

Ryan N. Gutenkunst
<http://gutengroup.mcb.arizona.edu>

Education

- 1998–2002 California Institute of Technology, Pasadena, CA; B.S. with Honor, Physics
2002–2008 Cornell University, Ithaca, NY; Ph.D., Physics
Dissertation Title: “Sloppiness, Modeling, and Evolution in Biochemical Networks”
Dissertation Advisor: Prof. James P. Sethna

Employment

- 2007–2008 Postdoctoral Fellow, Cornell University
Mentors: Prof. Scott H. Williamson and Prof. Carlos D. Bustamante
2009–2010 Postdoctoral Fellow, Los Alamos National Laboratory
Mentor: Dr. Byron Goldstein
2010–2017 Assistant Professor, Dept of Molecular and Cellular Biology, University of Arizona
2017–present Associate Professor with Tenure
2017–present Associate Department Head
Affiliations: Departments of Ecology & Evolutionary Biology and Epidemiology & Biostatistics; Graduate Interdisciplinary Programs (GIDPs) in Applied Mathematics, Statistics, and Genetics; BIO5 Institute

Honors and Awards

- 1998–2002 National Merit Scholar, American Standard Corporation
2000, 2001 Summer Undergraduate Research Fellowship, California Institute of Technology
2002–2004 NSF Integrative Graduate Education and Research Traineeship (IGERT) in Nonlinear Systems, Cornell University
2004 Honorable Mention, NSF Graduate Research Fellowship
2004–2006 NIH Molecular Biophysics Training Grant, Cornell University
2009–2010 Center for Nonlinear Studies postdoctoral appointment, Los Alamos National Lab
2013 Distinguished Early-Career Teaching Award, University of Arizona, College of Science
2014 Kavli Fellow, US National Academy of Sciences and The Kavli Foundation

Service/Outreach

Local Outreach

- 2013 Leader, Tucson Festival of Books: Book club on Armand Leroi’s “Mutants”
2016 Pen Pal, Laffer Middle School science students
2016 Speaker, UA Science Cafe: “Genetic engineering: From Jurassic Park to Gattaca”

Departmental Service

- 2010–2013 Co-Chair, MCB/CMM/CBC/IMB joint departmental retreat committee
2012–2013 Chair, MCB website committee
2013–present Member, MCB website committee
2012, 2016, 2017 Member, MCB faculty peer evaluation committee
2012 Member, MCB faculty search committee

2015–2017	Member, MCB discretionary fund allocation committee
2016	Member, MCB astrobiology faculty search committee
2017	Member, MCB cancer bioinformatics search committee
2017–present	Director of Graduate Studies, MCB track of Professional Science Master's in Applied Biosciences GIDP
2017–present	Director of Graduate Studies, MCB Accelerated Master's Program

College/University Service

2012	Internal reviewer, Packard Fellowships for Science and Engineering
2012–2016	Mentor for Arizona Assurance and Arizona Science, Engineering, and Mathematics Scholars
2013	Internal reviewer, Blavatnik Awards for Young Scientists
2014	Member, MCB/CBC/EEB/CS joint faculty search committee
2014	Member, Statistics GIDP graduate advisory committee
2017	Internal reviewer, Basic/Clinical Partnerships seed grant, UA Cancer Center
2017–present	Member, Steering Committee for NIH T32 training grant “Computational and mathematical modeling of biomedical systems”

National/International Service

2009–present	Lecturer, q-bio Summer School on Cellular Information Processing
2010, 2013, 2017	Panelist, National Science Foundation
2013	Co-Organizer, Banff International Research Station workshop on “Mathematical Tools for Evolutionary Systems Biology”
2014	Co-Organizer, symposium on “Evolutionary Systems Biology of Networks” at the Annual Meeting of the Society for Molecular Biology and Evolution
2015–present	Associate Editor, BMC Evolutionary Biology
2016	Lecturer, Workshop on Population and Speciation Genomics, Český Krumlov, Czech Republic

