

**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

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

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, SMBE Virtual Lab Meeting program
2023	Organizer, PopSim satellite meeting, Cold Spring Harbor Laboratory
2023	Organizing Committee, Population, Evolutionary, and Quantitative Genetics conference

#### Ad-hoc Journal Reviewer

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 (4), 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), GigaScience (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)

#### External Thesis Reviewer

McGill University (Canada, 1)

## Publications/Creative Activity

Key: <sup>O</sup>-Gutenkunst group trainee, <sup>C</sup>-corresponding author, <sup>E</sup>-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<sup>C</sup>, 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**<sup>C</sup>, 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**<sup>C</sup>, 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**<sup>C</sup>, 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<sup>C</sup>, 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<sup>C</sup>, **Gutenkunst RN**, Myers CR (2008) Sloppiness, robustness, and evolvability in systems biology. *Current Opinion in Biotechnology* 19:389.
9. Andrés AM<sup>C</sup>, 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<sup>C</sup> (2009) Global distribution of genomic diversity underscores rich complex history of continental human populations. *Genome Research* 19:795.

11. **Gutenkunst RN<sup>C</sup>**, 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<sup>C</sup>, 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<sup>C</sup> (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<sup>C</sup> (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<sup>C</sup> (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<sup>C</sup>**, 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<sup>E</sup>, **Gutenkunst RN<sup>E</sup>**, Wilbe Ramsay K, Alaeus A, Albert J, Leitner T<sup>C</sup> (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<sup>C</sup> (2011) Effect of 1918 PB1-F2 expression on influenza A virus infection kinetics. *PLoS Computational Biology* 7:e1001081.
21. Xu X<sup>E</sup>, Liu X<sup>E</sup>, Ge S<sup>E</sup>, Jensen JD<sup>E</sup>, Hu F<sup>E</sup>, Li X<sup>E</sup>, Dong Y<sup>E</sup>, **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<sup>C</sup>, Wang J<sup>C</sup>, Wang W<sup>C</sup> (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<sup>C</sup> (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<sup>C</sup>, 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<sup>O</sup>, **Gutenkunst RN**, Serio TR<sup>C</sup> (2014) Loss of N-terminal acetylation suppresses a prion phenotype by modulating global protein folding. *Nature Communications* 5:4383.
25. Jilkine A<sup>O</sup>, **Gutenkunst RN**<sup>C</sup> (2014) Effect of dedifferentiation on time to mutation acquisition in stem cell-driven cancers. *PLoS Computational Biology* 10:e1003481.
26. Robinson JD<sup>C</sup>, Coffman AJ<sup>O</sup>, 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<sup>C</sup> (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<sup>E</sup>, Mannakee BK<sup>OE</sup>, Knecht W, Liberles DA<sup>C</sup>, **Gutenkunst RN**<sup>C</sup> (2015) Characterizing selective pressures on the pathway for de novo biosynthesis of pyrimidines in yeast. *BMC Evolutionary Biology* 15:232.
29. Pandya S<sup>O</sup>, Struck TJ<sup>O</sup>, Mannakee BK<sup>O</sup>, Paniscus M<sup>O</sup>, **Gutenkunst RN**<sup>C</sup> (2015) Testing whether metazoan tyrosine loss was driven by selection against promiscuous phosphorylation. *Molecular Biology and Evolution* 32:144.
