

## Ganeshkumar Ganapathy

National Evolutionary Synthesis Center (NESCent) at Duke University  
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### RESEARCH EXPERTISE

Population genomics, phylogenetics, statistical evolutionary biology, computational biology, combinatorial algorithms.

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### EDUCATION

**NESCent, Duke University** Postdoctoral fellowship, December 2006-present.

Principal collaborator: Dr. Marcy Uyenoyama

Statistical evolutionary biology and population genetics: human-chimp-gorilla ancestral population genomics; statistical models and methods to analyze genomic SNP data; a sample-based approach to estimate character-specific diversification rates.

**University of Texas at Austin** Ph.D, 2000-2006.

Advisors: Dr. Tandy Warnow and Dr. Vijaya Ramachandran

Algorithms and heuristics for combinatorial optimization in phylogenetics: ML and MP phylogenetic estimation; identifying congruences between phylogenetic trees and between area cladograms.

**Birla Institute of Technology and Science, Pilani, India** B.E. (Hons.) Computer Science, 1999.

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### FELLOWSHIPS AND GRANTS

- NESCent postdoctoral fellowship. Ancestral population genomics with an explicit model of coalescent with recombination. 2008-2009.
  - NESCent postdoctoral fellowship. New disc-covering methods for maximum likelihood, and pattern identification in biogeography. 2006-2008.
  - Student travel grant, University of Texas at Austin, 2004.
  - Microelectronics and Computer Development graduate fellowship, University of Texas at Austin, 2000-2001.
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### PEER-REVIEWED JOURNAL PUBLICATIONS

1. J. Dutheil, G. Ganapathy, M. K. Uyenoyama, A. Hobolth, M. Schierup and T. Mailund. Speciation times and effective population sizes using an explicit model of the coalescent with recombination: Application to the Human-Chimp-Gorilla-Orangutan system. To appear in *Genetics*, 2009. doi:10.1534/genetics.109.103010
2. G. Ganapathy and M. K. Uyenoyama. Site frequency spectra from genomic SNP surveys. *Theoretical Population Biology*, 75(4), pages 346-354, 2009.
3. G. Ganapathy, H. Le, B. Goodson, R. Jansen, V. Ramachandran, and T. Warnow. Pattern identification in biogeography. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, vol. 3, no. 4, pages 334-346, 2006.

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## PEER-REVIEWED CONFERENCE PUBLICATIONS

*(In computer science, conference proceedings are the primary outlet for original work and are thus peer-reviewed with high rejection rates and considered the equivalent of a journal publication.)*

4. G. Ganapathy, B. Goodson, R. Jansen, V. Ramachandran, and T. Warnow. Pattern identification in biogeography. In Proceedings of the Fifth International Workshop on Algorithms in Bioinformatics (WABI), pages 112–127, 2005. ([estimated impact factor in the top 25%](#))
5. G. Ganapathy, V. Ramachandran, and T. Warnow. On contract-and-refine-transformations between phylogenetic trees. In Proceedings of the Fifteenth ACM-SIAM Symposium on Discrete Algorithms (SODA), pages 893–902, 2004. (estimated impact factor in the top 9%: [assessment 1](#), [assessment 2](#))
6. G. Ganapathy, V. Ramachandran, and T. Warnow. Better hill-climbing searches for parsimony. In Proceedings of the Third International Workshop on Algorithms in Bioinformatics (WABI), pages 245–258, 2003. ([estimated impact factor in the top 25%](#))
7. G. Ganapathy and T. Warnow. Approximating the complement of the maximum compatible subset of leaves of  $k$  trees. In Proceedings of the Fifth International Workshop on Approximation Algorithms for Combinatorial Optimization (APPROX), pages 122–134, 2002. ([estimated impact factor in the top 25%](#))
8. G. Ganapathy and T. Warnow. Finding the maximum compatible tree for a bounded number of trees with bounded degree is solvable in polynomial time. In Proceedings of the First International Workshop on Algorithms and Bioinformatics (WABI), pages 156–163, 2001. ([estimated impact factor in the top 25%](#))

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## OPINION AND COMMENTARY

9. B. W. Sidlauskas, G. Ganapathy, S. Price, E. Hazkani-Covo, L. W. McCall, P. Spaeth, K. P. Jenkins, R. Scherle and H. Lapp, D. M. Kidd. Linking big: The continuing promise of evolutionary synthesis. To appear in *Evolution*, 2009.

