

Education

- 2006 – 2010 **Massachusetts Institute of Technology**
Ph.D. in Computer Science
Supervisor: Assoc. Prof. Manolis Kellis
Thesis title: Methods and Analysis of Genome-scale Gene Family Evolution Across Multiple Species
GPA: 4.9/5.0
- 2004–2006 **Massachusetts Institute of Technology**
Masters of Science in Electrical Engineering and Computer Science
Supervisor: Assoc. Prof. Manolis Kellis
Thesis title: Probabilistic Framework for Genome-wide Phylogeny and Orthology Determination
Thesis earned the MIT William A. Martin Award for best M.S. thesis in the field of Computer Science
GPA: 5.0/5.0
- 2000–2004 **University of Minnesota**
Bachelor of Science in Mathematics, Bachelor of Science in Computer Science
GPA: 3.872/4.0 (*summa cum laude*)
UMTYMP (University of Minnesota Talented Youth Math Program), Solar Vehicle Project

Research Experience

- 4/2011 – Present **Cornell - Biological Statistics and Computational Biology** Ithaca, NY
Postdoctoral Researcher
Developing models in phylogenetics and population genetics. Supervised by Assoc. Prof. Adam Siepel.
- 9/2010 – 4/2011 **MIT - Computer Science and Artificial Intelligence** Cambridge, MA
Postdoctoral Researcher
Integrated computational models from phylogenetics and population genetics. Supervised by Assoc. Prof. Manolis Kellis.
- 2004 – 2010 **MIT - Computer Science and Artificial Intelligence** Cambridge, MA
Masters Thesis, Ph.D. Thesis
Developed phylogenomic algorithms for analyzing gene duplications and losses in multiple mammalian, fungal, and fly genomes. Supervised by Assoc. Prof. Manolis Kellis.
- Summer 2004 **Yahoo Research Labs** Pasadena, CA
Research Intern
Developed prototypes of personalized web search, parallel PageRank, clustered search, and sparse matrix and graph visualization tools. Supervised by Dr. Leonid Zhukov.
- Summer 2003 **Bioinformatics Summer Institute at University of Minnesota** Minneapolis, MN
Research Intern
Developed a bootstrap clustering algorithm for use on E. coli microarray data using MANOVA.
- 2002 – 2004 **University of Minnesota - Computer Science Department** Minneapolis, MN
Undergraduate Research Assistant
Developed gCLUTO, a graphical interface to Prof. George Karypis's CLUTO data clustering library.
- Summer 2002 **Army High Performance Computing Research Center** Minneapolis, MN
Research Intern
Wrote a frontend and visualizations for the CLUTO data clustering library.
- Spring 2002 **University of Minnesota - Computer Science Department** Minneapolis, MN
Undergraduate Research Assistant
Wrote C and Perl programs for classifying genes by regulatory sequences in promoters regions.