30. Coffman AJ<sup>O</sup>, Hsieh P<sup>O</sup>, Gravel S, **Gutenkunst RN**<sup>C</sup> (2016) Computationally efficient composite likelihood statistics for demographic inference. *Molecular Biology and Evolution* 33:591.
31. Edwards TC, Tollis M, Hsieh P<sup>O</sup>, **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<sup>O</sup>, Veeramah KR, Lachance J, Tishkoff SA, Wall JD, Hammer MF<sup>C</sup>, **Gutenkunst RN**<sup>C</sup> (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<sup>O</sup>, Woerner AE, Wall JD, Lachance J, Tishkoff SA, **Gutenkunst RN**, Hammer MF<sup>C</sup> (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<sup>O</sup>, **Gutenkunst RN**<sup>C</sup> (2016) Selection on network dynamics drives differential rates of protein domain evolution. *PLoS Genetics* 12:e1006132.
35. Ragsdale AP<sup>O</sup>, Coffman AJ<sup>O</sup>, Hsieh P<sup>O</sup>, Struck TJ<sup>O</sup>, **Gutenkunst RN**<sup>C</sup> (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<sup>O</sup>, Hallmark B, Watkins J, Karafet TM, Osipova LP, **Gutenkunst RN**<sup>C</sup>, Hammer MF<sup>C</sup> (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<sup>C</sup>, **Gutenkunst R**, Ackerman M, Spitze K, Ye Z, Maruki T, Jia Z (2017) Population genomics of *Daphnia pulex*. *Genetics* 206:315.
38. Qi X<sup>C</sup>, An H, Ragsdale AP<sup>O</sup>, 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<sup>OC</sup>, **Gutenkunst RN**<sup>C</sup> (2017) Inferring demographic history using two-locus statistics. *Genetics* 206:1037.
40. Mannakee BK<sup>OC</sup>, Balaji U, Witkiewicz AK, **Gutenkunst RN**<sup>C</sup>, Knudsen ES<sup>C</sup> (2018) Sensitive and specific post-call filtering of genetic variants in xenograft and primary tumors. *Bioinformatics* 34:1713.
41. Struck TJ<sup>O</sup>, Mannakee BK<sup>O</sup>, **Gutenkunst RN**<sup>C</sup> (2018) The impact of genome-wide association studies on biomedical research publications. *Human Genomics* 12:38.
42. Adrion JK<sup>E</sup>, Cole CB<sup>E</sup>, Dukler N<sup>E</sup>, Galloway JG<sup>E</sup>, Gladstein AL<sup>E</sup>, Gower G<sup>E</sup>, Kyriazis CC<sup>E</sup>, Ragsdale AP<sup>E</sup>, Tsambos G<sup>E</sup>, Baumdicker F, Carlson J, Cartwright RA, Durvasula A, Kim BY, McKenzie P, Messer PW, Noskova E, Vecchy DO, Racimo F, Struck TJ<sup>O</sup>, Gravel S, **Gutenkunst RN**, Lohmeuller KE, Ralph PL, Schrider DR, Siepel A, Kelleher J<sup>C</sup>, Kern AD<sup>C</sup> (2020) A community-maintained standard library of population genetic models. *eLife* 9:e54967.
43. Blischak PD<sup>OC</sup>, 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<sup>O</sup>, **Gutenkunst RN**<sup>C</sup> (2020) BATCAVE: Calling somatic mutations with a tumor- and site-specific prior. *NAR: Genomics and Bioinformatics* 2:lqaa004.
45. Huang X<sup>O</sup>, Fortier AL<sup>O</sup>, Coffman AJ<sup>O</sup>, Struck TJ<sup>O</sup>, Irby MN<sup>O</sup>, James JE<sup>O</sup>, León-Burguete JE<sup>O</sup>, Ragsdale AP<sup>O</sup>, **Gutenkunst RN**<sup>C</sup> (2021) Inferring genome-wide correlations of mutation fitness effects between populations. *Molecular Biology and Evolution* 38:4588.
46. **Gutenkunst RN**<sup>C</sup> (2021) dadi.CUDA: Accelerating population genetic inference with Graphics Processing Units. *Molecular Biology and Evolution* 38:2177.
47. Blischak PD<sup>OC</sup>, 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<sup>E</sup>, Ragsdale AP<sup>E</sup>, Bisschop G, **Gutenkunst RN**, Hartfield M, Noskova E, Schiffels S, Struck TJ<sup>O</sup>, Kelleher J<sup>C</sup>, Thornton K (2022) Demes: a standard format for demographic models. *Genetics* 222:iyac131.
49. Marchi N<sup>E</sup>, Winkelbach L<sup>E</sup>, Schulz I<sup>E</sup>, Bami M<sup>E</sup>, 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<sup>O</sup>, **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<sup>C</sup>, Burger J<sup>C</sup>, Excoffier L<sup>C</sup> (2022) The genomic origins of the world's first farmers. *Cell* 185:1842.
