

Ryan N. Gutenkunst
<http://gutengroup.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 & Cellular Biology, University of Arizona
2017–2023 Associate Professor with Tenure
2023–present Professor with Tenure
Affiliations: Departments of Ecology & Evolutionary Biology and Epidemiology & Biostatistics; Graduate Interdisciplinary Programs (GIDPs) in Applied BioSciences, Applied Mathematics, Cancer Biology, Data Science & Statistics, and Genetics; BIO5 Institute
2017–2023 Associate Department Head
2023 Interim Department Head
2024–present Department Head

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
2009 3rd place, District 23 Toastmasters Humorous Speech Contest
2014 Kavli Fellow, US National Academy of Sciences and The Kavli Foundation
2021 Finisher, Ironman Arizona

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”
2019 Discussion with Tucson Hard Sci-Fi Writers & Artists Galactic Cabal
2020 Speaker, UA Science Cafe: “Genetic Testing: Hype versus Reality”

2023-present Host, high school researchers in my group (4)

National Outreach

2018–2021 Skype-a-Scientist with K-12 students

Departmental Service

| | |
|------------------------|--|
| 2010–2013 | Co-Chair, MCB/CMM/CBC/IMB joint departmental retreat committee |
| 2012–present | Member, Undergraduate curriculum committee |
| 2012–2013 | Chair, Website committee |
| 2013–2015 | Member, Website committee |
| 2012, 2016, 2017, 2021 | Member, Faculty peer evaluation committee |
| 2012 | Member, Faculty search committee |
| 2015–2017 | Member, Discretionary fund allocation committee |
| 2016 | Member, Astrobiology faculty search committee |
| 2017 | Member, Cancer bioinformatics search committee |
| 2017–2023 | Director of Graduate Studies, MCB Accelerated Master's Program |
| 2018 | Co-chair, MCB Academic Program Review committee |
| 2018–present | Faculty mentor for Prof. Megha Padi |
| 2019–2021 | Faculty mentor for Prof. Betül Kaçar |
| 2021 | Member, Department Head search committee |
| 2022 | Member, Discretionary fund allocation committee |
| 2022 | Member, Professor of Practice hiring committee |
| 2022–2023 | Director, Undergraduate and Master's Education |

College/University Service

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| 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” |
| 2017–2023 | Director of Graduate Studies, MCB track of Professional Science Master's in Applied Biosciences GIDP |
| 2018, 2019 | Internal reviewer, Research, Discovery & Innovation grants |
| 2019, 2020 | Internal reviewer, Astronaut Scholarship |
| 2020–present | Member, Executive Committee for Genetics GIDP |
| 2022 | Chair, College of Science committee for resolution of grade appeal |
| 2022–present | Member, Design Committee for Applied Statistics and Data Science Professional Science Master's Degree |
| 2023–present | Faculty Advisor, UA TriCats triathlon club team |
| 2023 | Internal reviewer, CNRS-UA Arizona Graduate Research Fellowship & International Mobility |
| 2023 | Co-Organizer, Arizona-Los Alamos Days meeting |

National/International Service

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|--------------|--|
| 2010 | Panelist, National Science Foundation |
| 2013 | 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 Ecology and Evolution (previously BMC Evolutionary Biology) |
| 2017 | Panelist, National Science Foundation |
| 2018 | Co-organizer, workshop on Population Genomics Simulation at Cold Spring Harbor Laboratory |
| 2019, 2021 | Organizer, Arizona Population Genetics Group workshop |
| 2020 | Panelist, National Science Foundation |
| 2020 | Lecturer, SACNAS meeting on NSF GRFP application, University of Houston |
| 2021 | Panelist, National Science Foundation |
| 2021 | Panelist, National Science Foundation |
| 2023 | Supervisor, SMCBE Virtual Lab Meeting program |
| 2023 | Organizer, PopSim satellite meeting, Cold Spring Harbor Laboratory |
| 2023 | Organizing Committee, Population, Evolutionary, and Quantitative Genetics conference |
| 2024–present | Organizer, Genomic History Inference Strategies Tournament (GHIST) |