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## TALKS AND CONFERENCE PRESENTATIONS

1. Human-Chimp-Gorilla ancestral population genomics using an explicit model of the coalescent with recombination. Evolution meeting, University of Idaho, June 12-16, 2009.
2. Human-Chimp-Gorilla ancestral population genomics using an explicit model of the coalescent with recombination. Cornell University, April 12, 2009.
3. Human-Chimp-Gorilla ancestral population genomics using an explicit model of the coalescent with recombination. Bioinformatics Research Center, North Carolina State University, Raleigh, USA, Sep. 11, 2008 (*invited*).
4. Introductory phylogenetics. video-conference guest lecture delivered to undergraduate students at the University of Puerto Rico. February 2007.
5. On contract-and-refine transformations between phylogenetic trees. Fifteenth ACM/SIAM Symposium on Discrete Algorithms, New Orleans, USA, Jan. 11-13, 2004.
6. Better hill-climbing searches for parsimony. Third International Workshop on Algorithms in Bioinformatics, Budapest, Hungary, Sep. 15-20, 2003.

7. Approximating the complement of the maximum compatible tree of  $k$  trees. Fifth International Workshop on Approximation Algorithms for Combinatorial Optimization, Rome, Italy, Sep. 17-21, 2002.
  8. Finding the maximum compatible tree for a bounded number of trees with bounded degree is solvable in polynomial time. First International Symposium on Algorithms in Bioinformatics, Aarhus, Denmark, August 28-31, 2001.
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## TEACHING AND MENTORING

### Student mentoring

- Mentees: two Duke University undergraduate students, Alexandra Balaban and Perry Zheng.
  - Duration: Three semesters in 2008-2009.
  - Responsibilities: Teaching basic statistics, evolutionary biology and programming, project management, and general academic advising.
  - Project: Design and implementation of methods to estimate speciation and extinction rates that may depend on a character state.
- Mentee: Duke University graduate student, Nihshanka Debroy.
  - Duration: One semester (fall 2007).
  - Project: Design and implementation of a simulator for a stochastic model of speciation and extinction with migration.
- Served as mentor to two undergraduate students through the Undergraduate Diversity at SSE/SSB program at the 2009 annual Evolution meeting.

**Computer Science** Teaching assistant, UT Austin, five semesters between 2001-2006.

- Courses: graduate algorithms, undergraduate algorithms and discrete mathematics.
- Responsibilities: held tutorial sessions, prepared and evaluated tests, quizzes and exams.

**Engineering** Undergraduate teaching assistant, UT Austin, fall 1998.

- Course: senior-level control systems.
  - Responsibilities: helped prepare tutorial assignments, and helped students solve them in class.
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## PROFESSIONAL SERVICES AND AFFILIATIONS

### Conference Organization

Program committee member, 9<sup>th</sup> International Workshop on Algorithms in Bioinformatics, 2009

### External reviewer

- Journals: Molecular Biology and Evolution, Genetics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Bioinformatics, Journal of Biomedical Informatics, Theoretical Computer Science;
- Conferences: RECOMB, WABI, COCOON.

### Professional memberships

Society for the Study of Evolution, 2009-2010

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## WORK EXPERIENCE

Software Engineer

Silicon Automation Systems (now Sasken), Bangalore, India, 1999-2000  
Designed and implemented a MPEG-2 video decoder in C++

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## REFERENCES

1. **Dr. Tandy Warnow** (Ph.D. Dissertation Advisor)  
Professor, Department of Computer Sciences  
Co-Director, Center for Computational Biology and Bioinformatics  
University of Texas at Austin  
  
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1 University Station C0500, Austin, TX 78712-0233 USA
2. **Dr. Vijaya Ramachandran** (Ph.D. Dissertation Advisor)  
Blakemore Regents Professor, Department of Computer Sciences  
University of Texas at Austin  
  
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Address: Department of Computer Sciences, The University of Texas at Austin  
1 University Station C0500, Austin, TX 78712-0233 USA
3. **Dr. Marcy K. Uyenoyama** (collaborator, 2007-present)  
Professor, Department of Biology  
Duke University  
  
Phone: (Office) (919) 660-7350 (Fax) (215) 660-7293  
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4. **Dr. Asger Hobolth** (collaborator, 2007-present)  
Associate Professor, Department of Mathematical Sciences  
University of Aarhus  
  
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