50. Prata KE<sup>C</sup>, 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<sup>EC</sup>, Tse JY<sup>EC</sup>, Sokol ES, Masterson M, Bansal P, Rabinowitz I, Tarleton CA, Dobroff AS, Smith TL, Bocklage TJ, Mannakee BK<sup>O</sup>, **Gutenkunst RN**, Bischoff JE, Ness SA, Riedlinger GM, Groisberg R, Pasqualini R, Ganesan S<sup>C</sup>, Arap W<sup>C</sup> (2022) Genomic landscape of lymphatic malformations: A case series and response to the PI3K $\alpha$  inhibitor Alpelisib in an N-of-One clinical trial. *eLife* 11:e74510.
  52. Blischak PD<sup>OC</sup>, Sajan M<sup>O</sup>, Barker MS, **Gutenkunst RN**<sup>C</sup> (2023) Demographic history inference and the polyploid continuum. *Genetics* 224:iyad107.  
☆ Featured by the editors of *Genetics*.
  53. Lauterbur ME<sup>E</sup>, Cavassim MIA<sup>E</sup>, Gladstein AL<sup>E</sup>, Gower G<sup>E</sup>, Pope NS<sup>E</sup>, Tsambos G<sup>E</sup>, 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<sup>C</sup> (2023) Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations. *eLife* 12:RP84874.
  54. Tuffaha M, Varakunan S, Castellano D<sup>O</sup>, **Gutenkunst RN**, Wahl LM<sup>C</sup> (2023) Shifts in mutation bias promote mutators by altering the distribution of fitness effects. *American Naturalist* 202:503.
  55. Tran LN<sup>O</sup>, Sun CK<sup>O</sup>, Struck TJ<sup>O</sup>, Sajan M<sup>O</sup>, **Gutenkunst RN**<sup>C</sup> (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<sup>O</sup>, Ragsdale AP<sup>O</sup>, Transtrum MK, **Gutenkunst RN**<sup>C</sup> (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<sup>C</sup>, Eyre-Walker A, **Gutenkunst RN**, Lohmueller KE, Jensen JD<sup>C</sup> (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<sup>O</sup>, Li P, **Gutenkunst RN**<sup>C</sup> (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, Kuczynski 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<sup>O</sup>, Struck TJ<sup>O</sup>, Davey S, **Gutenkunst RN** (2022) dadi-cli. <https://github.com/xin-huang/dadi-cli>
4. Tran LN<sup>O</sup>, Tran LN<sup>O</sup>, Sun CK<sup>O</sup>, Struck TJ<sup>O</sup>, **Gutenkunst RN** (2023) donni – Demography Optimization via Neural Network Inference. <https://github.com/Intran26/donni>

## **Publications in Progress**

#### Refereed Journal Articles

1. Huang X<sup>OE</sup>, Struck TJ<sup>OE</sup>, Davey SW, **Gutenkunst RN**<sup>C</sup> (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<sup>O</sup>, Serrano Colomé C, **Gutenkunst RN**, Wahl LM<sup>C</sup> (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<sup>E</sup>, Castellano D<sup>OE</sup>, **Gutenkunst RN**<sup>C</sup>, Ramos-Onsins SE<sup>C</sup> (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

## 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%
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

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

#### 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
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”

#### 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 “Multi-allele population genomics for inference of demography and natural selection” Left to become postdoc with Prof. Simon Gravel at McGill University.

Brian Mannakee	Fall 2019	Now faculty in Integrative Biology at University of Wisconsin—Madison. Ph.D. in Biostatistics “Statistical methods for improving low frequency variant calling in cancer genomics” Awarded an NSF Graduate Research Fellowship Left to become Bioinformatics Scientist at Foundation Medicine.
Linh Tran	In progress	Ph.D. in Genetics

#### 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
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 Kuhlwiilm 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