

Contact	Department of Biology Tufts University 200 College St Medford, MA 02155 Lawrence.Uricchio@tufts.edu	https://scholar.google.com/citations?user=XyVUpZYAAAAJ uricchio.github.io
Positions	2021- 2018-2021 2015-2018	<i>Assistant Professor</i> , Department of Biology, Tufts University <i>Postdoctoral Scholar</i> , Integrative Biology, University of California, Berkeley <i>Postdoctoral Fellow</i> , Biology, Stanford University
Education	2014 2011 2009 2005	<i>PhD</i> , Bioinformatics, University of California, San Francisco <i>MS</i> , Computer Science, University of Chicago <i>MS</i> , Biophysical Sciences, University of Chicago <i>BA</i> , Physics, Carleton College
Honors	2016-2018 2015-2016 2014 2014 2013 2012-2014 2005 2005 2005 2005 2002	NIH IRACDA Postdoctoral Fellow, Stanford University & SJSU CEHG Postdoctoral Fellow, Stanford University Discovery Fellow, UCSF ASHG trainee award for excellence in human genetics research, semi-finalist Teaching Assistant Excellence Award, UCSF Achievement Rewards for College Scientists Fellow, UCSF Distinction in the physics major, Carleton College Phi Beta Kappa (academic honor society), Carleton College Sigma Xi (scientific research honor society), Carleton College Magna Cum Laude, Carleton College Dean's list, Carleton College

Articles

Published

- [1] EBEL ER, **URICCHIO LH**, PETROV DA, EGAN ES (2022) Revisiting the malaria hypothesis: accounting for polygenicity and pleiotropy. *Trends in Parasitology*, **38**(4).
- [2] COUPER LI, FARNER JE, CALDWELL JM, CHILDS ML, HARRIS MJ, KIRK DG, NOVA N, SHOCKET M, SKINNER EB, **URICCHIO LH**, EXPOSITO-ALONSO M, MORDECAI EA. (2021) How will mosquitoes adapt to climate warming?. *eLife*, **10**, e69630.
- [3] SONG C, **URICCHIO LH**, MORDECAI EA, SAAVEDRA S. (2021) Understanding the emergence of contingent and deterministic exclusion in multispecies communities. *Ecology Letters*, **24**, 2155–2168.
- [4] **URICCHIO LH** (2020) Evolutionary perspectives on polygenic selection, missing heritability, and GWAS. *Human Genetics*, **139**(1), 5–21.
- [5] SEVERSON AL, **URICCHIO LH**, ARBISSER IM, GLASSBERG EC, ROSENBERG NA. (2019) Analysis of author gender in TPB, 1991-2018. *Theoretical Population Biology*, **127**, 1–6.
- [6] **URICCHIO LH**, PETROV DA, ENARD D. (2019) Exploiting selection at linked sites to infer the rate and strength of adaptation. *Nature Ecology & Evolution*, **3**(6), 977–984.
- [7] HERNANDEZ RD, **URICCHIO LH**, HARTMAN K, YE C, DAHL A, ZAITLEN N. (2019) Ultrarare variants drive substantial cis heritability of human gene expression. *Nature Genetics*, **51**(9), 1349–1355.
- [8] **URICCHIO LH**[†], KITANO HC[†], GUSEV A, ZAITLEN NA. (2019) An evolutionary compass for detecting signals of polygenic selection and mutational bias. *Evolution Letters*, **3**(1), 69–79.
- [9] **URICCHIO LH**, DAWS SC, SPEAR ER, MORDECAI EA. (2019) Priority effects and nonhierarchical competition shape species composition in a complex grassland community. *The American Naturalist*, **193**(2), 213–226.