Ad-hoc Journal Reviewer / Guest Editor

Science (1), Cell (3), Proceedings of the National Academy of Sciences USA (2), eLife (1), Molecular Biology and Evolution (8), Genome Research (2), PLoS Genetics (5), PLoS Computational Biology (3), Molecular Systems Biology (2), Molecular Ecology (4), Genetics (14), Evolution (3), Proceedings of the Royal Society B (1), Molecular Cancer Research (1), Bioinformatics (2), Molecular Ecology Resources (1), G3: Genes, Genomes, Genetics (1), Journal of Molecular Evolution (1), IET Systems Biology (1), BMC Bioinformatics (1), BMC Systems Biology (3), BMC Evolutionary Biology (3), Giga-Science (3), 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 (US, 3), National Environmental Research Council (UK, 1), Natural Sciences and Engineering Research Council (Canada, 1), Estonian Research Council (5), Vienna Science and Technology Fund (1), Wellcome Trust (UK, 2), Human Frontiers Science Program (International, 1), Biotechnology and Biological Sciences Research Council (UK, 1), Israel Science Foundation (2), United States-Israel Binational Science Foundation (1), University of Missouri Research Board (1), Nevada IDeA Network of Biomedical Research Excellence (1)

Promotion & Tenure Package Reviewer

7 (Years and institutions not listed to protect confidentiality)

Publications/Creative Activity

Key: ^O-Gutenkunst group trainee, ^C-corresponding author, ^E-contributed equally, *-substantially based on work done as a graduate student.

In the scientific fields to which I've contributed most, the authors with the greatest roles in carrying out the work are listed first, and the authors with the greatest roles in supervision are listed last. Conventions for corresponding author vary.

Refereed Journal Articles

1. Black ED, **Gutenkunst RN** (2003) An introduction to signal extraction in interferometric gravitational wave detectors. *American Journal of Physics* 71:365.
2. *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.
3. ***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.
4. ***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.
5. ***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*
6. *Myers CR, **Gutenkunst RN**, Sethna JP (2007) Python unleashed on systems biology. *Computing in Science & Engineering* 9:34.
7. *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.
9. 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.
10. 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.

12. 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.
13. 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.
15. 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.
16. 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.
☆ Featured: Wade N. (2011) Roots of disease found to vary by continent. *New York Times*.
17. **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.
☆ Featured: Stolte D (2011) First analysis of orangutan genome yields surprises. *UANews*.
19. 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.
20. 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.
21. 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.
22. 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.

24. Holmes WM, Mannakee BK^O, **Gutenkunst RN**, Serio TR^C (2014) Loss of N-terminal acetylation suppresses a prion phenotype by modulating global protein folding. *Nature Communications* 5:4383.
25. Jilkin A^O, **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^O, Hickerson MJ, **Gutenkunst RN** (2014) Sampling strategies for frequency spectrum-based population genomic inference. *BMC Evolutionary Biology* 14:254.
27. 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.
28. Hermansen RA^E, Mannakee BK^O, 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^O, Struck TJ^O, Mannakee BK^O, Paniscus M^O, **Gutenkunst RN**^C (2015) Testing whether metazoan tyrosine loss was driven by selection against promiscuous phosphorylation. *Molecular Biology and Evolution* 32:144.
30. Coffman AJ^O, Hsieh P^O, Gravel S, **Gutenkunst RN**^C (2016) Computationally efficient composite likelihood statistics for demographic inference. *Molecular Biology and Evolution* 33:591.
31. Edwards T^C, Tollis M, Hsieh P^O, **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.
32. Hsieh P^O, 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^O, 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.
34. Mannakee BK^O, **Gutenkunst RN**^C (2016) Selection on network dynamics drives differential rates of protein domain evolution. *PLoS Genetics* 12:e1006132.
35. Ragsdale AP^O, Coffman AJ^O, Hsieh P^O, Struck TJ^O, **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*.
36. Hsieh P^O, Hallmark B, Watkins J, Karafet TM, Osipova LP, **Gutenkunst RN**^C, Hammer MF^C (2017) Exome sequencing provides evidence of polygenic adaptations and deciphers demographic prehistory in indigenous Siberian populations. *Molecular Biology and Evolution* 34:2913.
☆ Press release on EurekaAlert.