Publications

1. Wu, [Rasmussen](#), Bansal, Kellis. *TreeFix: statistically informed gene tree error correction using species trees*. submitted. 2012.
2. Choi, [Rasmussen](#), Hubisz, Gronau, Stanhope, Siepel. *Inferring homologous recombination and horizontal gene transfer using whole genomes of *Streptococcus pyogenes* and *S. dysgalactiae* ssp. *equisimilis**. submitted. 2012.
3. [Rasmussen](#), Kellis. *Unified modeling of gene duplications, losses, and coalescence using a locus tree*. Genome Research. 2012.
4. Bergwitz, [Rasmussen](#), DeRobertis, Wee, Sinha, Chen, Huang, Perrimon. *Roles of Major Facilitator Superfamily Transporters in Phosphate Response in *Drosophila**. PLoS One. 2012.
5. Wu, [Rasmussen](#), Kellis. *Evolution at the sub-gene level: gene architecture rearrangements in the *Drosophila* phylogeny*. Molecular Biology and Evolution. 2011.
6. Lindblad-Toh, Garber, Zuk, Lin, Parker, Washietl, Kheradpour, Ernst, Jordan, Mauceli, Ward, Lowe, Holloway, Clamp, Gnerre, Alföldi, Beal, Chang, Clawson, Cuff, Di Palma, Fitzgerald, Flicek, Guttman, Hubisz, Jaffe, Jungreis, Kent, Kostka, Lara, Martins, Masingham, Moltke, Raney, [Rasmussen](#), Robinson, Stark, Vilella, Wen, Xie, Zody, Broad Institute Sequencing Platform and Whole Genome Assembly Team, Worley, Kovar, Muzny, Gibbs, Baylor College of Medicine Human Genome Sequencing Center, Warren, Mardis, Weinstock, Wilson, Genome Institute at Washington University, Birney, Margulies, Herrero, Green, Haussler, Siepel, Goldman, Pollard, Pedersen, Lander, Kellis. *A high-resolution map of evolutionary constraint in the human genome based on 29 eutherian mammals*. Nature. 2011.
7. [Rasmussen](#), Kellis. *A Bayesian Approach for Fast and Accurate Gene Tree Reconstruction*. Molecular Biology and Evolution. 2010.
8. Organ, [Rasmussen](#), Baldwin, Kellis, and Edwards. *A Phylogenomic Approach to the Evolutionary Dynamics of Gene Duplication in Birds*. In *Evolution After Gene Duplication*. (Eds.) K. Dittmar and D. Liberles. Wiley & Sons. 2010.
9. Butler, [Rasmussen](#), Lin, Santos, Sakthikumar, Munro, Rheinbay, Grabherr, Forche, Reedy, Agrafioti, Arnaud, Bates, Brown, Brunke, Costanzo, Fitzpatrick, de Groot, Harris, Hoyer, Hube, Klis, Kodira, Lennard, Logue, Martin, Neiman, Nikolaou, Quail, Quinn, Santos, Schmitzberger, Sherlock, Shah, Silverstein, Skrzypek, Soll, Staggs, Stansfield, Stumpf, Sudbery, Thyagarajan, Zeng, Berman, Berriman, Heitman, Gow, Lorenz, Birren, Kellis, Cuomo. *Evolution of pathogenicity and sexual reproduction in eight *Candida* genomes*. Nature 459: 657-662. 2009.
10. Lin, Deoras, [Rasmussen](#), Kellis. *Performance and Scalability of Discriminative Metrics for Comparative Gene Identification in 12 *Drosophila* Genomes*. PLoS Comput Biol. 2008.
11. [Rasmussen](#), Kellis. *Accurate gene-tree reconstruction by learning gene- and species-specific substitution rates across multiple complete genomes*. Genome Research 17: 1932-1942. 2007.
12. Stark, Lin, Kheradpour, Pederson, Parts, Carlson, Crosby, [Rasmussen](#), Roy, Deroas, Ruby, Brennecke, FlyBase curators, Berkeley *Drosophila* Genome Project, Hodges, Hinrichs, Caspi, Paten, Park, Han, Maeder, Polansky, Robson, Aerts, vanHelden, Hassan, Gilbert, Eastman, Rice, Weir, Hahn, Park, Dewey, Pachter, Kent, Haussler, Lai, Bartel, Hannon, Kaufman, Eisen, Clark, Smith, Celniker, Gelbart, Kellis. *Discovery of functional elements in 12 *Drosophila* genomes using evolutionary signatures*. Nature 450: 219-232. 2007.
13. *Drosophila* 12 Genomes Consortium. *Evolution of genes and genomes on the *Drosophila* phylogeny*. Nature 450: 203-218. 2007.
14. [Rasmussen](#), Deshpande, Karypis, Johnson, Crow, and Retzel. *wCLUTO: A Web-Enabled Clustering Toolkit*. Plant Physiology. 2003.
15. [Rasmussen](#) and Karypis. *gCLUTO: An interactive clustering, visualization, and analysis system*. University of Minnesota Technical Report #04-021. 2004.

