

# CV: Daniel B. Weissman *(Last updated: July 19, 2019)*

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Math & Science Center N244, Dept. of Physics, Emory University, Atlanta, GA 30322

## Education

PhD, Stanford University (2010) Physics. Thesis: “Epistasis and Evolution”.

Advisors: Marc Feldman, Daniel Fisher

BA, Harvard College (2005) Physics and Mathematics

## Positions

2015– : Assistant Professor of Physics, Emory University

2014–2015 : Postdoctoral researcher, UC Berkeley (adviser: Oskar Hallatschek)

2014: Research Fellow, Simons Institute for the Theory of Computing, UC Berkeley

2010–2013: Postdoctoral researcher, IST Austria (adviser: Nicholas Barton)

## Concurrent positions

2017–: Core Faculty, Initiative in the Theory and Modeling of Living Systems (TMLS), Emory University

2017– : Associated Assistant Professor of Biology, Emory University

2015–: Faculty, Population Biology, Ecology, and Evolution (PBEE) Graduate Program, Emory University

## Funding

### Current

2019-2021: co-I, NIH R21 AI138079-01A1, “*C. trachomatis* within-host genomic diversity and transmission between female anatomic sites”, \$469k total.

2018–2023: co-PI, NSF PoLS 1806833 subcontract from Georgia Tech, “Formation of High a High-Flux Student Research Network (HF-SRN) as a Laboratory for Enhancing Interaction in the PoLS SRN”, \$500k total.

2017–2022: Simons Investigator Award in the Mathematical Modeling of Living Systems, \$660k total.

## Teaching

Emory:

Physics 152: Intro Electricity & Magnetism (Spring 2019)

Physics 731R: Quantitative Population Biology (Spring 2018)

Physics 365: Electricity & Magnetism (Fall 2015, Fall 2016, Fall 2017)

Physics 421: Thermodynamics (Spring 2017)

Co-instructor, IBS 592: Quantitative Methods in PBEE (Spring 2018)

Co-instructor, IBS 594: Evolutionary Biology (Spring 2016)

University of Vienna: Co-instructor, Molecular Population Genetics (Spring 2013)

Stanford and IST Austria: Teaching assistant for undergraduate and graduate courses in physics, mathematics, and biology (2008–2012)

Harvard University: Tutor, Physics Question Center (2003–2005)

See Service/Outreach below for K-12 teaching

## Awards and honors

2017: Simons Investigator Award in the Mathematical Modeling of Living Systems (as listed above)  
2014: Postdoc travel award, Society for Molecular Biology and Evolution (declined)  
2014: Research Fellowship, Simons Institute for the Theory of Computing  
2012: 2<sup>nd</sup> prize, postdoc/faculty talks, Population Genetics Group, Glasgow  
2008–2010: Stanford Graduate Fellowship  
2005–2008: NSF Graduate Research Fellowship  
2005: University of Cambridge, Herchel Smith Scholarship (declined)  
2005: *Summa cum laude* (Harvard), highest honors (Physics Department)  
2005: Stride-Rite Award for outreach and service (Harvard)  
2005: Phi Beta Kappa  
2001–2005: John Harvard Scholar  
2002–2003: Detur Prize (Harvard)

## Awards and honors to group members

2018: Emory PBEE Student of the Year, Brent Allman  
2018: Travel Award, U. Washington Summer Institute in Statistics and Modeling of Infectious Disease, Brent Allman  
2018: Communicate Your Science Award, Genetics Society UK, Mahan Ghafari  
2017-2020: NSF Graduate Research Fellowship, Brent Allman  
2017: Travel Award, NIMBioS workshop on Connecting Biological Data with Mathematical Models, Brent Allman  
2017: Emory McMullan Award, Caroline Holmes  
2017: Emory Evidence-Focused Mini-Grant for Teaching, Brent Allman  
2016: Travel Award, 10<sup>th</sup> q-bio conference, Mahan Ghafari  
2016: Scholarship, q-bio Summer School, Mahan Ghafari  
2016: Emory professional development Travel Award, Mahan Ghafari

## Talks and conferences

### External invited talks

“Evolution in space” (2019) Physics Colloquium, Georgia Institute of Technology  
“Learning influenza infection dynamics from genetic data” (2018) ITS Symposium, CUNY Graduate Center  
“Clones, sex, and hitchhiking in space” (2018) Bar-Ilan University  
“Evolution in spatially-structured populations” (2018) ITS Symposium, CUNY Graduate Center  
“Inferring population dynamics from genetic diversity with minimal assumptions” (2017) Quantitative Biology Seminar, Cold Spring Harbor Laboratory  
“Minimal-assumption historical inference from population-genomic data” (2017) Harvard University  
“Inferring population dynamics from genomic diversity” (2017) Tel Aviv University  
“Genetic diversity in adapting, spatially-extended populations” (2014) Biology seminar, San Francisco State University  
“The effect of gene interactions on evolution” (2014) Physics colloquium, Emory University  
“The rate and dynamics of complex adaptation” (2013) Ecology & Evolution seminar, University of Lausanne  
“The genomic effects of selective sweeps” (2012) Biomathematics seminar, University of Vienna  
“The dynamics of complex adaptation” (2012) University of St. Andrews