Ad-hoc Journal Reviewer

Science (1), Cell (1), eLIFE (1), Proceedings of the National Academy of Sciences USA (1), Genome Research (1), Molecular Systems Biology (2), PLoS Computational Biology (3), PLoS Genetics (4), Molecular Biology and Evolution (3), Molecular Ecology (3), Genetics (6), Evolution (2), IET Systems Biology (1), BMC Systems Biology (3), BMC Evolutionary Biology (2), Bioinformatics (1), Theoretical Population Biology (2), Molecular BioSystems (1), Bulletin of Mathematical Biology (1), Journal of Computational and Graphical Statistics (1), Physical Biology (1), Philosophical Transactions of the Royal Society B (1), PLoS ONE (5), Interface Focus (1), Frontiers in Evolutionary and Population Genetics (2), Life Sciences (1), Biotechnology Progress (1), Garland Science (1), W.H. Freeman and Company (1)

Ad-hoc Proposal Reviewer

National Science Foundation (2), Wellcome Trust (1), Biotechnology and Biological Sciences Research Council (UK, 1); National Environmental Research Council (UK, 1); Estonian Research Council (1); Vienna Science and Technology Fund (1); University of Missouri Research Board (1)

Publications/Creative Activity

Publications from research carried out as Assistant Professor are annotated to clarify the work and my contribution. Key: *italics*-Gutenkunst group trainee, ^C-corresponding author, ^E-contributed equally

Refereed Journal Articles

39. Lynch M^C, **Gutenkunst R**, Ackerman M, Spitze K, Ye Z, Maruki T, Jia Z (2017) Population genomics of *Daphnia pulex*. *Genetics* 206:315.
38. Qi X^C, An H, *Ragsdale AP*, Hall TE, **Gutenkunst RN**, Pires JC, Barker MS (2017) Genomic inferences of domestication events are corroborated by written records in *Brassica rapa*. *Molecular Ecology* 206:315.
37. *Ragsdale AP*^C, **Gutenkunst RN**^C (2017) Inferring demographic history using two-locus statistics. *Genetics* 206:1037.
36. *Coffman AJ*, *Hsieh P*, Gravel S, **Gutenkunst RN**^C (2016) Computationally efficient composite likelihood statistics for demographic inference. *Molecular Biology and Evolution* 33:591.
35. Edwards T^C, Tollis M, *Hsieh P*, **Gutenkunst RN**, Liu Z, Kusumi K, Culver M, Murphy RW (2016) Assessing models of speciation under different biogeographic scenarios; an empirical study using multi-locus and RNA-seq analyses. *Ecology and Evolution* 6:379.
34. *Hsieh P*, Veeramah KR, Lachance J, Tishkoff SA, Wall JD, Hammer MF^C, **Gutenkunst RN**^C (2016) Whole-genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. *Genome Research* 26:279.
☆ Featured in the *Arizona Daily Star*.
33. *Hsieh P*, Woerner AE, Wall JD, Lachance J, Tishkoff SA, **Gutenkunst RN**, Hammer MF^C (2016) Model-based analyses of whole genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. *Genome Research* 26:291.
32. *Mannakee BK*, **Gutenkunst RN**^C (2016) Selection on network dynamics drives differential rates of protein domain evolution. *PLoS Genetics* 12:e1006132.
31. *Ragsdale AP*, *Coffman AJ*, *Hsieh P*, *Struck TJ*, **Gutenkunst RN**^C (2016) Triallelic population genomics for inferring correlated fitness effects of same site nonsynonymous mutations. *Genetics* 203:513.
☆ Highlighted by the editors of *Genetics*.
30. Hermansen RA^E, *Mannakee BK*^E, Knecht W, Liberles DA^C, **Gutenkunst RN**^C (2015) Characterizing selective pressures on the pathway for de novo biosynthesis of pyrimidines in yeast. *BMC Evolutionary Biology* 15:232.
29. *Pandya S*, *Struck TJ*, *Mannakee BK*, *Paniscus M*, **Gutenkunst RN**^C (2015) Testing whether meta-zoan tyrosine loss was driven by selection against promiscuous phosphorylation. *Molecular Biology and Evolution* 32:144.

