

## Justin Silverman

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CONTACT INFORMATION	Justin.Silverman@duke.edu justin-silverman.com statsathome.com
RESEARCH INTERESTS	Computational and statistical methods for sequence count data ( <i>e.g.</i> , microbiome surveys, gene expression studies, single cell RNA-seq), uncertainty quantification, Bayesian decision theory, time-series analysis, compositional data analysis.
EDUCATION	<p><b>MD/PhD Candidate</b>, Duke University 2012-2020 PhD in Computational Biology and Bioinformatics <i>Thesis</i>: Bayesian Multivariate Count Models for the Design and Analysis of Microbiome Studies <i>Mentors</i>: Dr. Lawrence David and Dr. Sayan Mukherjee PhD graduation in 2019, MD graduation in 2020</p> <p><b>Research Technician</b>, Johns Hopkins University 2011-2012 <i>Mentor</i>: Dr. Nina Markovic</p> <p><b>Bachelors of Science</b>, Johns Hopkins University 2007-2011 Double Major in Physics and Biophysics, Minor in Mathematics</p>
PUBLICATIONS	<p>[* denotes equal contribution]</p> <p>Morton J*, Marotz C*, Washburne A, <b>Silverman JD</b>, Edlund A, Zaramela L, Zengler K, Knight R. (2019) Establishing microbial measurement standards with reference frames. <i>Nature Communications</i>, 2719; DOI: 0.1038/s41467-019-10656-5</p> <p>Villa MM*, Bloom RJ*, <b>Silverman JD</b>, 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. <i>bioRxiv</i> 630822; DOI:10.1101/630822</p> <p><b>Silverman JD</b>, Bloom RJ, Jiang S, Durand HK, Mukherjee S, David LA. (2019) Measuring and Mitigating PCR Bias in Microbiome Data. <i>bioRxiv</i> 604025; DOI:10.1101/604025</p> <p><b>Silverman JD</b>, Roche K, Holmes ZC, David LA, Mukherjee S. (2019) Bayesian Multinomial Logistic Normal Models Through Marginally Latent Matrix-T Processes. <i>arXiv</i>:1903.11695</p> <p><b>Silverman JD</b>, Roche K, Mukherjee S, David LA. (2018) Naught all zeros in sequence count data are the same. <i>bioRxiv</i> 477794; DOI:10.1101/477794.</p> <p><b>Silverman JD</b>*, Shenhav L*, David LA, Halperin E, Mukherjee S. (2018) Statistical Considerations in the Design and Analysis of Longitudinal Microbiome Studies. <i>bioRxiv</i> 448332; DOI:10.1101/448332 (<i>Invited Review at mSystems</i>)</p> <p><b>Silverman JD</b>, Durand HK, Bloom RJ, Mukherjee S, David LA. (2018) Dynamic linear models guide design and analysis of microbiota studies within artificial human guts. <i>Microbiome</i>. 6:202 DOI:10.1186/s40168-018-0584-3</p> <p>Shenhav L, Furman O, Barischoe L, Thompson M, <b>Silverman JD</b>, Mizrahi I, Halperin E. (2018) Modeling the temporal dynamics of the gut microbial community in adults</p>

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]

Holmes Z, **Silverman JD**, Dressman H, Zhengzheng W, Armstrong S, Seed P, Rawls J, David L. (2019) Butyrate production by gut microbiota from children with obesity is linked to bacterial community composition and prebiotic choice. (*Submitted to mBio*)

**Silverman JD**, Mukherjee S, David LA. Rethinking base-scale inference in sequence count data through total augmentation. (*In Preparation*)

PATENTS AND  
SOFTWARE

**Justin D. Silverman** (2019) Multinomial logistic-normal linear models using a marginal Laplace approximation (*stray*)

**Justin D. Silverman** (2017) Dynamic linear models for microbiota studies (MAL-LARD)

**Justin Silverman** (2016) philr: Phylogenetic partitioning based ILR transform for metagenomics data. R package version 1.0.0. <http://bioconductor.org/packages/phlir/> (Downloaded 2951 times; September 6th, 2018).

**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	<b>Referee</b>	publons.com/author/1257294/justin-d-silverman
		Annals of Applied Statistics PLoS Computational Biology mSystems Microbiome Genome Biology ( <i>In Conjunction with Lawrence David</i> )
	<b>Session Organizer</b>	IMS Invited Session at JSM 2018 “Longitudinal Modeling and Experimental Design for Investigating Host Associated Microbiota”
INVITED TALKS	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	<i>Modeling time evolution and therapeutic effect in human microbiota</i> , The 7 <sup>th</sup> 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

TEACHING EXPERIENCE	DOmath 2018 Research Program: Stochastic Properties of Dynamical Systems: Project Manager	Summer 2018
	Human Microbiome Seminar Guest Lecturer, University of North Carolina, Chapel Hill	Spring 2017
	Statistical Methods in Computational Biology Teaching Assistant and Guest Lecturer, Duke University	Spring 2017
	Spectroscopy (Quantum Mechanics for Biophysics) Teaching Assistant, Johns Hopkins University	Fall 2011
REFERENCES	<b>Sayan Mukherjee</b> , Professor, Department of Statistical Science, Duke University, (919) 684-4608 <a href="mailto:sayan@stat.duke.edu">sayan@stat.duke.edu</a>	
	<b>Lawrence David</b> , Assistant Professor, Center for Genomic and Computational Biology, Duke University, (919) 668-5388 <a href="mailto:lawrence.david@duke.edu">lawrence.david@duke.edu</a>	
	<b>Juan Jose Egozcue</b> , Professor, Department of Civil and Environmental Engineering, Polytechnic University of Catalonia, <a href="mailto:juan.jose.egozcue@upc.edu">juan.jose.egozcue@upc.edu</a>	
	<b>Vera Pawlowsky-Glahn</b> , Professor, Department of Computer Science and Applied Math, University of Girona, ++34-972-418170, <a href="mailto:vera.pawlowsky@udg.edu">vera.pawlowsky@udg.edu</a>	
	<b>Greg Gloor</b> , Professor, Department of Biochemistry, University of Western Ontario, (519) 661-2111, <a href="mailto:ggloor@uwo.ca">ggloor@uwo.ca</a>	
	<b>David Simel</b> , Professor, Department of Medicine, Duke University, (919) 286-6941, <a href="mailto:david.simel@duke.edu">david.simel@duke.edu</a>	