society (AMS)'s Mathematical Reviews (MR), refereed 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 a program committee member of one international conference: the Fifth International Conference on Language and Automata Theory and Applications (LATA 2011) in Tarragona (Spain). My current Microsoft Academic Search ranking is #2 out of 203 researchers from Ochanomizu University.

教育内容 / Educational Pursuits

Lecturer at Ochanomizu University for the "Rigaku Souron" course (2010-12-06). Lecturer at "The 3rd CompView Fall School on Algorithmic Bioinformatics", organized by Global COE: CompView at Tokyo Institute of Technology (2010-09-01).

研究計画

I wish to continue my current research projects as well as consider some new related topics. For example, I have recently become interested in data compression and will work with Dr. Sadakane at National Institute of Informatics (NII) in Tokyo on a novel, promising type of data compression which we call "CRAM: Compressed Random Access Memory". Basically, it allows a compressed file to be modified without decompressing the entire file. In another project, Dr. Sung at National University of Singapore and I are going to create new algorithms for computing consensus trees for multi-labeled phylogenetic trees. I expect to publish several good papers in international conferences and reputable journals, and to collaborate with researchers from many different countries.

メッセージ

A few projects for graduate students are available. Please contact me if you are interested.