37. 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^O, 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.
39. Ragsdale AP^{OC}, **Gutenkunst RN^C** (2017) Inferring demographic history using two-locus statistics. *Genetics* 206:1037.
40. Mannakee BK^{OC}, Balaji U, Witkiewicz AK, **Gutenkunst RN^C**, Knudsen ES^C (2018) Sensitive and specific post-call filtering of genetic variants in xenograft and primary tumors. *Bioinformatics* 34:1713.
41. Struck TJ^O, Mannakee BK^O, **Gutenkunst RN^C** (2018) The impact of genome-wide association studies on biomedical research publications. *Human Genomics* 12:38.
42. Adrion JK^E, Cole CB^E, Dukler N^E, Galloway JG^E, Gladstein AL^E, Gower G^E, Kyriazis CC^E, Ragsdale AP^E, Tsambos G^E, Baumdicker F, Carlson J, Cartwright RA, Durvasula A, Kim BY, McKenzie P, Messer PW, Noskova E, Vecchyo DO, Racimo F, Struck TJ^O, Gravel S, **Gutenkunst RN**, Lohmeuller KE, Ralph PL, Schrider DR, Siepel A, Kelleher J^C, Kern AD^C (2020) A community-maintained standard library of population genetic models. *eLife* 9:e54967.
43. Blischak PD^{OC}, Barker MS, **Gutenkunst RN** (2020) Inferring the demographic history of inbred species from genome-wide SNP frequency data. *Molecular Biology and Evolution* 37:2124.
44. Mannakee BK^O, **Gutenkunst RN^C** (2020) BATCAVE: Calling somatic mutations with a tumor- and site-specific prior. *NAR: Genomics and Bioinformatics* 2:lqaa004.
45. Huang X^O, Fortier AL^O, Coffman AJ^O, Struck TJ^O, Irby MN^O, James JE^O, León-Burguete JE^O, Ragsdale AP^O, **Gutenkunst RN^C** (2021) Inferring genome-wide correlations of mutation fitness effects between populations. *Molecular Biology and Evolution* 38:4588.
46. **Gutenkunst RN^C** (2021) dadi.CUDA: Accelerating population genetic inference with Graphics Processing Units. *Molecular Biology and Evolution* 38:2177.
47. Blischak PD^{OC}, Barker MS, **Gutenkunst RN** (2021) Chromosome-scale inference of hybrid speciation and admixture with convolutional neural networks. *Molecular Ecology Resources* 21:2676.
48. Gower G^E, Ragsdale AP^E, Bisschop G, **Gutenkunst RN**, Hartfield M, Noskova E, Schiffels S, Struck TJ^O, Kelleher J^C, Thornton K (2022) Demes: a standard format for demographic models. *Genetics* 222:iyac131.
49. Marchi N^E, Winkelbach L^E, Schulz I^E, Bami M^E, Hofmanová Z, Blöcher J, Reyna-Blanco CS, Diekmann Y, Thiéry A, Kapopoulou A, Link V, Piuze V, Kreutzer S, Figarska SM, Ganiatsou E, Pukaj A, Struck TJ^O, **Gutenkunst RN**, Karul N, Gerritsen F, Pechtl J, Peters J, Zeeb-Lanz A, Lenneis E, Teschler-Nicola M, Triantaphyllou S, Stefanović S, Papageorgopoulou C, Wegmann D^C, Burger J^C, Excoffier L^C (2022) The genomic origins of the world's first farmers. *Cell* 185:1842.

