# CV: Daniel B. Weissman

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### 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)

2006–2010: Research assistant, Stanford University (advisers: Marcus Feldman, Daniel Fisher)

### **Fellowships**

2014: Research Fellowship, Simons Institute for the Theory of Computing

2008–2010: Stanford Graduate Fellowship

2005–2008: NSF Graduate Research Fellowship

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

## Invited/prize talks

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

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

"The rate and dynamics of complex adaptation." (2013) University of Lausanne: Department of Ecology & Evolution seminar.

"The genomic effects of selective sweeps." (2012) University of Vienna.

"The dynamics of complex adaptation." (2012) University of St. Andrews.

"Patterns of diversity in adapting, spatially-extended populations." (2012) Population Genetics Group, Glasgow. 2<sup>nd</sup> prize, postdoc/faculty talks.

"The effects of sweeps in large sexual populations." (2012) University of Edinburgh: Institute of Evolutionary Biology seminar.

"The rate of complex adaptation." (2010) University of Illinois at Urbana-Champaign.

### **Publications**

- 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.
- **DBW**, Hallatschek O (2016) Minimal-assumption inference from population-genomic data. bioRxiv: 084459.
- Delarue M, **DBW**, Hallatschek O (2016) A simple molecular mechanism explains multiple patterns of cell-size regulation. bioRxiv: 083725.
- 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.