“The effects of sweeps in large sexual populations” (2012) Institute of Evolutionary Biology seminar, University of Edinburgh  
 “The rate of adaptation in large sexual populations” (2011) Stanford University  
 “The rate of complex adaptation” (2010) University of Illinois at Urbana-Champaign  
 “The dynamics of complex adaptation” (2010) IST Austria  
 “The dynamics of complex adaptation” (2010) University of Pennsylvania  
 “Complex adaptations: crossing fitness valleys” (2010) KITP, UC Santa Barbara  
 “Complex adaptations and disease” (2010) UCLA

## Invited conference talks

*TBD (2020) Workshop on Mathematics of Microbial Evolution: Beyond the Limits of Classical Theory, Banff International Research Station*  
*TBD (2019) Workshop on Out-of-Equilibrium Processes in Evolution and Ecology, Banff International Research Station - Casa Matemática Oaxaca*  
 “Inferring spatial dynamics from genetic diversity” (2019) Telluride Science Research Center Workshop on Emergent Simplicity in Biophysical Dynamics  
 “Evolutionary theory: goals and methods” (2019) Telluride Science Research Center Workshop on Emergent Simplicity in Biophysical Dynamics  
 “Clones, sex, and hitchhiking in space” (2018) Theory and Biology conference, Simons Foundation  
 “Hitchhiking in space” (2017) Feldman II, Stanford University  
 “Minimal-assumption inference from genomes” (2016) Populations, Evolution, and Physics conference, Aspen Center for Physics

## Publications

Ghafari M, **DBW** (2019) The expected time to cross extended fitness plateaus. *Theoretical Population Biology*: accepted, preprint available at [www.biorxiv.org/content/10.1101/343053v1](http://www.biorxiv.org/content/10.1101/343053v1).  
 Li ZRT, Zarnitsyna VI, Lowen AC, **DBW**, Koelle K, Kohlmeier JE, Antia R, Garcia-Sastre A (2019) Why Are CD8 T Cell Epitopes of Human Influenza A Virus Conserved? *Journal of Virology* 93: e01534–18.  
 Allman BE, **DBW** (2018) Hitchhiking in space: ancestry in adapting, spatially extended populations. *Evolution* 72: 722–734.  
 Holmes CM, Nemenman I, **DBW** (2018) Increased adaptability to sudden environmental change can more than make up for the two-fold cost of males. *Europhysics Letters* 123: 58001.  
**DBW**, Hallatschek O (2017) Minimal-assumption inference from population-genomic data. *eLife* 6: e24836.  
 Delarue M, **DBW**, Hallatschek O (2017) A simple molecular mechanism explains multiple patterns of cell-size regulation. *PLoS ONE* 12: e0182633.  
 Sobel Leonard A, **DBW**, Greenbaum BD, Ghedin E, Koelle K (2017) Transmission bottleneck size estimation from pathogen deep-sequencing data, with an application to human influenza A virus. *Journal of Virology* 91: e00171–17.  
 Van Cleve J, **DBW** (2015) Measuring ruggedness in fitness landscapes. *Proceedings of the National Academy of Sciences* 112: 7345–7346.  
 Arbilly M, **DBW**, Grodzinski U, Feldman MW (2014) Arms races between producers and scroungers can drive the evolution of social cognition. *Behavioral Ecology* 25: 487–495.  
**DBW** (2014) Stress-induced variation can cause average mutation and recombination rates to be positively correlated with fitness. *ALIFE* 14: 43–44.

- DBW**, Hallatschek O (2014) The rate of adaptation in large sexual populations with linear chromosomes. *Genetics* 196: 1167–1183.
- Trotter MV, **DBW**, Peterson GI, Peck KM, Masel J (2014) Cryptic genetic variation can make “irreducible complexity” a common mode of adaptation in sexual populations. *Evolution* 68: 3357–3367.
- DBW**, Barton NH (2012) Limits to the rate of adaptive substitution in sexual populations. *PLoS Genetics* 8: e1002740.
- DBW**, Feldman MW, Fisher DS (2010) The rate of fitness-valley crossing in sexual populations. *Genetics* 186: 1389–1410.
- DBW**, Desai MM, Fisher DS, Feldman MW (2009) The rate at which asexual populations cross fitness valleys. *Theoretical Population Biology* 75: 286–300.
- Desai MM, **DBW**, Feldman MW (2007) Evolution can favor antagonistic epistasis. *Genetics* 177: 1001–1010.