50. Prata KE^C, Riginos C, **Gutenkunst RN**, Latijnhouwers K, Sánchez JA, Englebert N, Hay K, Bongaerts P (2022) Deep connections: divergence histories with gene flow in mesophotic *Agaricia* corals. *Molecular Ecology* 31:2511.
51. Shaheen MF^{EC}, Tse JY^{EC}, Sokol ES, Masterson M, Bansal P, Rabinowitz I, Tarleton CA, Dobroff AS, Smith TL, Bocklage TJ, Mannakee BK^O, **Gutenkunst RN**, Bischoff JE, Ness SA, Riedlinger GM, Groisberg R, Pasqualini R, Ganesan S^C, Arap W^C (2022) Genomic landscape of lymphatic malformations: A case series and response to the PI3K α inhibitor Alpelisib in an N-of-One clinical trial. *eLife* 11:e74510.
52. Blischak PD^{OC}, Sajan M^O, Barker MS, **Gutenkunst RN^C** (2023) Demographic history inference and the polyploid continuum. *Genetics* 224:iyad107.
☆ Featured by the editors of *Genetics*.
53. Lauterbur ME^E, Cavassim MIA^E, Gladstein AL^E, Gower G^E, Pope NS^E, Tsambos G^E, Adrion J, Belsare S, Biddanda A, Caudill V, Cury J, Echevarria I, Haller BC, Hasan AR, Huang X, Iasi LNM, Noskova E, Obšteter J, Pavinato VAC, Pearson A, Peede D, Perez MF, Rodrigues MF, Smith CCR, Spence JP, Teterina A, Tittes S, Unneberg P, Vazquez JM, Waples RK, Wohns AW, Wong Y, Baumdicker F, Cartwright RA, Gorjanc G, **Gutenkunst RN**, Kelleher J, Kern AD, Ragsdale AP, Ralph PL, Schrider DR, Gronau I^C (2023) Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations. *eLife* 12:RP84874.
54. Tuffaha M, Varakunan S, Castellano D^O, **Gutenkunst RN**, Wahl LM^C (2023) Shifts in mutation bias promote mutators by altering the distribution of fitness effects. *American Naturalist* 202:503.
55. Tran LN^O, Sun CK^O, Struck TJ^O, Sajan M^O, **Gutenkunst RN^C** (2024) Computationally efficient demographic history inference from allele frequencies with supervised machine learning. *Molecular Biology and Evolution* 41:msae077.

Reviews & Commentaries

1. **Gutenkunst RN** (2002) Extracting light from water: Sonoluminescence. *Caltech Undergraduate Research Journal* 2:16.
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.
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.
4. Mannakee BK^O, Ragsdale AP^O, 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.
5. Johri P^C, Eyre-Walker A, **Gutenkunst RN**, Lohmueller KE, Jensen JD^C (2022) On the prospect of achieving accurate joint estimation of selection with population history. *Genome Biology and Evolution* 14:evac088.

Non-refereed Manuscripts

1. ***Gutenkunst RN**, Sethna JP (2007) Adaptive mutation in a geometrical model of chemotype evolution. arXiv. <https://doi.org/10.48550/arXiv.0712.3240>
2. Loewe L, Swain P, **Gutenkunst R** (2013) Mathematical Tools for Evolutionary Systems Biology. Banff International Research Station 5-day workshop report. <http://www.birs.ca/workshops/2013/13w5080/report13w5080.pdf>
3. Wang X^O, Li P, **Gutenkunst RN**^C (2017) Systematic effects of mRNA secondary structure on gene expression and molecular function in budding yeast. bioRxiv. <https://doi.org/10.1101/138792>

Software

1. ***Gutenkunst RN**, Atlas JC, Casey FP, Kuczenski RS, Waterfall JJ, Myers CR, Sethna JP (2007) SloppyCell. <http://github.com/GutenkunstLab/SloppyCell>
2. **Gutenkunst RN** (2009) dadi – Diffusion Approximations for Demographic Inference. <https://bitbucket.org/gutenkunstlab/dadi>
3. Huang X^O, Struck TJ^O, Davey S, **Gutenkunst RN** (2022) dadi-cli. <https://github.com/xin-huang/dadi-cli>
4. Tran LN^O, Sun CK^O, Struck TJ^O, **Gutenkunst RN** (2023) donni – Demography Optimization via Neural Network Inference. <https://github.com/Intran26/donni>