28. Holmes WM, Mannakee BK, **Gutenkunst RN**, Serio TR^C (2014) Loss of N-terminal acetylation suppresses a prion phenotype by modulating global protein folding. *Nature Communications* 5:4383.
27. Jilkine A, **Gutenkunst RN**^C (2014) Effect of dedifferentiation on time to mutation acquisition in stem cell-driven cancers. *PLoS Computational Biology* 10:e1003481.
26. Robinson JD^C, Coffman AJ, Hickerson MJ, **Gutenkunst RN** (2014) Sampling strategies for frequency spectrum-based population genomic inference. *BMC Evolutionary Biology* 14:254.
25. Veeramah K, **Gutenkunst RN**, Woerner A, Watkins J, Hammer M^C (2014) Evidence for increased levels of positive and negative selection on the X chromosome versus autosomes in humans. *Molecular Biology and Evolution* 31:2267.
24. Ma X, Kelley JL, Eilertson K, Musharoff S, Degenhardt JD, Martins AL, Vinar T, Kosiol C, Siepel A, **Gutenkunst RN**, Bustamante CD^C (2013) Population genomic analysis of ten genomes reveals a rich speciation and demographic history of orang-utans (*Pongo pygmaeus* and *Pongo abelii*). *PLoS ONE* 8:e77175.
23. Smith AM^C, Adler FR, Ribeiro RM, **Gutenkunst RN**, McAuley JL, McCullers JA, Perelson AS (2013) Kinetics of coinfection with influenza A virus and *Streptococcus pneumoniae*. *PLoS Pathogens* 9:e1003238.
22. Xu X^E, Liu X^E, Ge S^E, Jensen JD^E, Hu F^E, Li X^E, Dong Y^E, **Gutenkunst RN**, Fang L, Huang L, Li J, He W, Zhang G, Zheng X, Zhang F, Li Y, Yu C, Kristiansen K, Zhang X, Wang J, Wright M, McCouch S, Nielsen R^C, Wang J^C, Wang W^C (2012) Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. *Nature Biotechnology* 30:105.
21. Chylek LA, Hu B, Blinov ML, Emonet T, Faeder JR, Goldstein B, **Gutenkunst RN**, Haugh JM, Lipniacki T, Posner RG, Yang J, Hlavacek WS^C (2011) Guidelines for visualizing and annotating rule-based models. *Molecular BioSystems* 7:2779.
20. Gravel S, Henn BM, **Gutenkunst RN**, Indap AR, Marth GT, Clark AG, Yu F, Gibbs RA, The 1000 Genomes Project, Bustamante CD^C (2011) Demographic history and rare allele sharing among human populations. *Proceedings of the National Academy of Sciences USA* 108:11983.
19. **Gutenkunst RN**^C, Coombs D, Starr T, Dustin ML, Goldstein B (2011) A biophysical model of cell adhesion mediated by immunoadhesin drugs and antibodies. *PLoS ONE* 6:e19701.
18. The Orangutan Genome Sequencing Consortium (2011) Comparative and demographic analysis of orang-utan genomes. *Nature* 469:529.
17. Skar H^E, **Gutenkunst RN**^E, Wilbe Ramsay K, Alaeus A, Albert J, Leitner T^C (2011) Daily sampling of an HIV-1 patient with slowly progressing disease displays persistence of multiple env subpopulations consistent with neutrality. *PLoS ONE* 6:e21747.
16. Smith AM, Adler FR, McAuley JL, **Gutenkunst RN**, Ribeiro RM, McCullers JA, Perelson AS^C (2011) Effect of 1918 PB1-F2 expression on influenza A virus infection kinetics. *PLoS Computational Biology* 7:e1001081.

