Lawrence Hart Uricchio   *computational biology, evolutionary & statistical genetics, quantiative ecology, mentorship & teaching*

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	University of California, Berkeley	`https://uricchio.github.io/`
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Education	2015 -	*Postdoc*, UC Berkeley & Stanford University
	2014	*PhD*, Bioinformatics, University of California, San Francisco
	2011	*MS*, Computer Science, University of Chicago
	2009	*MS*, Biophysical Sciences, University of Chicago
	2005	*BA*, Physics, Carleton College

Honors & Fellowships	2016 - 2018	NIH IRACDA Postdoctoral Fellow, Stanford University
	2015 - 2016	CEHG Postdoctoral Fellow, Stanford University
	2014	Discovery Fellow, UCSF
	2014	ASHG trainee award for excellence in human genetics research, semi-finalist
	2013	Teaching Assistant Excellence Award, UCSF
	2012 - 2014	Achievement Rewards for College Scientists Fellow, UCSF
	2005	Distinction in the physics major, Carleton College
	2005	Phi Beta Kappa (academic honor society), Carleton College
	2005	Sigma Xi (scientific research honor society), Carleton College
	2005	Magna Cum Laude, Carleton College
	2002	Dean's list, Carleton College

Publications

Articles & editorials

1. Hernandez RD, **Uricchio LH**, Hartman K, Ye J, Dahl A, Zaitlen N. Ultra-rare variants drive substantial cis-heritability of human gene expression. *Nature Genetics*, accpeted, 2019.

2. **Uricchio LH**[†]. Evolutionary perspectives on polygenic selection, missing heritability, and GWAS. *Human Genetics*, in press, June 2019.

3. **Uricchio LH**[†], Petrov DA, Enard D[†]. Exploiting selection at linked stites to infer the rate and strength of adaptation. *Nature Ecology & Evolution*, 3:977–984, June 2019.

4. Severson AL[‡], **Uricchio LH**[‡], Arbisser IM[‡], Glassberg EC, Rosenberg NA. Analysis of author gender in TPB, 1991–2018. *Theoretical Population Biology*, 127:1–6, June 2019.

5. Gignoux CR, Torgerson DG, Pino-Yanes M, **Uricchio LH**, Galanter J *et al.* 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, Mar 2019.

6. **Uricchio LH**[‡†], Kitano HC[‡], Gusev A, Zaitlen NA[†]. An evolutionary compass for detecting polygenic selection and mutational bias. *Evolution Letters*, 3(1):69–79, Feb 2019.

7. **Uricchio LH**[†], Daws SC, Spear ER, Mordecai EA[†]. Priority effects and non-hierarchical competition shape species composition in a complex grassland community. *The American Naturalist*, 193(2):213–226, Feb 2019.

8. Goldberg A, **Uricchio LH**, Rosenberg NA. Natural selection in human populations. *Oxford Bibliographies in Evolutionary Biology*, Aug 2018.

9. **Uricchio LH**, Warnow T, Rosenberg NA. 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, Nov 2016.

10. **Uricchio LH**[†], Zaitlen NA, Ye CJ, Witte JS, Hernandez RD[†]. Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. *Genome Research*, 26:863–873, July 2016.

11. **Uricchio LH**, Torres R, Witte JS, Hernandez RD. Population genetic simulations of complex phenotypes with implications for rare variant association tests. *Genetic Epidemiology*, 39(1):35–44, Jan 2015.

12. **Uricchio LH**, Hernandez RD. Robust forward simulations of recurrent hitchhiking. *Genetics*, 197(1):221–236, May 2014.

13. Maher MC[‡], **Uricchio LH**[‡], Torgerson DG, Hernandez RD. Population genetics of rare variants and complex diseases. *Human Heredity*, 74(3-4):118–128, Apr 2013.

14. **Uricchio LH**, Chong JX, Ross KD, Ober C, Nicolae DL. Accurate imputation of rare and common variants in a founder population from a small number of sequenced individuals. *Genetic Epidemiology*, 36(4):312–319, May 2012.

15. Çalışkan M, Chong JX, **Uricchio L**, Anderson R, Chen P *et al*. 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, Apr 2011.

16. Miller LS, Pietras EM, **Uricchio LH**, Hirano K, Rao S *et al*. Inflammasome-mediated production of IL-1β is required for neutrophil recruitment against staphylococcus aureus in vivo. *Journal of Immunology*, 179(10):6933–6942, Nov 2007.

17. Pattanayak AK, Brooks DWC, de La Fuente A, **Uricchio L**, Holby E *et al*. Coarse-grained entropy decrease and phase-space focusing in hamiltonian dynamics. *Physical Review A*, 72(1):013406, Jul 2005.