Publications in Progress

Refereed Journal Articles

1. Huang X^{OEC}, Struck TJ^{OE}, Davey SW, **Gutenkunst RN**^C (submitted) dadi-cli: Automated and distributed population genetic model inference from allele frequency spectra. Preprint at <https://doi.org/10.1101/2023.06.15.545182>
2. Tuffaha MZ, Castellano D^O, Serrano Colomé C, **Gutenkunst RN**, Wahl LM^C (submitted) Non-hypermutator cancers access driver mutations through reversals in germline mutational bias. Preprint at <https://doi.org/10.1101/2024.04.30.591900>
3. Vourlaki I-T^E, Castellano D^{OE}, **Gutenkunst RN**^C, Ramos-Onsins SE^C (submitted) Detection of domestication signals through the analysis of the full distribution of fitness effects using forward simulations and polygenic adaptation. Preprint at <https://doi.org/10.1101/2022.08.24.505198>

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
- 2017 Systems Biology Seminar, Boston University, Boston, MA
- 2018 Bioinformatics Forum, University of Pennsylvania, Philadelphia, PA
- 2018 Institute for Genomics and Evolutionary Medicine, Temple University, Philadelphia, PA
- 2021 School of Biological Sciences, Washington State University, Pullman, WA
- 2022 Department of Biological Sciences, Northern Arizona University, Flagstaff, AZ

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
- 2022 Software Tools for Open Science, National Institutes of Health, Online
- 2023 National Association of Biology Teachers Professional Development Conference, Baltimore, MD
- 2024 Advancing R1 Teaching Faculty for Undergraduate Learning (ARTFUL) Conference, Houston, TX

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, Tempe, 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
- 2017 International Society for Evolution, Ecology, and Cancer Annual Meeting, Tempe, AZ
- 2018 Population, Evolutionary, and Quantitative Genetics, Madison, Wisconsin
- ☆ Contributed abstract selected for platform lightning talk presentation
- 2018 Probabilistic Modeling in Genomics, Cold Spring Harbor, NY
- ☆ Contributed abstract selected for platform presentation
- 2019 Society for Molecular Biology and Evolution Annual Meeting, Manchester, UK
- ☆ Contributed abstract selected for platform presentation
- 2020 The Allied Genetics Conference, Online
- 2022 Probabilistic Modeling in Genomics, Online
- 2022 Population, Evolutionary, and Quantitative Genetics, Pacific Grove, CA
- ☆ Contributed abstract selected for platform presentation
- 2022 Society for Molecular Biology and Evolution Everywhere, Online
- ☆ Contributed abstract selected for platform presentation
- 2023 Probabilistic Modeling in Genomics, Cold Spring Harbor, NY
- 2023 Society for the Study of Evolution Annual Meeting, Albuquerque, NM
- 2024 The Allied Genetics Conference, Washington, DC
- 2025 Society for Molecular Biology and Evolution Annual Meeting, Puerto Vallarta, MX
- ☆ Organized and led GHIST kickoff workshop

Grants and Contracts

Current Federal Research Support

- | | |
|-----------------|--|
| 2/12/19–1/31/24 | NIH R01 GM127348: \$1,472,436 (No-cost extension to 1/31/25) PI: Ryan Gutenkunst Joint Inferences of Natural Selection Between Sites and Populations Role: PI (16.6% effort) Additional administrative supplement of \$199,665 awarded in 2020 from NIH Office of Data Science Strategy to support work with Nirav Merchant to bring cloud computing to dadi |
| 5/1/23–2/29/28 | NIH R35 GM149235: \$1,667,719 PI: Ryan Gutenkunst Genomic Inferences of History and Selection across Populations and Time |