15. Colvin J, Monine MI, **Gutenkunst RN**, Hlavacek WS, Von Hoff DD, Posner RG^C (2010) RuleMonkey: software for stochastic simulation of rule-based models. *BMC Bioinformatics* 11:404.
14. The 1000 Genomes Project Consortium (2010) A map of human genome variation from population-scale sequencing. *Nature* 467:1061.
13. Andrés AM^C, Hubisz MJ, Indap A, Torgerson DG, Degenhardt JD, Boyko AR, **Gutenkunst RN**, White TJ, Green ED, Bustamante CD, Clark AG, Nielsen R (2009) Targets of balancing selection in the human genome. *Molecular Biology and Evolution* 26:2755.
12. Auton A, Bryc K, Boyko AR, Lohmueller KE, Novembre J, Reynolds A, Indap A, Wright MH, Degenhardt JD, **Gutenkunst RN**, King KS, Nelson MR, Bustamante CD^C (2009) Global distribution of genomic diversity underscores rich complex history of continental human populations. *Genome Research* 19:795.
11. **Gutenkunst RN**^C, Hernandez RD, Williamson SH, Bustamante CD (2009) Inferring the joint demographic history of multiple populations from multidimensional SNP frequency data. *PLoS Genetics* 5:e1000695.
10. Nielsen R^C, Hubisz MJ, Hellmann I, Torgerson D, Andrés AM, Albrechtsen A, **Gutenkunst R**, Adams MD, Cargill M, Boyko A, Indap A, Bustamante CD, Clark AG (2009) Darwinian and demographic forces affecting human protein coding genes. *Genome Research* 19:838.
9. Casey FP^C, Waterfall JJ, **Gutenkunst RN**, Myers CR, Sethna JP (2008) Variational method for estimating the rate of convergence of Markov-chain Monte Carlo algorithms. *Physical Review E* 78:046704.
8. Daniels BC, Chen YJ, Sethna JP^C, **Gutenkunst RN**, Myers CR (2008) Sloppiness, robustness, and evolvability in systems biology. *Current Opinion in Biotechnology* 19:389.
7. Casey FP^C, Baird D, Feng Q, **Gutenkunst RN**, Waterfall JJ, Myers CR, Brown KS, Cerione RA, Sethna JP (2007) Optimal experimental design in an epidermal growth factor receptor signalling and down-regulation model. *IET Systems Biology* 1:190.
6. **Gutenkunst RN**^C, Casey FP, Waterfall JJ, Myers CR, Sethna JP (2007) Extracting falsifiable predictions from sloppy models. *Annals of the New York Academy of Sciences* 1115:203.
5. **Gutenkunst R**^C, Newlands N, Lutcavage M, Edelstein-Keshet L (2007) Inferring resource distributions from Atlantic bluefin tuna movements: an analysis based on net displacement and length of track. *Journal of Theoretical Biology* 245:243.
4. **Gutenkunst RN**^C, Waterfall JJ, Casey FP, Brown KS, Myers CR, Sethna JP (2007) Universally sloppy parameter sensitivities in systems biology models. *PLoS Computational Biology* 3:e189.
 ☆ Featured in *Biomedical Computation Review*.
 ☆ "Exceptional" evaluation on *Faculty of 1000: Biology*
3. Myers CR, **Gutenkunst RN**, Sethna JP (2007) Python unleashed on systems biology. *Computing in Science & Engineering* 9:34.

2. Waterfall JJ, Casey FP, **Gutenkunst RN**, Brown KS, Myers CR, Brouwer PW, Elser V, Sethna JP (2006) Sloppy-model universality class and the Vandermonde matrix. *Physical Review Letters* 97:150601.
1. Black ED, **Gutenkunst RN** (2003) An introduction to signal extraction in interferometric gravitational wave detectors. *American Journal of Physics* 71:365.

Reviews & Commentaries

4. *Mannakee BK, Ragsdale AP, Transtrum MK, **Gutenkunst RN**^C* (2016) Sloppiness and the geometry of parameter space. In D Gomez-Cabrero, L Geris editors, *Uncertainty in Biology: a Computational Modeling Approach*, pages 271–291. Springer International, Switzerland.
3. Transtrum MK, **Gutenkunst RN**, Chen Y, Machta BB, Sethna JP (2011) Discussion of “Riemannian manifold Langevin and Hamiltonian Monte Carlo methods” by Girolami and Calderhead. *Journal of the Royal Statistical Society: Series B* 73: 199.
2. Ramachandran S, Tang H, **Gutenkunst RN**, Bustamante CD (2010) Genetics and genomics of human population structure. In MR Speicher, AG Motulsky, SE Antonarakis, editors, *Vogel and Motulsky’s Human Genetics: Problems and Approaches*, pages 589–615. Springer Verlag, Germany.
1. **Gutenkunst RN** (2002) Extracting light from water: Sonoluminescence. *Caltech Undergraduate Research Journal* 2:16.

Non-refereed Manuscripts

2. Laurence Loewe, Peter Swain, **Ryan Gutenkunst** (2013) Mathematical Tools for Evolutionary Systems Biology. Banff International Research Station 5-day workshop report.
1. **Gutenkunst RN**, Sethna JP (2007) Adaptive mutation in a geometrical model of chemotype evolution. arXiv:0712.3240.

