# Justin Silverman

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| CONTACT INFORMATION | `Justin.Silverman@duke.edu` | justin-silverman.com<br>statsathome.com |

RESEARCH INTERESTS

Computational and statistical methods for sequence count data (*e.g.,* microbiome surveys, gene expression studies, single cell RNA-seq), uncertainty quantification, Bayesian decision theory, time-series analysis, compositional data analysis.

EDUCATION

**MD/PhD Candidate**, Duke University                 2012-2020
  PhD in Computational Biology and Bioinformatics
  *Thesis:* Bayesian Multivariate Count Models for the Design
       and Analysis of Microbiome Studies
  *Mentors:* Dr. Lawrence David and Dr. Sayan Mukherjee
  PhD graduation in 2019, MD graduation in 2020

**Research Technician**, Johns Hopkins University          2011-2012
  *Mentor:* Dr. Nina Markovic

**Bachelors of Science**, Johns Hopkins University          2007-2011
  Double Major in Physics and Biophysics, Minor in Mathematics

PUBLICATIONS

[* denotes equal contribution]

Villa MM*, Bloom RJ*, **Silverman JD**, Durand HK, Jiang S, Wu A, Huang S, You L, David LA. (2019) High-throughput isolation and culture of human gut bacteria with droplet microfluidics. *bioRxiv* 630822; DOI:10.1101/630822

**Silverman JD**, Bloom RJ, Jiang S, Durand HK, Mukherjee S, David LA. (2019) Measuring and Mitigating PCR Bias in Microbiome Data. *bioRxiv* 604025; DOI:10.1101/604025

**Silverman JD**, Roche K, Holmes ZC, David LA, Mukherjee S. (2019) Bayesian Multinomial Logistic Normal Models Through Marginally Latent Matrix-T Processes. *arXiv* :1903.11695

**Silverman JD**, Roche K, Mukherjee S, David LA. (2018) Naught all zeros in sequence count data are the same. *bioRxiv* 477794; DOI:10.1101/477794.

**Silverman JD**\*, Shenhav L*, David LA, Halperin E, Mukherjee S. (2018) Statistical Considerations in the Design and Analysis of Longitudinal Microbiome Studies. *bioRxiv* 448332; DOI:10.1101/448332 (*Invited Review at mSystems*)

**Silverman JD**, Durand HK, Bloom RJ, Mukherjee S, David LA. (2018) Dynamic linear models guide design and analysis of microbiota studies within artificial human guts. *Microbiome.* 6:202 DOI:10.1186/s40168-018-0584-3

Shenhav L, Furman O, Bariscoe L, Thompson M, **Silverman JD**, Mizrahi I, Halperin E. (2018) Modeling the temporal dynamics of the gut microbial community in adults and infants. *bioRxiv* 212993. DOI:10.1101/212993. (*Submitted to PLoS Computational Biology*)

Washburne AD, **Silverman JD**, Morton JT, Becker D, Crowley D, Mukherjee S, David LA, Plowright R. (2018) Phylofactorization - a graph partitioning algorithm to

identify phylogenetic scales of ecological data. *Ecological Monographs* 00(00):e01353. DOI:10.1002/ecm.1353

**Silverman JD**, Silverman RK. (2018) The Bayesian Sorting Hat: A Decision-Theoretic Approach to Size-Constrained Clustering. arXiv:1710.06047. (*In Revision at Journal of Machine Learning Research*)

Midani FS, Weil AA, Chowdhury F, Begum YA, Khan AI, Debela, MD, Durand HK, Reese AT, Nimmagadda SN, **Silverman JD**, Ellis CN, Ryan ET, Calderwood SB, Harris JB, Qadri F, David LA, LaRocque RC. (2018) Human gut microbiota predicts susceptibility to *Vibrio cholerae* infection. *The Journal of Infectious Diseases.* 218:4 DOI:10.1093/infdis/jiy192

**Silverman JD**, Washburne AD, Mukherjee S, David LA. (2017) A phylogenetic transform enhances analysis of compositional microbiota data. *eLife* 6:e21887 DOI: 10.7554/eLife.21887

Washburne AD, **Silverman JD**, Leff JW, Bennett DJ, Darcy JL, Mukherjee S, Fierer N, David LA. (2017) Phylogenetic factorization of compositional data yields lineage-level associations in microbiome datasets. *PeerJ* 5:e2969 DOI:10.7717/peerj.2969

| PUBLICATIONS SUBMITTED AND IN PREPARATION | [* denotes equal contribution]<br><br>Morton J*, Marotz C*, **Silverman JD**, Washburne A, Edlund A, Zaramela L, Zengler K, Knight R. Establishing microbial measurement standards with reference frames (*In Revision at Nature Communications*)<br><br>**Silverman JD**, Mukherjee S, David LA. Rethinking base-scale inference in sequence count data through total augmentation. (*In Preparation*) |
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| PATENTS AND SOFTWARE | **Justin D. Silverman** (2019) Multinomial logistic-normal linear models using a marginal Laplace approximation (*stray*)<br><br>**Justin D. Silverman** (2017) Dynamic linear models for microbiota studies (MALLARD)<br><br>**Justin Silverman** (2016) philr: Phylogenetic partitioning based ILR transform for metagenomics data. R package version 1.0.0. http://bioconductor.org/packages/philr/ (Downloaded 2951 times; September 6th, 2018).<br><br>**Justin David Silverman**, Adam Sean Jermyn, Nina Markovic. (2015) *System for Lightweight Image Processing.* U.S. Patent 9,097,739. |
| FUNDED RESEARCH | Collaborative Quantitative Approaches to Problems in Basic and Clinical Sciences, Pilot Grant ($50,000) — Authored (Submitting PIs: Lawrence David and Sayan Mukherjee) "A geometric approach to modeling human microbiota dynamics"      2016-2017 |