- [10] GIGNOUX CR, TORGERSON DG, PINO-YANES M, **URICCHIO LH**, GALANTER J, ROTH LA, ENG C, HU D, NGUYEN EA, HUNTSMAN S et al. (2019) An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos. *Journal of Allergy and Clinical Immunology*, **143**(3), 957–969.
- [11] GOLDBERG A, **URICCHIO LH**, ROSENBERG NA (2018) Natural selection in human populations. *Oxford Bibliographies in Evolutionary Biology*, DOI:10.1093/OBO/9780199941728-0112.
- [12] **URICCHIO LH**, WARNOW T, ROSENBERG NA (2016) An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees. *BMC Bioinformatics*, **17**(14), 241–250.
- [13] **URICCHIO LH**[†], ZAITLEN NA, YE CJ, WITTE JS, HERNANDEZ RD[†]. (2016) Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. *Genome Research*, **26**, 863–873. († *co-corresponding authors*).
- [14] **URICCHIO LH**, TORRES R, WITTE JS, HERNANDEZ RD. (2015) Population genetic simulations of complex phenotypes with implications for rare variant association tests. *Genetic Epidemiology*, **39**(1), 35–44.
- [15] **URICCHIO LH**, HERNANDEZ, RD. (2014) Robust forward simulations of recurrent hitchhiking. *Genetics*, **197**(1), 221–236.
- [16] MAHER MC[‡], **URICCHIO LH**[‡], TORGERSON DG, HERNANDEZ RD. (2013) Population genetics of rare variants and complex diseases. *Human Heredity*, **74**(3-4), 118–128. (‡ *denotes equal contributions; recommended to the Faculty of 1000*).
- [17] **URICCHIO LH**, CHONG JX, ROSS KD, OBER C, NICOLAE DL. (2012) Accurate imputation of rare and common variants in a founder population from a small number of sequenced individuals. *Genetic Epidemiology*, **36**(4), 312–319.
- [18] ÇALIŞKAN M, CHONG JX, **URICCHIO L**, ANDERSON R, CHEN P et al. (2011) Exome sequencing reveals a novel mutation for autosomal recessive nonsyndromic mental retardation in the TECR gene on chromosome 19p13. *Human Molecular Genetics*, **20**(7), 1285–1289.
- [19] MILLER LS, PIETRAS EM, **URICCHIO LH**, HIRANO K, RAO S et al. (2007) Inflammasome-mediated production of IL-1 β is required for neutrophil recruitment against *Staphylococcus aureus* in vivo. *Journal of Immunology*, **179**(10), 6933–6942.
- [20] PATTANAYAK AK, BROOKS DWC, DE LA FUENTE A, **URICCHIO L**, HOLBY E et al. (2005) Coarse-grained entropy decrease and phase-space focusing in Hamiltonian dynamics. *Physical Review A*, **72**(1), 013406.

In progress

- [1] **URICCHIO LH**, BRUNS EL, HOOD M, BOOTS M, ANTONOVICS J. (2022) Multimodal disease transmission as a limiting factor for the spatial extent of a host plant. *Ecology*, **submitted**.
- [2] VISHER E, **URICCHIO LH**, BARTLETT L, DENAMUR N, YARCAN A, ALHASSANI D, BOOTS M (2022) The Evolution of Host Specialization in an Insect Pathogen. *Evolution*, **in revision**.
- [3] CASTELLANO D, **URICCHIO LH**, MUNCH K, ENARD D. Viruses rule over adaptation in conserved human proteins. (2019) *preprint available at* <https://www.biorxiv.org/content/10.1101/555060v1.abstract>.

Dissertation

- [1] **URICCHIO LH**. (2014) Models and forward simulations of selection, human demography, and complex traits. UNIVERSITY OF CALIFORNIA, SAN FRANCISCO.

Teaching	2022	Instructor, <i>Seminar in Ecology and Evolution</i> , Bio 244, Tufts University
	2022	Guest lecture, <i>Resilience seminar</i> , Bio 263, Tufts University
	2021	Instructor, <i>Computational Biology</i> , Bio 35, Tufts University
	2018	Co-instructor, <i>Evolutionary genetics</i> , San Jose State University
	2017	Co-instructor, <i>Ecology</i> , San Jose State University
	2017	Co-founder, <i>Stanford postdoc pedagogy miniseries</i> , Stanford University
	2016-2017	Guest lecturer, <i>Evolution</i> , Stanford University
	2015	Instructor, <i>Undergraduate Biology Exploration</i> , Stanford University
	2014	Graduate teaching assistant, <i>Computational Evolutionary Genomics</i> , UCSF
	2013	Graduate student instructor, <i>Computational Biology</i> , UC Berkeley
	2009	Guest lecturer, <i>Genes, Networks, and Cells</i> , University of Chicago
	2003-2004	Teaching assistant, tutor, & grader, <i>Introduction to Physics, Classical & Computational Mechanics, Contemporary Experimental Physics</i> , Carleton College
Mentorship	2022-	Undergrad research mentor for Daphne Garcia, Tufts Biology Dept & Summer Fellow
	2021-	Postdoc mentor for Dr. Adam Pepi, Tufts Biology Dept
	2021-	PhD mentor for Kasturi Lele, Tufts Biology Dept
	2021-	PhD mentor for SJ McGeady, Tufts Biology Dept
	2021-	PhD mentor for Alejandro Calderon, Tufts Biology Dept
	2021	Summer research mentor for Alice Lau, Tufts MS student and TIE Fellow
	2021	Summer research mentor for SJ McGeady, incoming Tufts PhD student
	2016	Summer research co-mentor for Alan Aw, Stanford undergraduate
	2013	Summer research co-mentor for Isela Hernandez, Biological Health Sciences Internship Program
	2010	Summer research co-mentor for Sam Neal, Summer Link High School Program
Service	2022	Canada Foundation for Innovation Grant Reviewer
	2021	NSF panelist (invited grant reviewer)
	2021-	Committee Member, Tufts Biology DEIJ committee
	2013-	Invited peer reviewer for <i>Genetics</i> , <i>BMC Evolutionary Biology</i> , <i>PLoS Genetics</i> , <i>Molecular Biology & Evolution</i> , <i>Genome Biology & Evolution</i> , <i>Molecular Ecology</i> , <i>Heredity</i> , <i>Theoretical Population Biology</i> , <i>Nature Genetics</i> , <i>American Journal of Human Genetics</i> , <i>Entropy</i> , <i>Functional Ecology</i> , <i>Peer Community in Evolutionary Biology</i> , <i>Journal of Allergy and Clinical Infection</i> , <i>eLife</i> , <i>PLoS ONE</i> , <i>G3</i> , <i>Evolution</i> , and <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i>
	2016	Committee Member & Presenter, Stanford Postdoc Pedagogy Journal Club
	2015-2016	Committee Member, Stanford CEHG diversity outreach committee
Competitive Funding	2016-2018	NIH IRACDA Fellow, Stanford & SJSU (\$53,600 per year)
	2016-2017	Stanford Teaching & Mentoring Academy Award (\$6,870)
	2015-2016	Stanford CEHG Postdoctoral Fellowship (\$50,000)
	2012-2014	UCSF Achievement Rewards for College Scientists Fellow (\$12,000 per year)
	2014	UCSF Discovery Fellow (\$4,000 for travel & research over 2 years)