‡ denotes equal contributions; † denotes corresponding author

In progress

1. Castellano D, **Uricchio LH**, Munch K, Enard D. Viruses rule over adaptation in conserved human proteins. to be submitted: *preprint at* `https://www.biorxiv.org/content/10.1101/555060v1`, 2019.

Dissertation

1. **Uricchio LH**. Models and forward simulations of selection, human demography, and complex traits. UNIVERSITY OF CALIFORNIA, SAN FRANCISCO, 2014.

Teaching	2018	Co-instructor, *Evolutionary genetics* (BIOL 118), San Jose State University*
	2017	Co-instructor, *Ecology* (BIOL 160), San Jose State University*
		*semester-long undergraduate courses for which I led 40-50% of instructional time.
	2017	Co-founder, *Stanford postdoc pedagogy miniseries*, Stanford University
	2015	Instructor, *Undergraduate Biology Exploration*, Stanford University
	2016-2017	Guest lecturer (twice), *Evolution*, Stanford University
	2014	Graduate teaching assistant, *Computational Evolutionary Genomics*, UCSF
	2013	Graduate student instructor, *Computational Biology*, UC Berkeley
	2009	Guest lecturer, *Genes, Networks, and Cells*, University of Chicago
	2003-2004	Teaching assistant, tutor, & grader, *Introduction to Physics, Classical & Computational Mechanics, Contemporary Experimental Physics*, Carleton College
Mentoring	2016	Student research co-mentor to Alan Aw, Rosenberg Lab
	2013	Student research mentor to Isela Hernandez, Biological Health Sciences Internship Program
	2010	Student research mentor to Sam Neal, Summer Link High School Program
	2006-2007	Co-supervisor/trainer of undergraduate lab members, UCLA
Service	2013-	Invited reviewer for *Genetics, Nature Genetics, BMC Evolutionary Biology, PLoS Genetics, Nature Ecology & Evolution, Molecular Biology & Evolution, Molecular Ecology, Heredity, Theoretical Population Biology, PLoS ONE, G3: Genes, Genomes, Genetics*, and *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
	2016	Committee member & session leader, 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. Exploiting selection at linked stites to infer the rate and strength of adaptation. *Evolution Meeting, Providence, RI.* **Talk**, 2019.

2. Genome-scale inference of adaptive evolution: new approaches for answering old questions. *Boise State University, Boise, ID.* **Seminar**, 2019.

3. Genome-scale inference of adaptive evolution: new approaches for answering old questions. *Chapman University, Orange, CA.* **Seminar**, 2019.

4. Evolutionary processes shaping the human genome. *Linfield College, McMinnville, OR.* **Seminar**, 2018.

5. Scientific teaching workshops for stanford postdocs. *Stanford Education Day, Stanford, CA.* **Talk**, 2018.

6. Modulation of adaptation rate by background selection in the human genome. *Bay Area Population Genomics Meeting, Santa Cruz, CA.* **Talk**, 2018.

7. Modulation of adaptation rate by background selection in the human genome. *American Society of Naturalists Meeting, Monterey, CA.* **Talk**, 2018.

8. Designing and implementing scientific teaching workshops for postdocs. *Stanford Teaching and Mentoring Academy seminar series, Stanford, CA.* **Talk**., 2018.

9. 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.

10. Detecting causal genetic variation in populations with complex evolutionary histories. *Univeristy of Washington, Bothell, WA.* **Seminar**, 2016.

11. Explosive growth and the genetic architecture of polygenic traits under selection. *American Society of Naturalists Meeting, Monterey, CA.* **Talk**, 2016.

12. Selection and explosive growth may hamper the performance of rare variant association tests. *Bay Area Population Genomics Meeting, Stanford, CA.* **Talk**, 2015.

13. Recent demography and natural selection hamper the power of rare variant association tests. *American Society of Human Genetics Meeting, San Diego, CA.* **Talk**, 2014.

14. 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.

15. Simulations and inference of simultaneous positive and negative selection. *Society of Molecular Biology and Evolution Meeting, San Juan, Puerto Rico.* **Poster**, 2014.

16. Parameter rescaling for forward simulations of recurrent hitchhiking. *Bay Area Population Genomics Meeting, San Francisco, CA.* **Poster**, 2013.

17. Forward simulations of recurrent selection and demographics with rescaled parameters. *American Society of Human Genetics Meeting, Boston, MA.* **Poster**, 2013.

18. Accurate pedigree-based imputation. *Department of Human Genetics, University of Chicago, Chicago, IL.* **Seminar**, 2011.

References

Associate Professor Ryan Hernandez, PhD *(PhD advisor)*
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