

# CV: Daniel B. Weissman

daniel.weissman@emory.edu; <http://weissmanlab.github.io>

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

2017– : Associated Assistant Professor of Biology, Emory University

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)

## Funding

2017–2022: Simons Investigator Award in the Mathematical Modeling of Living Systems

2008–2010: Stanford Graduate Fellowship

2005–2008: NSF Graduate Research Fellowship

2005: University of Cambridge, Herchel Smith Scholarship (declined)

## Invited talks

*TBD (2018) Theory and Biology conference, Simons Foundation.*

*“Inferring population dynamics from genetic diversity with minimal assumptions.” (12/2017) Quantitative Biology Seminar, Cold Spring Harbor Laboratory.*

“Hitchhiking in space.” (2017) Feldmania II, Stanford University.

“Minimal-assumption historical inference from population-genomic data.” (2017) Harvard University.

“Inferring population dynamics from genomic diversity.” (2017) Tel Aviv University.

“Minimal-assumption inference from genomes.” (2016) Populations, Evolution, and Physics conference, Aspen Center for Physics.

“Genetic diversity in adapting, spatially-extended populations.” (2014) Dept. of Biology seminar, San Francisco State University.

“The rate and dynamics of complex adaptation.” (2013) Dept. of 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 complex adaptation.” (2010) University of Illinois at Urbana-Champaign.

## Awards and honors

2014: Postdoc travel award, Society for Molecular Biology and Evolution (declined)

2012: 2<sup>nd</sup> prize, postdoc/faculty talks, Population Genetics Group, Glasgow

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)

## Teaching

- Emory:
  - Electricity & Magnetism; Fall 2015, Fall 2016, Fall 2017.
  - Thermodynamics; Spring 2017.
- 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 below for K-12 teaching experience.

## Service/outreach

- STEM Symposium: Recruitment committee, poster judge, program representative, 2016–present
- Stanford Science Bus: Science enrichment teacher in East Palo Alto Charter School, 2006–2010.
- Stanford Student Labor Action Coalition, 2006–2010.
- Boston Refugee Youth Enrichment: Science teacher, 2001–2005. Science director, 2002–2005. Summer school teacher, 2003. Support staff, 2005. Mentor, 2002–2010.
- Harvard Progressive Student Labor Movement, 2001–2005.
- East Central Illinois Refugee Mutual Assistance Center: Tutor, 2000–2001.

## Publications

- 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.
- DBW** (2016) Ancestry in adapting, spatially-extended populations. *bioRxiv*: 084426.
- 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.