Software

2. **Gutenkunst RN** (2009) *dadi* – Diffusion Approximations for Demographic Inference. <https://bitbucket.org/gutenkunstlab/dadi/> (Pronounced as “daddy”)
1. **Gutenkunst RN**, Atlas JC, Casey FP, Kuczynski RS, Waterfall JJ, Myers CR, Sethna JP (2007) SloppyCell. <http://sloppycell.sourceforge.net>

Publications in Progress

Refereed Journal Articles

4. *Hsieh P, Hallmark B, Watkins J, Karafet TM, Osipova LP, **Gutenkunst RN**^C, Hammer MF^C* (submitted) Exome sequencing provides evidence of polygenic adaptations and deciphers demographic prehistory in indigenous Siberian populations.

3. Leighton GM^C, Wang X, **Gutenkunst RN**, Dornhaus A (submitted) Behavioral Caste is Associated with Distinct Genetic Expression Profile in Workers in *Temnothorax rugatulus*
2. *Struck TJ, Mannakee BK, Gutenkunst RN^C* (submitted) How much research is spurred when a gene is associated with a complex disease? bioRxiv preprint <https://doi.org/10.1101/106773>.
1. Wang X, Li P, **Gutenkunst RN^C** (submitted) Systematic effects of mRNA secondary structure on gene expression and molecular function in budding yeast. bioRxiv preprint <https://doi.org/10.1101/138792>.

Conferences/Scholarly Presentations

External Departmental Seminars

- 2008 Department of Computational and Systems Biology, University of Pittsburgh, Pittsburgh, PA
- 2008 Mathematical Biology Program, University of British Columbia, Vancouver, Canada
- 2008 Santa Fe Institute, Santa Fe, NM
- 2009 Centre for Integrative Bioinformatics, Vrije University, Amsterdam, Netherlands
- 2009 Program in Bioinformatics and Integrative Biology, University of Massachusetts, Worcester, MA
- 2010 Department of Biology, Boston College, Boston, MA
- 2010 Department of Physics, Emory University, Atlanta, GA
- 2010 q-bio Summer School, Los Alamos, NM
- 2010 BIO5 Institute, University of Arizona
- 2011 Department of Engineering Sciences and Applied Mathematics, Northwestern University Chicago, IL
- 2013 Mathematical Biology Research Program, University of Utah, Salt Lake City, UT
- 2013 Networks Seminar, University of Houston, Houston, TX
- 2015 Program in Computational Biology, University of Pittsburgh and Carnegie Mellon University Pittsburgh, PA
- 2015 Department of Biology, Temple University, Philadelphia, PA
- 2015 Center for Computational Biology, University of California, Berkeley, CA
- 2016 Department of Physics and Astronomy, Brigham Young University, Provo, UT
- 2017 Center for Bioinformatics Research, Indiana University, Bloomington, IN

Invited Conference Presentations

- 2009 Banff International Research Station Workshop: New Mathematical Challenges from Molecular Biology and Genetics, Banff, Canada
- 2009 Lorentz workshop: Data Analysis, Parameter Identification and Experimental Design in Systems Biology, Leiden, Netherlands
- 2012 Mathematical Biosciences Institute workshop: Robustness in Biological Systems, Columbus, OH
- 2012 American Mathematical Society Fall Western Sectional Meeting, Tucson, AZ
- 2014 Indonesian-American Kavli Frontiers of Science Symposium, Medan, Indonesia
- 2015 Society for Molecular Biology and Evolution Annual Meeting, Vienna, Austria
- 2016 Symposium on Cell Signaling, Santa Fe, NM

Select Contributed Conference Presentations

- 2005 Sixth International Conference on Systems Biology, Boston, MA
 - ☆ Contributed abstract selected for platform presentation in student symposium
- 2007 Society for Molecular Biology and Evolution Annual Meeting, Halifax, Canada
 - ☆ Contributed abstract selected for platform presentation
- 2008 Cornell Postdoc Research Day
 - ☆ Winner of a Best Poster Presentation award
- 2010 FASEB Summer Research Conference: Immunoreceptors, Keystone, CO
 - ☆ Contributed abstract selected for platform presentation
- 2010 Fourth Annual q-bio Conference on Cellular Information Processing, Santa Fe, NM
 - ☆ Contributed abstract selected for platform presentation
- 2010 iEvoBio (Informatics for Phylogenetics, Evolution and Biodiversity) Conference, Portland, OR
 - ☆ Contributed abstract selected for platform presentation
- 2011 Society for the Study of Evolution Annual Meeting, Portland, OR
- 2011 Society for Molecular Biology and Evolution Annual Meeting, Kyoto, Japan
 - ☆ Contributed abstract selected for platform presentation
- 2011 Mechanisms of Protein Evolution, Denver, CO
- 2013 Banff International Research Station Workshop: Mathematical Tools for Evolutionary Systems Biology, Banff, Canada
- 2013 Society for Mathematical Biology Annual Meeting, Phoenix, AZ
- 2013 Society for Molecular Biology and Evolution Annual Meeting, Chicago, IL
- 2014 Society for Molecular Biology and Evolution Annual Meeting, San Juan, PR
 - ☆ Contributed abstract selected for platform presentation
- 2016 Biology of Genomes, Cold Spring Harbor, NY
- 2016 Allied Genetics, Orlando, FL
 - ☆ Contributed abstract selected for platform presentation