Role: PI (29.8% 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)
- 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 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 572A | 8 students, 3 units | 25% |
| 2011, Fall | Cell Systems, MCB 572A | 28 students, 3 units | 33% |
| 2012, Spring | Key Concepts in Quantitative Biology, MCB 315 | 15 students, 4 units | 60% |
| 2012, Fall | Key Concepts in Quantitative Biology, MCB 315 | 13 students, 4 units | 80% |
| 2012, Fall | Cell Systems, MCB 572A | 18 students, 4 units | 50% |
| 2013, Fall | Key Concepts in Quantitative Biology, MCB 315 | 12 students, 4 units | 100% |
| 2014, Fall | Cell Systems, MCB 572A | 18 students, 4 units | 33% |
| 2014, Fall | Introductory Biology I, MCB 181 | 336 students, 3 units | 15% |
| 2014, Fall | Key Concepts in Quantitative Biology, MCB 315 | 15 students, 4 units | 100% |
| 2015, Fall | Introductory Biology I, MCB 181 | 350 students, 3 units | 15% |
| 2015, Fall | Key Concepts in Quantitative Biology, MCB 315 | 11 students, 4 units | 100% |
| 2015, Fall | Cell Systems, MCB 572A | 19 students, 4 units | 33% |
| 2016, Fall | Key Concepts in Quantitative Biology, MCB 315 | 8 students, 4 units | 100% |
| 2016, Fall | Cell Systems, MCB 572A | 13 students, 4 units | 50% |
| 2018, Fall | Genomic Medicine Colloquium, MCB 195B | 18 students, 1 unit | 100% |
| 2018, Fall | Quantitative Biology, MCB 315 | 13 students, 3 units | 100% |
| 2018, Fall | Scientific Communication, MCB 575 | 7 students, 3 units | 50% |
| 2019, Fall | Big Data in Molecular Biology and Biomedicine, MCB 447 | 7 students, 3 units | 100% |
| 2020, Fall | Genomic Medicine Colloquium, MCB 195B | 15 students, 1 unit | 100% |

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|--------------|--|----------------------|------|
| 2020, Fall | Quantitative Biology, MCB 315 | 19 students, 3 units | 67% |
| 2020, Fall | Scientific Communication, MCB 575 | 10 students, 3 units | 50% |
| 2021, Fall | Genomic Medicine Colloquium, MCB 195B | 18 students, 1 unit | 100% |
| 2021, Fall | Big Data in Molecular Biology and Biomedicine, MCB 447/547 | 16 students, 3 units | 50% |
| 2021, Fall | Scientific Communication, MCB 575 | 5 students, 3 units | 50% |
| 2022, Fall | Genomic Medicine Colloquium, MCB 195B | 20 students, 1 unit | 100% |
| 2022, Fall | Quantitative Biology, MCB 315 | 22 students, 3 units | 50% |
| 2022, Fall | Scientific Communication, MCB 575 | 10 students, 3 units | 50% |
| 2023, Spring | Genetics, Ancestry, and Race, MCB 295E | 25 students, 1 unit | 100% |
| 2023, Fall | Genetics, Ancestry, and Race, MCB 295E | 39 students, 1 unit | 100% |
| 2023, Fall | Big Data in Molecular Biology and Biomedicine, MCB 447/547 | 19 students, 3 units | 33% |

Guest Lectures

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|------------------|--|
| 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 |
| 2022 | Race, Ethnicity, and the American Dream, ANTH 150 |

Individual Trainee Contact

Collaborations with Undergraduates on Research Projects

| | | |
|--------------------|-------------------------|---|
| Travis Woodrow | Fall 2012–Spring 2013 | Computer Science |
| Michael Iuzzolino | Summer 2013 | Mathematics |
| Jose Leon-Burguete | Winter 2017 | Genomic Sciences, National Autonomous University of Mexico (J-1 Student Intern) |
| Setayesh Odmidian | Spring 2019–Summer 2019 | Biology |
| Mathews Sajan | Fall 2019–Spring 2023 | Pre-Health and Business |
| Connie Sun | Summer 2020–Spring 2023 | Ecology & Evolutionary Biology and Computer Science |
| Olivia Fernflores | Spring 2022–present | Bioinformatics |
| Lilith Kotler | Fall 2023–present | Molecular & Cellular Biology |
| Sam Gibbon | Summer 2024–present | Neuroscience & Cognitive Science |