Presentations

- [1] Back to the future: the population genetics of adaptation in our rapidly changing world. *CSU East Bay, Hayward, CA. Seminar*, 2020.
- [2] Adaptation and constraint through the lens of genome-wide association studies. *University of Wisconsin, Madison, WI. Seminar*, 2020.
- [3] Adaptation and constraint through the lens of genome-wide association studies. *Temple University, Philadelphia, PA. Seminar*, 2020.

- [4] Adaptation and constraint through the lens of genome-wide association studies. *Tufts University, Somerville, MA. Seminar*, 2020.
- [5] Adaptation and constraint through the lens of genome-wide association studies. *Vanderbilt University, Nashville, TN. Seminar*, 2020.
- [6] Evolutionary perspectives on human complex traits and missing heritability. *CSUN, Northridge, CA. Seminar*, 2019.
- [7] Can modern genomic sequence data fulfill their evolutionary potential?. *Indiana University, Bloomington, IN. Seminar*, 2019.
- [8] Statistical inference of evolutionary processes from genomic data. *Macalester College, St. Paul, MN. Seminar*, 2019.
- [9] Can modern genomic sequence data fulfill their evolutionary potential?. *Cornell University, Ithaca, NY. Seminar*, 2019.
- [10] Exploiting selection at linked sites to infer the rate and strength of adaptation. *Evolution Meeting, Providence, RI. Talk*, 2019.
- [11] Genome-scale inference of adaptive evolution: new approaches for answering old questions. *Boise State University, Boise, ID. Seminar*, 2019.
- [12] Genome-scale inference of adaptive evolution: new approaches for answering old questions. *Chapman University, Orange, CA. Seminar*, 2019.
- [13] Evolutionary processes shaping the human genome. *Linfield College, McMinnville, OR. Seminar*, 2018.
- [14] Scientific teaching workshops for Stanford postdocs. *Stanford Education Day, Stanford, CA. Talk*, 2018.
- [15] Modulation of adaptation rate by background selection in the human genome. *Bay Area Population Genomics Meeting, Santa Cruz, CA. Talk*, 2018.
- [16] Modulation of adaptation rate by background selection in the human genome. *American Society of Naturalists Meeting, Monterey, CA. Talk* (2018).
- [17] Designing and implementing scientific teaching workshops for postdocs. *Stanford Teaching and Mentoring Academy seminar series, Stanford, CA. Talk* (2018).
- [18] An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees. *RECOMB Comparative Genomics Meeting, Montreal, Canada. Talk* (2016).
- [19] Explosive growth and the genetic architecture of polygenic traits under selection. *American Society of Naturalists Meeting, Monterey, CA. Talk* (2016).
- [20] Selection and explosive growth may hamper the performance of rare variant association tests. *Bay Area Population Genomics Meeting, Stanford, CA. Talk* (2015).
- [21] Recent demography and natural selection hamper the power of rare variant association tests. *American Society of Human Genetics Meeting, San Diego, CA. Talk* (2014).
- [22] Model-based simulations of selection and demography with implications for heritable phenotypes and rare variant association tests. *UC Berkeley Center for Theoretical Evolutionary Genomics, Berkeley, CA. Talk* (2014).
- [23] Simulations and inference of simultaneous positive and negative selection. *Society of Molecular Biology and Evolution Meeting, San Juan, Puerto Rico. Poster* (2014).
- [24] Parameter rescaling for forward simulations of recurrent hitchhiking. *Bay Area Population Genomics Meeting, San Francisco, CA. Poster* (2013).
- [25] Forward simulations of recurrent selection and demographics with rescaled parameters. *American Society of Human Genetics Meeting, Boston, MA. Poster* (2013).
- [26] Accurate pedigree-based imputation. *Department of Human Genetics Seminar, University of Chicago, Chicago, IL. Talk* (2011).

- [27] Simultaneous measurement of myosin-II kinetics and cellular traction forces. *HHMI Interfaces Scholars Meeting, Chevy Chase, MD. Poster* (2008).