

Mukul S. Bansal

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Voice: (515) 520 1017
- Research Interests** **Algorithms** and Problem Solving in general. In particular, algorithmic and theoretical problems motivated by phylogenetics and computational biology, graph theoretic algorithms, combinatorial optimization, approximation algorithms.
- Education** **Ph.D. Candidate**, Fall 2004 - Present *G.P.A.* 3.90 /4.0
Department of Computer Science *Advisor:* David Fernández-Baca
Iowa State University, Ames, Iowa

Master of Science, Fall 2006 *G.P.A.* 3.90 /4.0
Department of Computer Science *Advisor:* David Fernández-Baca
Iowa State University, Ames, Iowa
Thesis Title: Algorithms for minimum bipartite fill-in and the gene-duplication problem

Bachelor of Technology, July 2004
Department of Computer Science and Engineering
International Institute of Information Technology, Hyderabad, India
- Awards and Honors**
- Awarded the Dr. Robert Stewart Early Research Recognition Award by the Department of Computer Science at Iowa State University, for the academic year 2007–2008. It is awarded competitively to one graduate student each academic year.
 - Awarded the Premium for Academic Excellence (PACE) Award during Fall 2004 and spring 2005. It is awarded competitively to approximately 10% of incoming graduate students at Iowa State University.
 - Secured 99th percentile in the Physics Olympiad at state level in India (1999).
 - Secured a top ten position in the Regional Mathematics Olympiad (state level) conducted by the National Board of Higher Mathematics in India (1998).
- Journal and Conference Publications**
- Mukul S. Bansal and Oliver Eulenstein, “An $\Omega(n^2/\log n)$ Speed-Up of TBR Heuristics for the Gene-Duplication Problem”, *IEEE/ACM Transactions on Computational Biology and Bioinformatics (In press)*.
- Mukul S. Bansal and Oliver Eulenstein, “The Multiple Gene Duplication Problem Revisited”, *ISMB 2008; Bioinformatics* 2008, 24(13): i132–i138.
- Mukul S. Bansal and Oliver Eulenstein, “The Gene-Duplication Problem: Near-Linear Time Algorithms for NNI Based Local Searches”, *ISBRA 2008, LNCS/LNBI 4983*: 14–25.
- A. Wehe, Mukul S. Bansal, J. G. Burleigh and O. Eulenstein, “DupTree: A program for large-scale phylogenetic analyses using gene tree parsimony”, *Bioinformatics* 2008, 24(13): 1540–1541.
- Mukul S. Bansal, Jianrong Dong and David Fernández-Baca, “Comparing and Aggregating Partially Resolved Trees”, *LATIN 2008, LNCS 4957*: 72–83.
- J. G. Burleigh, Mukul S. Bansal, André Wehe and O. Eulenstein, “Locating Multiple Gene Duplications Through Reconciled Trees”, *RECOMB 2008, LNCS/LNBI 4955*: 273–284.
- Duhong Chen, J. G. Burleigh, Mukul S. Bansal and David Fernández-Baca, “PhyloFinder: An Intelligent Search Engine for Phylogenetic Tree Databases”, *BMC Evolutionary Biology* 2008, 8:90.
- Mukul S. Bansal and Oliver Eulenstein, “An $\Omega(n^2/\log n)$ Speed-Up of TBR Heuristics for the Gene-Duplication Problem”, *WABI 2007, LNCS/LNBI 4645*: 124–135.

Mukul S. Bansal, J. G. Burleigh, O. Eulenstein and A. Wehe, "Heuristics for the Gene-Duplication Problem: A $\Theta(n)$ Speed-Up for the Local Search", *RECOMB 2007, LNCS/LNBI 4453*: 238–252.

Mukul S. Bansal and V.Ch.Venkaiah, "A Note on Finding a Maximum Clique in a Graph Using BDDs", *Australasian Journal of Combinatorics*, 32 (2005): 253–258.

Technical Reports

Mukul S. Bansal and V. Ch. Venkaiah, "Improved Fully Polynomial Time Approximation Scheme for the 0-1 Multiple-choice Knapsack Problem", *SIAM Conference on Discrete Mathematics*, 2004; *Tech. Report No. IIT/TR/2004/3, International Institute of Information Technology, India*.

Research Software

DupTree: This is a tool box that allows the user to heuristically search for a species supertree that best reconciles the input gene trees under the gene duplication model. Joint work with André Wehe (with support from Oliver Eulenstein). This toolbox can be downloaded from <http://genome.cs.iastate.edu/CBL/DupTree/>.

ExactMGD: This is a program that can be used to infer (and identify) the smallest number of multiple gene duplication episodes that can reconcile the given gene trees with a given species tree. It is based on the multiple gene duplication model introduced by Guigó et al. in 1996.

PhyloFinder: This is an intelligent search engine for phylogenetic tree databases. Joint work with Duhong Chen, J.G. Burleigh and David Fernández-Baca. An implementation of PhyloFinder using TreeBASE data is available at <http://pilin.cs.iastate.edu/phylofinder/>.

Work Experience

Visiting Researcher: Sanderson Lab, University of Arizona

Summer 2007: Worked with Prof. Mike Sanderson on computational problems related to multiple gene duplication and polyploidy.

Research Assistant: Iowa State University

Spring, Fall 2007: Worked on problems related to gene and genome duplication and computing distances between phylogenetic trees.

Spring, Summer 2006: Worked on problems related to chordal bipartite graphs, and gene duplication.

Summer 2005: Worked on problems related to phylogenetics and chordal bipartite graphs.

Teaching Assistant: Iowa State University

Spring 2008: ComS 418/518: Computational Geometry (graduate level course).

Fall 2006: ComS 511: Design and Analysis of Algorithms (graduate level course).

Fall 2005: ComS 228: Introduction to Data Structures Using Java.

Summer 2005: ComS 227: Introduction to Object Oriented Programming (using Java).

Spring 2005: ComS 228: Introduction to Data Structures Using C++.

Fall 2004: ComS 227: Introduction to Object Oriented Programming (using C++).

Relevant Graduate Level Courses

Design and Analysis of Algorithms, Theory of Computation, Advanced Topics in the Analysis of Algorithms, Game Theory, Fundamental Algorithms in Computational Biology, Modern Graph Theory, Advanced Algorithms in Computational Biology, Principles of Operating Systems, Introduction to Parallel Algorithms and Programming, Advanced Topics in Database Systems.

Technologies

Programming Languages: C, C++, Java

Platforms: Linux, Solaris, Win 9x/ME/2K/XP

Other Technologies: MySQL, MPI, POSIX Threads, HTML

References

Available upon request.