Collaborations with Graduate Students on Research Projects (Lab Rotations)

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

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|-------------------|-------------|--|
| Amber Koslucher | Summer 2018 | Biostatistics |
| Hao Zhang | Spring 2019 | Arizona Biological & Biomedical Sciences |
| Theodore Meissner | Fall 2021 | Applied Mathematics |
| Yanghuan Yu | Fall 2021 | Arizona Biological & Biomedical Sciences |
| Stephen Cooke | Spring 2023 | Ecology & Evolutionary Biology |
| Raymond Hon | Spring 2024 | Arizona Biological & Biomedical Sciences |
| Heng Wu | Spring 2024 | Applied Mathematics |

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 and Computer Science “Optimization in the demographic simulation software dad” |
| 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” |
| Alyssa Fortier | Spring 2018 | B.S. in Molecular & Cellular Biology and Mathematics “Improving the robustness of dominance and selection inference” Awarded a NSF Graduate Research Fellowship |
| Megan Irby | Spring 2020 | B.S. in Molecular & Cellular Biology and Mathematics “The joint distribution of fitness effects of wild tomatoes and a brief introduction to linkage in DFE inference” |
| Amy Fan | Spring 2023 | B.S. in Molecular & Cellular Biology and Statistics & Data Science “Modeling selection bias on recombination rates inferred through linkage disequilibrium” |
| Olivia Fernflores | Spring 2024 | B.S. in Molecular & Cellular Biology “Inferring the Demographic History and Joint Distribution of Fitness Effects in the Wild House Mouse, <i>Mus musculus domesticus</i> ” Beckman Scholar |

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” Left to become postdoc with Prof. Evan Eichler at the University of Washington. Now faculty in Genetics, Cell Biology, and Development at the University of Minnesota. |
| Aaron Ragsdale | Fall 2017 | Ph.D. in Applied Mathematics |

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|----------------|-------------|--|
| Brian Mannakee | Fall 2019 | <p>“Multi-allele population genomics for inference of demography and natural selection”</p> <p>Left to become postdoc with Prof. Simon Gravel at McGill University. Now faculty in Integrative Biology at University of Wisconsin—Madison.</p> <p>Ph.D. in Biostatistics</p> <p>“Statistical methods for improving low frequency variant calling in cancer genomics”</p> <p>Awarded an NSF Graduate Research Fellowship</p> <p>Left to become Bioinformatics Scientist at Foundation Medicine.</p> |
| Linh Tran | Summer 2024 | <p>Ph.D. in Genetics</p> <p>“Computationally efficient, cost-effective, and interpretable machine learning methods for population genomic inference”</p> |