Talks

1. 11/2011. Guest lecturer for BTRY 4840/6840 Computational Genomics. Cornell, NY. *Gene trees and species trees*.
2. 11/2011. Guest lecturer for 6.878/6.047 Computational Biology. MIT, MA. *Phylogenetics, Population Genetics, and Genomes*.
3. 12/2010. NIMBioS Working Group: Inferring Patterns and Processes of Gene Diversification by Reconciling Gene Trees and Species Trees. Knoxville, TN. *Gene families undergoing duplications, losses, and coalescence*.

4. 11/2010. Guest lecturer for 6.878/6.047 Computational Biology. MIT, MA.
Phylogenetics, Population Genetics, and Genomes.
5. 6/2010. Bertinoro Computational Biology. Bertinoro, Italy.
Reconciliation of duplications, losses, and coalescence.
6. 2/2010. MBI: Inference in Stochastic Models of Sequence Evolution. Ohio State, OH.
Bayesian reconstruction of gene families.
7. 11/2009. Guest lecturer for 6.878/6.047 Computational Biology. MIT, MA.
Algorithms for Phylogenomics.
8. 7/2009. Quest for Orthologs. Wellcome Trust Sanger Institute, Hinxton, UK.
Efficient Bayesian Reconstruction and Reconciliation of Thousands of Gene Family Phylogenies Across Multiple Complete Genomes.
9. 4/2007. Genome Analysis Program. Broad Institute of MIT and Harvard, MA.
Phylogenomics of mammalian, fly, and fungal genomes.
10. 10/2005. Meetings on Genome Informatics. Cold Spring Harbor Laboratory, NY.
Multiple genome phylogeny for ortholog and paralog detection.

Teaching Experience

Fall 2006, 2008	6.878/6.047 and 6.895/6.085 Computational Biology: Genomes, Networks, Evolution <i>Teaching Assistant</i> Developed course materials including lectures, homework assignments, midterms, and finals. Led weekly recitations.	MIT
Summer 2003	University of Minnesota - Institute of Technology Center for Education (ITCEP) <i>Teaching Assistant</i> Worked with gifted middle and high school students for several math, science, and engineering summer programs at the University of Minnesota. Responsibilities included teaching and tutoring.	MN

Software Developed

- **DLCoal** (Duplications, Losses, and Coalescence) - Phylogenetic software.
<http://compbio.mit.edu/dlcoal>
- **SPIMAP** (SPecies Inferred Maximum A Posteriori Reconstruction) - Phylogenetic software.
<http://compbio.mit.edu/spimap>
- **SPIDIR** (SPecies Inferred Distance-based Reconstruction) - Phylogenetic software.
<http://compbio.mit.edu/spidir>
- **gCLUTO** - Graphical clustering toolkit
<http://glaros.dtc.umn.edu/gkhome/views/cluto>; <http://mattrasmus.com/umn/gcluto>
- **SUMMON** - Scientific visualization prototyping and scripting library.
<http://mattrasmus.com/summon>
- **KeepNote** - Cross-platform note-taking and organization software.
<http://keepnote.org>

Honors & Awards

Cornell Center for Comparative and Population (3CPG) Genomics Fellowship (2011)
 William A. Martin Award for best M.S. thesis in the field of Computer Science (2006)
 Ruth L. Kirschstein National Research Service Award (2004-2007)
 Barry M. Goldwater Scholarship (2003)
 CRA Outstanding Undergraduate Award, Honorable Mention (2003) Frank Louk Scholarship (2003) Lando Scholarship (2002), Ella Thrope Math Scholarship (2001, 2002, 2003), Math Undergrad Scholarship (2001), Iron Range Scholarship (2001), IT Honors Undergraduate Research Assistant Scholarship (2001), Minnesota Technology, Inc. Scholarship (2001, 2002)