

# CV: Daniel B. Weissman *(Last updated: June 3, 2021)*

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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”.

Advisers: 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: Nick 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

2021-2023: Sloan Research Fellowship, \$75k total

2021-2022: PI, Synergy II Nexus Award, “Mapping the eco-evolutionary landscape of antibiotic resistance and virulence in the bacterial pathogen *Staphylococcus aureus*”, \$83k total

2020-2023: co-PI, Emory MP3 Initiative Seed Grant, “Characterizing molecular regulation of *Acinetobacter baumannii* phenotypes to understand its spread dynamics in a host community”, \$300k total

2018–2023: co-PI, NSF PoLS 1806833 subcontract from Georgia Tech, “Formation of a High-Flux Student Research Network (HF-SRN) as a Laboratory for Enhancing Interaction in the PoLS SRN”, \$500k total, subcontract \$100k total

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

### Completed

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

## Teaching

Emory:

Physics 152: Intro to Electricity & Magnetism (Spring 2019)

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

Physics 421: Thermodynamics (Spring 2017, Spring 2020, Spring 2021)

Physics 502: Mathematical Physics (Fall 2019)  
Physics 731R: Quantitative Population Biology (Spring 2018)  
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

2021: Sloan Research Fellowship (as listed above)  
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

2021, Brent Allman: Berl Boykin Fierce Leadership Award, Emory Office of LGBT Life  
2021, Brent Allman: Bouchet Graduate Honor Society induction  
2019, Brent Allman: Kharen Fulton Diversity Award, Emory Laney Graduate School  
2018, Brent Allman: Student of the Year, Emory PBEE  
2018, Brent Allman: Travel Award, U. Washington Summer Institute in Statistics and Modeling of Infectious Disease  
2018, Mahan Ghafari: Communicate Your Science Award, Genetics Society UK  
2017–2020, Brent Allman: Graduate Research Fellowship, NSF  
2017, Brent Allman: Travel Award, NIMBioS workshop on Connecting Biological Data with Mathematical Models  
2017, Caroline Holmes: McMullan Award, Emory College  
2017, Brent Allman: Evidence-Focused Mini-Grant for Teaching, Emory Laney Graduate School  
2016, Mahan Ghafari: Travel Award, 10<sup>th</sup> q-bio conference  
2016, Mahan Ghafari: Scholarship, q-bio Summer School  
2016, Mahan Ghafari: Professional development Travel Award, Emory Laney Graduate School  
2015–2020, Tyler Smith: Woodruff Fellowship, Emory Laney Graduate School

## Talks and conferences

### Invited talks

- “Inferring dispersal patterns and gene interactions from genetic sequencing data” (2021) Networks Seminar, University of Houston
- “Inferring spatial dynamics from genetic diversity and gene interactions from large bacterial phylogenies” (2021) Workshop on Quantitative Evolution, Phylogeny and Ecology: From Models to Data and Back, Institut Henri Poincaré, Paris
- Cancelled due to COVID* (2020) Workshop on the Mathematics of Microbial Evolution: Beyond the Limits of Classical Theory, Banff International Research Station, Canada
- “Evolution in space” (2020) Bioinformatics and Genomics Seminar, University of North Carolina, Charlotte
- “Evolution in space” (2019) Physics Colloquium, Georgetown University
- “Evolution in space” (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
- “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
- “Clones, sex, and hitchhiking in space” (2018) Theory and Biology conference, Simons Foundation
- “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
- “Hitchhiking in space” (2017) Feldman 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) 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

## Publications

- Allman BE, Koelle K, **DBW** (2021) Heterogeneity in viral infections increases the rate of deleterious mutation accumulation. *bioRxiv*. DOI: 10.1101/2021.05.07.443113.
- Ghafari M, Lumby CK, **DBW**, Illingworth CJR (2020) Inferring transmission bottleneck size from viral sequence data using a novel haplotype reconstruction method. *Journal of Virology* 94: e00014–20.
- Rybnikov S, **DBW**, Hübner S, Korol AB (2020) Fitness dependence preserves selection for recombination across diverse mixed mating systems. *bioRxiv*. DOI: 10.1101/2020.09.29.318238.
- Smith T, **DBW** (2020) Isolation by distance in populations with long-range dispersal. *bioRxiv*. DOI: 10.1101/2020.06.24.168211.
- Ghafari M, **DBW** (2019) The expected time to cross extended fitness plateaus. *Theoretical Population Biology* 129: 54–67.
- 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.