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 |
| Miao Zhang | Spring 2018 | Ph.D. in Statistics |
| Nicholas Kappler | Spring 2018 | Ph.D. in Applied Mathematics |
| Ariella Gladstein | Summer 2018 | Ph.D. in Ecology & Evolutionary Biology |
| Nicholas Helle | Summer 2018 | P.S.M. in Applied Biosciences |
| Arron Sullivan | Fall 2018 | Ph.D. in Molecular & Cellular Biology |
| David Jones | Spring 2019 | P.S.M. in Applied Biosciences |
| David Waid | Spring 2019 | P.S.M. in Applied Biosciences |
| Kun Xiong | Spring 2019 | Ph.D. in Molecular & Cellular Biology |
| Luke Kosinski | Summer 2020 | Ph.D. in Molecular & Cellular Biology |
| Robert Porter | Summer 2020 | P.S.M. in Applied Biosciences |
| Robert Betterton | Fall 2020 | P.S.M. in Applied Biosciences |
| Minhao Chen | Spring 2021 | P.S.M. in Applied Biosciences |
| Quinea Lassiter | Spring 2021 | P.S.M. in Applied Biosciences |
| Elizabeth Ogunbunmi | Spring 2021 | P.S.M. in Applied Biosciences |
| Cathryn Sephus | Spring 2021 | M.S. in Molecular & Cellular Biology |
| Christopher Carnahan | Summer 2021 | P.S.M. in Applied Biosciences |
| Adam Grant | Summer 2021 | Ph.D. in Cancer Biology |
| Nicole Walker | Spring 2022 | P.S.M. in Applied Biosciences |
| Chenlu Di | Fall 2022 | Ph.D. in Ecology & Evolutionary Biology |
| Ondrej Cernicky | Spring 2023 | M.S. in Molecular & Cellular Biology |
| Joshua Hack | Spring 2023 | M.S. in Molecular & Cellular Biology |
| Annalisa Medina | Spring 2023 | P.S.M. in Applied Biosciences |
| Alexandra Sundman | Spring 2023 | M.S. in Molecular & Cellular Biology |

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|--------------------|-------------|---|
| Shane Thomas | Spring 2023 | Ph.D. in MCB with Emphasis in Science Education |
| Alhan Yazdi | Spring 2023 | P.S.M. in Applied Biosciences |
| Heather Connick | Winter 2023 | P.S.M. in Applied Biosciences |
| Matt Miller | Spring 2024 | M.S. in Molecular & Cellular Biology |
| Ulises Hernandez | In progress | Ph.D. in Ecology & Evolutionary Biology |
| Qiuyu Jiang | In progress | Ph.D. in Ecology & Evolutionary Biology |
| Mary Reed-Weston | In progress | Ph.D. in Genetics |
| Genavieve Sandoval | In progress | Ph.D. in Ecology & Evolutionary Biology |
| Sawsan Wehebi | In progress | Ph.D. in Genetics |
| Andrew Wheeler | In progress | Ph.D. in Genetics |
| Jiawen Yang | In progress | Ph.D. in Cancer Biology |

Postdoctoral Scholars Trained

| | |
|-------------------|--|
| Alexandra Jilkine | July 2011–July 2013 Left to become Assistant Professor of Applied Mathematics and Computational Mathematics and Statistics at the University of Notre Dame |
| Xia Wang | January 2015–January 2018 (co-advised with Prof. Guang Yao) Left to become postdoc with Prof. Helen Zhang at the University of Arizona. |
| Paul Blischak | September 2018–December 2020 (co-advised with Prof. Mike Barker and supported by an NSF Plant Genome fellowship) Left to become Data Scientist at Bayer Crop Science |
| Xin Huang | November 2019–June 2021 Left to become a postdoc with Martin Kuhlwilm at the University of Vienna |
| Jennifer James | August 2020–April 2021 Left with a Wenner-Gren Post-PhD Fellowship to work with Martin Lascoux at Uppsala University |
| David Castellano | December 2021–present |
| Emanuel Fonseca | May 2022–present |
| Justin Conover | March 2023–present (co-advised with Prof. Mike Barker and supported by an NSF Plant Genome fellowship) |

Contributions to Instructional Innovations and Collaborations

Teaching Workshops Delivered

| | |
|-----------|---|
| 2009–2017 | 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 |
| 2020–present | Member, Master's in Genetics curriculum committee |

Curriculum Development

I developed the curricula for the MCB 315: Qualitative Biology and for MCB 447/547: Big Data in Molecular Biology and Biomedicine. I also developed a two-week computational cancer lab for the AIM-Bio reformed MCB 181L: Introductory Biology Laboratory. In addition, I developed two 1-unit colloquia courses: MCB 195B: Genomic Medicine and MCB 295E: Genetics, Ancestry, and Race.

Teaching Awards

Department and College

2013 Distinguished Early-Career Teaching Award, College of Science