Grants and Contracts

Current Federal Research Support

- 9/01/14–1/31/18 DARPA WF911NF-14-1-0395: \$3,630,769
 - PI: Mihai Surdeanu; Co-Is: Kobus Barnard, Angus Forbes, Ryan Gutenkunst, Clayton Morrison, Guang Yao
 - REACH: Reading and assembling contextual and holistic big mechanisms from text
 - Role: Co-PI (8.3% effort)
- 9/01/16–8/31/19 NSF DUE-1625015: \$598,690
 - PI: Molly Bolger; Co-PIs: Lisa Elfring, Jennifer Katcher
 - Authentic scientific practices in the classroom: a model-based-inquiry curriculum for the introductory biology laboratory
 - Role: Senior personnel (4.1% effort)

Past Federal Research Support

- 3/1/12–2/29/16 NSF DEB-1146074: \$551,964
 - PI: Ryan Gutenkunst
 - Demographic history inference from genomic linkage and allele frequency spectra
 - Role: PI (16.6% effort)

Past Institutional Research Support

6/1/15–5/31/16 University of Arizona Center for Insect Science: \$10,000
PI: Anna Dornhaus; Co-Is: Ryan Gutenkunst, Gavin Leighton
Testing the genetic toolkit of social behavior hypothesis using detailed descriptions of behavior and RNA-sequencing experiments in *Temnothorax rugatulus*

Extent of Teaching

List of courses taught

2010, Fall	Cell Systems, MCB 572	8 students	25%
2011, Fall	Cell Systems, MCB 572	28 students	33%
2012, Spring	Key Concepts in Quantitative Biology, MCB 315	15 students	60%
2012, Fall	Cell Systems, MCB 572	18 students	50%
2012, Fall	Key Concepts in Quantitative Biology, MCB 315	13 students	80%
2013, Fall	Key Concepts in Quantitative Biology, MCB 315	12 students	100%
2014, Fall	Cell Systems, MCB 572	18 students	33%
2014, Fall	Key Concepts in Quantitative Biology, MCB 315	15 students	100%
2014, Fall	Introductory Biology I, MCB 181	336 students	15%
2015, Fall	Cell Systems, MCB 572	19 students	33%
2015, Fall	Key Concepts in Quantitative Biology, MCB 315	11 students	100%
2015, Fall	Introductory Biology I, MCB 181	350 students	15%
2016, Fall	Cell Systems, MCB 572	13 students	50%
2016, Fall	Key Concepts in Quantitative Biology, MCB 315	8 students	100%

Guest lectures

2010	Quantitative Biology colloquium, MATH 596A (4 sessions)
2010, 2013	Research Topics in Computer Science, CSC 296H/496H
2011	Introduction to Biophysics, PHYS 430/530
2011	Genetic and Molecular Networks, MCB 546
2011	Recent Advances in Genetics, GENE 670
2011, 2013, 2014	Functional and Evolutionary Genomics, ECOL 453/553
2013	Complex Systems: Networks & Self-organization in Biology, ECOL 496H/596H
2014, 2015, 2016	Initiative for Maximizing Student Development colloquium, MCB 595E
2014, 2016	Introduction to Modeling in Biology, ECOL 519
2015	Bioinformatics, ECOL 346
2016	Seminar in Bioinformatics, ECOL 296B

Individual Trainee Contact

Collaborations with undergraduates on research projects

Travis Woodrow	Fall 2012–Spring 2013	Computer Science
Michael Iuzzolino	Summer 2013	Mathematics
Alyssa Fortier	Fall 2015–present	Molecular and Cellular Biology
Jose Leon-Burguete	Winter 2017	Genomic Sciences, National Autonomous University of Mexico (J-1 Student Intern)

