

# CV: Daniel B. Weissman *(Last updated: June 9, 2023)*

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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

2023–: Associate Professor of Physics, Emory University

2015–2023: 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

2022-2027: PI, NSF 2146260 (PHY), “CAREER: Quantifying Adaptation and Recombination in Pathogen Populations”, \$817k total

2021-2023: Sloan Research Fellowship FG-2021-16667, \$75k total

2021-2022: PI, Synergy II Nexus Award / MP3 Initiative Seed Grant, “Mapping the eco-evolutionary landscape of antibiotic resistance and virulence in the bacterial pathogen *Staphylococcus aureus*”, \$83k total, no-cost extension through 2023

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 1806833 (PHY) subcontract from Georgia Tech, “Collaborative Research: Formation of a High-Flux Student Research Network (HF-SRN) as a Laboratory for Enhancing Interaction in the PoLS SRN”, \$1.9M total, subcontract \$500k total

2017–2022: Simons Investigator Award in the Mathematical Modeling of Living Systems 508600, \$660k total, no-cost extension through 2023

### 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, Spring 2023)

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

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

Physics 502: Mathematical Physics (Fall 2019\*, Spring 2022\*, Fall 2022<sup>†</sup>)

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)

\**now relabeled Physics 702: Advanced Mathematical Methods*

<sup>†</sup>*now renamed Physics 502: Mathematical Methods*

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)

## 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)

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

2022, Brent Allman: Presidential Member, Genetics Society of America

2022, Brent Allman: Heart of Emory Award, Office of Campus Life

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

- “SARS-CoV-2 adaptation at the population and individual levels” (2023) Workshop on the Mathematics of Microbial Evolution: Beyond the Limits of Classical Theory, Banff International Research Station, Canada
- “SARS-CoV-2 evolution within and between hosts” (2022) Physics Colloquium, University of Florida
- “Chronic infections likely drive SARS-CoV-2 adaptation” (2022) Mathematics and Statistics of Genomic Epidemiology, Banff International Research Station - Casa Matemática Oaxaca
- “Adaptation in space” (2022) Towards an Integrative View of Adaptation: Bridging Population and Quantitative Genetics, KITP, UC Santa Barbara
- “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
- “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

### Invited talks prior to Emory

- “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

- Båvik LM, Mehta RS, **DBW** (2023) 50 shades of greenbeard: robust evolution of altruism based on similarity of complex phenotypes. *Proceedings of the Royal Society B: Biological Sciences*: accepted. DOI: 10.1101/2022.05.26.493612.
- Mehta RS, Petit III RA, Read TD, **DBW** (2023) Detecting patterns of accessory genome coevolution in *Staphylococcus aureus* using data from thousands of genomes. *BMC Bioinformatics* 24: 243. DOI: 10.1186/s12859-023-05363-4.
- Rybnikov SR, Frenkel Z, Hübner S, **DBW**, Korol AB (2023) Modeling the evolution of recombination plasticity: a prospective review. *BioEssays*: 2200237. DOI: 10.1002/bies.202200237.
- Smith T, **DBW** (2023) Isolation by distance in populations with power-law dispersal. *G3: Genes, Genomes, Genetics*: jkad023. DOI: 10.1093/g3journal/jkad023.
- Allman BE, Koelle K, **DBW** (2022) Heterogeneity in viral populations increases the rate of deleterious mutation accumulation. *Genetics* 222 (2): iyac127. DOI: <https://doi.org/10.1093/genetics/iyac127>.
- Ghafari M, Liu Q, Dhillon A, Katzourakis A, **DBW** (2022) Investigating the evolutionary origins of the first three SARS-CoV-2 variants of concern. *Frontiers in Virology* 2: 942555. DOI: 10.3389/fviro.2022.942555.
- Koelle K, Lin J, Zhu H, Antia R, Lowen AC, **DBW** (2022) Masks do no more than prevent transmission: theory and data undermine the variolation hypothesis. *medRxiv*. DOI: 10.1101/2022.06.28.22277028.
- Min J, Gupta M, Desai MM, **DBW** (2022) Spatial structure alters the site frequency spectrum produced by hitchhiking. *Genetics* 222 (3): iyac139. DOI: 10.1093/genetics/iyac139.
- Scherer EM, Babiker A, Adelman MW, Allman B, Key A, Kleinhenz JM, Langsjoen RM, Nguyen PV, Onyechi I, Sherman JD, Simon TW, Soloff H, Tarabay J, Varkey J, Webster AS, Weiskopf D, **DBW**, Xu Y, Waggoner JJ, Koelle K, Rouphael N, Pouch SM, Piantadosi A (2022) SARS-CoV-2 evolution and immune escape in immunocompromised patients. *New England Journal of Medicine* 386: 2436–2438.
- Rybnikov S, **DBW**, Hübner S, Korol AB (2021) Fitness dependence preserves selection for recombination across diverse mixed mating strategies. *Journal of Theoretical Biology* 528: 110849.
- 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.
- 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.

- Sobel Leonard A, **DBW**, Greenbaum B, Ghedin E, Koelle K (2019) Correction for Sobel Leonard et al., “Transmission bottleneck size estimation from pathogen deep-sequencing data, with an application to human influenza A virus”. *Journal of Virology* 93.
- 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.