| HONORS AND AWARDS | | |
|---|---|---|
| Best Young Presentation (Compositional Data Analysis Workshop) | | 2017 |
| Mitchell Meritorious Research Travel Award | | 2017 |
| Phi Beta Kappa (JHU Highest Honors for Arts and Sciences) | | 2011 |
| Donald E. Kerr Memorial Award for Excellence in Physics | | 2011 |
| H. Keffer Hartline Award for Outstanding Scholarship in Biophysics | | 2011 |
| JHU Office of Greek Life Senior Academic Excellence Award | | 2011 |
| Goldwater Scholar | | 2010 |
| Provost Undergraduate Research Award | | 2010 |
| Materials Research Science and Engineering Center, Summer REU | | 2010 |
| Sigma Pi Sigma (Physics Honor Society, Invitation Only) | | 2010 |

SERVICE

**Referee**     publons.com/author/1257294/justin-d-silverman
Annals of Applied Statistics
PLoS Computational Biology
mSystems
Genome Biology *(In Conjunction with Lawrence David)*

**Session Organizer**     IMS Invited Session at JSM 2018
"Longitudinal Modeling and Experimental Design for Investigating Host Associated Microbiota"

| INVITED TALKS | |
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| Symposium on Advances in Genomics, Epidemiology and Statistics: Philadelphia | 2019 |
| Biostatistics Seminar Series at University of Massachusetts: Amherst, MA | 2019 |
| Simons Foundation: New York, NY | 2019 |
| Penn State University: State College, PA | 2019 |
| University of Chicago: Chicago, IL | 2019 |
| Computational Molecular Biology Seminar at Brown: Providence, RI | 2018 |
| Center of Statistical Genetics Seminar, Univ of Michigan: Ann Arbor, MI | 2018 |
| IMS Invited Session at JSM: Vancouver, BC | 2018 |
| Probabilistic Microbial Modeling Symposium: San Diego, CA | 2018 |
| ENAR Geometry and Topology in Statistical Inference: Atlanta, GA | 2018 |
| Wharton Statistics Seminar Series: Philadelphia, PA | 2018 |
| Universitat Politècnica de Catalunya: Barcelona, Spain | 2018 |
| Seminar in Compositional Data: Girona, Spain | 2017 |
| Health Analytics Workshop at Duke University: Durham, NC | 2016 |

CONFERENCE TALKS

*Modeling time evolution and therapeutic effect in human microbiota*, The $7^{th}$ International Workshop on Compositional Data Analysis, Abbadia San Salvatore, Italy. (June 2017)

| RESEARCH MENTORSHIP | |
|---|---|
| Kim Roche (Graduate) | 2018-2019 |
| Katie Sparks (Undergraduate) | 2012 |
| Chris Weddel (High School) | 2011-2012 |
| Adam Jermyn (High School) | 2011-2012 |
| Roberto Rivera (Undergraduate) | 2011 |

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| <span style="font-variant:small-caps">Teaching Experience</span> | DOmath 2018 Research Program:<br>Stochastic Properties of Dynamical Systems: Project Manager | Summer 2018 |
| | Human Microbiome Seminar<br>Guest Lecturer, University of North Carolina, Chapel Hill | Spring 2017 |
| | Statistical Methods in Computational Biology<br>Teaching Assistant and Guest Lecturer, Duke University | Spring 2017 |
| | Spectroscopy (Quantum Mechanics for Biophysics)<br>Teaching Assistant, Johns Hopkins University | Fall 2011 |

<span style="font-variant:small-caps">References</span>

**Sayan Mukherjee**, Professor, Department of Statistical Science, Duke University, (919) 684-4608 `sayan@stat.duke.edu`

**Lawrence David**, Assistant Professor, Center for Genomic and Computational Biology, Duke University, (919) 668-5388 `lawrence.david@duke.edu`

**Juan Jose Egozcue**, Professor, Department of Civil and Environmental Engineering, Polytechnic University of Catelonia, `juan.jose.egozcue@upc.edu`

**Vera Pawlowsky-Glahn**, Professor, Department of Computer Science and Applied Math, University of Girona, ++34-972-418170, `vera.pawlowsky@udg.edu`

**Greg Gloor**, Professor, Department of Biochemistry, University of Western Ontario, (519) 661-2111, `ggloor@uwo.ca`

**David Simel**, Professor, Department of Medicine, Duke University, (919) 286-6941, `david.simel@duke.edu`