Collaborations with graduate students on research projects (lab rotations)

PingHsun Hsieh	Fall 2010	Ecology & Evolutionary Biology
Mary Pansiscus	Fall 2010	Genetics
Aaron Ragsdale	Fall 2011	Applied Mathematics
Liang Wu	Fall 2012	Ecology & Evolutionary Biology
Adam David Grant	Fall 2016	Arizona Biological and Biomedical Sciences

Mentoring and Career counseling

I mentor graduate students in the Initiative for Maximizing Student Development program on applying for National Science Foundation Graduate Research Fellowships.

Theses directed and in progress

Brian Mannakee	Spring 2012	B.S. in Biochemistry "Evolutionary rate at the protein domain level is constrained by importance to network dynamics"
Katherine Cunningham	Spring 2013	B.S. in Molecular & Cellular Biology "Optimization in the demographic simulation software <i>∂a∂i</i> "
Siddharth Pandya	Spring 2013	B.S. in Biochemistry "Directional selection on tyrosine frequencies in eukaryotes versus solvent accessibility"
Travis Struck	Spring 2016	M.S. in Molecular & Cellular Biology "Research effort and evolutionary properties of genes"
Brandon Jernigan	Spring 2017	B.S. in Chemical Engineering "Evolutionary rate covariation of domain families"

Dissertations directed and in progress

PingHsun Hsieh	Spring 2016	Ph.D. in Ecology and Evolutionary Biology (Co-advised with Prof. Michael Hammer) "Model-based population genetics in indigenous humans: Inferences of demographic history, adaptive selection, and African archaic admixture using whole-genome/exome sequencing data" Now postdoc with Prof. Evan Eichler at the University of Washington
Aaron Ragsdale	Fall 2017	Ph.D. in Applied Mathematics "Model-based population genetics in indigenous humans: Inferences of demographic history, adaptive selection, and African archaic admixture using whole-genome/exome sequencing data" Now postdoc with Prof. Simon Gravel at McGill University
Brian Mannakee	In progress	Ph.D. in Biostatistics

Service on other dissertation and graduate committees

Julio Cesar Ignacio Espinoza	Winter 2015	Ph.D. in Molecular & Cellular Biology
Cristina Howard	Spring 2015	Ph.D. in Molecular & Cellular Biology
Ryan Pace	Summer 2015	Ph.D. in Molecular & Cellular Biology
Dhruv Vig	Summer 2015	Ph.D. in Molecular & Cellular Biology
August Woerner	Summer 2016	Ph.D. in Genetics

Peter Vinton	Summer 2016	Ph.D. in Molecular & Cellular Biology
Consuelo Quinto Cortés	Fall 2016	Ph.D. in Genetics
Grant Schissler	Spring 2017	Ph.D. in Statistics
Samantha Anderson	In progress	Ph.D. in Ecology & Evolutionary Biology
Ariella Gladstein	In progress	Ph.D. in Ecology & Evolutionary Biology
Nicholas Kappler	In progress	Ph.D. in Applied Mathematics
Luke Kosinski	In progress	Ph.D. in Molecular and Cellular Biology
Arron Sullivan	In progress	Ph.D. in Molecular & Cellular Biology
Kun Xiong	In progress	Ph.D. in Molecular & Cellular Biology
Miao Zhang	In progress	Ph.D. in Statistics

Postdoctoral Scholars Trained

Alexandra Jilkine	July 2011–July 2013	Now Assistant Professor of Applied Mathematics and Computational Mathematics and Statistics at the University of Notre Dame
Xia Wang	January 2015–present	(co-advised with Prof. Guang Yao)

Contributions to Instructional Innovations and Collaborations

Teaching workshops delivered

2009–present	q-bio Summer School, Albuquerque, NM
2016	Workshop on Population and Speciation Genomics, Český Krumlov, Czech Republic

Collaborations on curricular committees

2011–2017	Member, Astrobiology undergraduate and graduate minor executive committee
2012–present	Member, Molecular & Cellular Biology undergraduate curriculum committee
2013–present	Member, Bioinformatics undergraduate major steering committee
2015	Member, Introductory Physics I redesign committee

Teaching Awards

Department and college

2013	Distinguished Early-Career Teaching Award, College of Science
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