San Francisco, CA 94122

Matthew D. Rasmussen

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http://mattrasmus.com

Work Experience

1/2022 – present	**insitro**	South San Francisco, CA

VP Software Engineering
Leading software engineering efforts such as LIMS, scientific pipelines (imaging, bioinformatics, cheminformatics), Data Engineering, DevOps, and IT.

10/2019 – 1/2022	**insitro**	South San Francisco, CA

VP Data Engineering
Leading software engineering efforts such as Data Engineering, DevOps, IT, Bioinformatics, and LIMS.

2/2019 – 10/2019	**Myriad Genetics**	South San Francisco, CA

VP Software Engineering
Led efforts including project planning, budget planning, recruiting, level guide, mentoring, and engineering career development plans.

4/2018 – 2/2019	**Counsyl**	South San Francisco, CA

Senior Director of Software Engineering
Continuing with my previous responsibilities, I managed two engineering managers, 15 software engineers, and several contractors.

5/2015 – 4/2018	**Counsyl**	South San Francisco, CA

Director of Software Engineering
Managed the Medical Genomics team at Counsyl, which included LIMS, variant curation, and patient reporting. I encouraged engineering proposals from the team, worked with stake holders (e.g. Lab Directors, Genetic Counselors, Product Managers) to gather requirements, and established development road maps. During this time, I continued significant software development and led software architecture decisions. Lastly, I recruited and ran the summer intern program for several years, developed workshops for the engineering team (e.g. advance PostgreSQL tricks, AWS APIs), and organized onboarding plans for new hires.

5/2013 – 5/2015	**Counsyl**	South San Francisco, CA

Software Engineer
Developed software for all of Counsyl's clinical diagnostic tests: ordering interfaces, variant interpretation, disease risk calculations, patient report generation, data pipelines (ETLs). Used Python, PostgreSQL, Django, Celery, React, Docker, AWS.

Research Experience

4/2011 – 5/2013	**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.

Education

2006 – 2010   **Massachusetts Institute of Technology**
Ph.D. in Computer Science
Supervisor: Assoc. Prof. Manolis Kellis
Thesis: Methods and Analysis of Genome-scale Gene Family Evolution Across Multiple Species

2004–2006   **Massachusetts Institute of Technology**
Masters of Science in Electrical Engineering and Computer Science
Supervisor: Assoc. Prof. Manolis Kellis
Thesis: Probabilistic Framework for Genome-wide Phylogeny and Orthology Determination
MIT William A. Martin Award for best M.S. thesis in the field of Computer Science

2000–2004   **University of Minnesota**
Bachelor of Science in Mathematics, Bachelor of Science in Computer Science
UMTYMP (University of Minnesota Talented Youth Math Program), Solar Vehicle Project

Software Experience

Programming languages: C/C++, JavaScript, Perl, Python (most proficient), R, SQL, UNIX shell scripting.

Software developed:

– **redun** - Yet another redundant workflow engine. Python-based workflow engine for data science.
  `https://github.com/insitro/redun`
– **ARGweaver** - Sampling and manipulating genome-wide ancestral recombination graphs (ARGs).
  `http://mdrasmus.github.io/argweaver/`
– **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`
– **SUMMON** - Scientific visualization prototyping and scripting library.
  `http://mattrasmus.com/summon`
– **KeepNote** - Cross-platform note-taking and organization software.
  `http://keepnote.org`
– **gCLUTO** - Graphical clustering toolkit
  `http://glaros.dtc.umn.edu/gkhome/views/cluto`; `http://mattrasmus.com/umn/gcluto`
– **Additional projects:** `http://mattrasmus.com`; `http://github.com/mdrasmus`

Publications

1. Yue F, Cheng Y, Breschi A, Vierstra J, Wu W, Ryba T, Sandstrom R, Ma Z, Davis C, Pope BD, Shen Y, Pervouchine DD, Djebali S, Thurman RE, Kaul R, Rynes E, Kirilusha A, Marinov GK, Williams BA, Trout D, Amrhein H, Fisher-Aylor K, Antoshechkin I, DeSalvo G, See L, Fastuca M, Drenkow J, Zaleski C, Dobin A, Prieto P, Lagarde J, Bussotti G, Tanzer A, Denas O, Li K, Bender MA, Zhang M, Byron R, Groudine MT, McCleary D, Pham L, Ye Z, Kuan S, Edsall L, Wu Y, Rasmussen MD, Bansal MS, Kellis M, Keller CA, Morrissey CS, Mishra T, Jain D, Dogan N, Harris RS, Cayting P, Kawli T, Boyle AP, Euskirchen G, Kundaje A, Lin S, Lin Y, Jansen C, Malladi VS, Cline MS, Erickson DT, Kirkup VM, Learned K, Sloan CA, Rosenbloom KR, Sousa BLD, Beal K, Pignatelli M, Flicek P, Lian J, Kahveci T, Lee D, Kent WJ, Santos MR, Herrero J, Notredame C, Johnson A, Vong S, Lee K, Bates D, Neri F, Diegel M, Canfield T, Sabo PJ, Wilken MS, Reh TA, Giste E, Shafer A, Kutyavin T, Haugen E, Dunn D, Reynolds AP, Neph S, Humbert R, Hansen RS, Bruijn MD, Selleri L, Rudensky A, Josefowicz S, Samstein R, Eichler EE, Orkin SH, Levasseur D, Papayannopoulou T, Chang K, Skoultchi A, Gosh S, Disteche C, Treuting P, Wang Y, Weiss MJ, Blobel GA, Cao X, Zhong S, Wang T, Good PJ, Lowdon RF, Adams LB, Zhou X, Pazin MJ, Feingold EA, Wold B, Taylor J, Mortazavi A, Weissman SM, Stamatoyannopoulos JA, Snyder MP, Guigo R, Gingeras TR, Gilbert DM, Hardison RC, Beer MA, Ren B, and Mouse ENCODE Consortium. *A comparative encyclopedia of DNA elements in the mouse genome.* Nature, 2014, 515, 355-364

2. Wu Y, Bansal MS, <u>Rasmussen MD</u>, Herrero J, Kellis M. *Phylogenetic Identification and Functional Characterization of Orthologs and Paralogs across Human, Mouse, Fly, and Worm*. bioRxivdoi: 10.1101/005736 2014.

3. <u>Rasmussen MD</u>, Hubisz MJ, Gronau I, Siepel A. *Genome-wide inference of ancestral recombination graphs*. PLoS Genetics. 2014.

4. Wu Y, <u>Rasmussen MD</u>, Bansal MS, Kellis M. *Most Parsimonious reconciliation in the presence of gene duplication, loss, and deep coalescence using labeled coalescent trees*. Genome Research. 2013.

5. Wu Y, <u>Rasmussen MD</u>, Bansal MS, Kellis M. *TreeFix: statistically informed gene tree error correction using species trees*. Systematic Biology. 2012.

6. Choi SC, <u>Rasmussen MD</u>, Hubisz MJ, Gronau I, Stanhope MJ, Siepel A. *Replacing and additive horizontal gene transfer in Streptococcus*. Molecular Biology and Evolution, 29(11):3309-20, 2012.

7. <u>Rasmussen MD</u>, Kellis M. *Unified modeling of gene duplications, losses, and coalescence using a locus tree*. Genome Research, 22(4):755-65, 2012.

8. Bergwitz C, <u>Rasmussen MD</u>, DeRobertis C, Wee MJ, Sinha S, Chen HH, Huang J, Perrimon N. *Roles of Major Facilitator Superfamily Transporters in Phosphate Response in Drosophila*. PLoS One, 7(2):e31730, 2012.

9. Wu Y, <u>Rasmussen MD</u>, Kellis M. *Evolution at the sub-gene level: gene architecture rearrangements in the Drosophila phylogeny*. Molecular Biology and Evolution, 29(2):689-705, 2011.

10. Lindblad-Toh K, Garber M, Zuk O, Lin MF, Parker BJ, Washietl S, Kheradpour P, Ernst J, Jordan G, Mauceli E, Ward LD, Lowe CB, Holloway AK, Clamp M, Gnerre S, Alföldi J, Beal K, Chang J, Clawson H, Cuff J, Di Palma F, Fitzgerald S, Flicek P, Guttman M, Hubisz MJ, Jaffe DB, Jungreis I, Kent WJ, Kostka D, Lara M, Martins AL, Massingham T, Moltke I, Raney BJ, <u>Rasmussen MD</u>, Robinson J, Stark A, Vilella AJ, Wen J, Xie X, Zody MC; Broad Institute Sequencing Platform and Whole Genome Assembly Team, Baldwin J, Bloom T, Chin CW, Heiman D, Nicol R, Nusbaum C, Young S, Wilkinson J, Worley KC, Kovar CL, Muzny DM, Gibbs RA; Baylor College of Medicine Human Genome Sequencing Center Sequencing Team, Cree A, Dihn HH, Fowler G, Jhangiani S, Joshi V, Lee S, Lewis LR, Nazareth LV, Okwuonu G, Santibanez J, Warren WC, Mardis ER, Weinstock GM, Wilson RK; Genome Institute at Washington University, Delehaunty K, Dooling D, Fronik C, Fulton L, Fulton B, Graves T, Minx P, Sodergren E, Birney E, Margulies EH, Herrero J, Green ED, Haussler D, Siepel A, Goldman N, Pollard KS, Pedersen JS, Lander ES, Kellis M. *A high-resolution map of human evolutionary constraint using 29 mammals*. Nature, 478(7370):476-82, 2011.

11. <u>Rasmussen MD</u>, Kellis M. *A Bayesian Approach for Fast and Accurate Gene Tree Reconstruction*. Molecular Biology and Evolution, 28(1):273-90, 2011.

12. Organ C, <u>Rasmussen MD</u>, Baldwin M, Kellis M, and Edwards SV. *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.

13. Butler G, <u>Rasmussen MD</u>, Lin MF, Santos MA, Sakthikumar S, Munro CA, Rheinbay E, Grabherr M, Forche A, Reedy JL, Agrafioti I, Arnaud MB, Bates S, Brown AJ, Brunke S, Costanzo MC, Fitzpatrick DA, de Groot PW, Harris D, Hoyer LL, Hube B, Klis FM, Kodira C, Lennard N, Logue ME, Martin R, Neiman AM, Nikolaou E, Quail MA, Quinn J, Santos MC, Schmitzberger FF, Sherlock G, Shah P, Silverstein KA, Skrzypek MS, Soll D, Staggs R, Stansfield I, Stumpf MP, Sudbery PE, Srikantha T, Zeng Q, Berman J, Berriman M, Heitman J, Gow NA, Lorenz MC, Birren BW, Kellis M, Cuomo CA. *Evolution of pathogenicity and sexual reproduction in eight Candida genomes*. Nature, 459(7247):657-62, 2009.

14. Lin MF, Deoras AN, <u>Rasmussen MD</u>, Kellis M. *Performance and Scalability of Discriminative Metrics for Comparative Gene Identification in 12 Drosophila Genomes*. PLoS Computational Biology, 4(4):e1000067, 2008.

15. <u>Rasmussen MD</u>, Kellis M. *Accurate gene-tree reconstruction by learning gene- and species-specific substitution rates across multiple complete genomes*. Genome Research, 17(12):1932-42, 2007.

16. Stark A, Lin MF, Kheradpour P, Pedersen JS, Parts L, Carlson JW, Crosby MA, <u>Rasmussen MD</u>, Roy S, Deoras AN, Ruby JG, Brennecke J; Harvard FlyBase curators; Berkeley Drosophila Genome Project, Hodges E, Hinrichs AS, Caspi A, Paten B, Park SW, Han MV, Maeder ML, Polansky BJ, Robson BE, Aerts S, van Helden J, Hassan B, Gilbert DG, Eastman DA, Rice M, Weir M, Hahn MW, Park Y, Dewey CN, Pachter L, Kent WJ, Haussler D, Lai EC, Bartel DP, Hannon GJ, Kaufman TC, Eisen MB, Clark AG, Smith D, Celniker SE, Gelbart WM, Kellis M. *Discovery of functional elements in 12 Drosphila genomes using evolutionary signatures*. Nature, 450(7167):219-32, 2007.

17. Drosophila 12 Genomes Consortium, et al. *Evolution of genes and genomes on the Drosophila phylogeny*. Nature, 450(7167):203-18, 2007.

18. <u>Rasmussen MD</u>, Deshpande MS, Karypis G, Johnson J, Crow JA, Retzel EF. *wCLUTO: A Web-Enabled Clustering Toolkit*. Plant Physiology, 133(2):510-6, 2003.

19. <u>Rasmussen MD</u> and Karypis G. *gCLUTO: An interactive clustering, visualization, and analysis system*. University of Minnesota Technical Report #04-021. 2004.

Talks

1. 12/2014. Phyloseminar. `http://phyloseminar.org`.
   Mathematical and Visualization Tools for Working with Ancestral Recombination Graphs.
2. 9/2014. Compbio Seminar. MIT, MA.
   Semi-supervised Learning for Clinical Variant Interpretation.
3. 3/2013. Probabilistic Modeling in Genomics. Janelia Farm, VA.
   Efficient Sampling of the Ancestral Recombination Graph.
4. 11/2012. Guest lecturer for 6.878/6.047 Computational Biology. MIT, MA.
   Phylogenomics.
5. 11/2012. Guest lecturer for OEB 275r Phylogenomics, Comparative Genomics and Adaptation. Harvard, MA.
   Multiple mechanisms of gene-tree/species-tree incongruence.
6. 9/2012. Genome Sciences, University of Washington. Seattle, WA.
   Bayesian Models for Genome-wide Analysis of Phylogenies and Populations.
7. 9/2012. Fred Hutchinson Cancer Research Center. Seattle, WA.
   Bayesian Models for Genome-wide Analysis of Phylogenies and Populations.
8. 11/2011. Guest lecturer for BTRY 4840/6840 Computational Genomics. Cornell, NY.
   Gene trees and species trees.
9. 11/2011. Guest lecturer for 6.878/6.047 Computational Biology. MIT, MA.
   Phylogenetics, Population Genetics, and Genomes.
10. 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.
11. 11/2010. Guest lecturer for 6.878/6.047 Computational Biology. MIT, MA.
    Phylogenetics, Population Genetics, and Genomes.
12. 6/2010. Bertinoro Computational Biology. Bertinoro, Italy.
    Reconciliation of duplications, losses, and coalescence.
13. 2/2010. MBI: Inference in Stochastic Models of Sequence Evolution. Ohio State, OH.
    Bayesian reconstruction of gene families.
14. 11/2009. Guest lecturer for 6.878/6.047 Computational Biology. MIT, MA.
    Algorithms for Phylogenomics.
15. 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.
16. 4/2007. Genome Analysis Program. Broad Institute of MIT and Harvard, MA.
    Phylogenomics of mammalian, fly, and fungal genomes.
17. 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**	MIT
	Teaching Assistant	
	Developed course materials including lectures, homework assignments, midterms, and finals. Led weekly recitations.	
Summer 2003	**University of Minnesota - Institute of Technology Center for Education (ITCEP)**	MN
	Teaching Assistant	
	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.	

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)