Justin Silverman

Contact Information	Justin.Silverman@duke.edu	justin-silverman.com 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

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]

Morton J*, Marotz C*, **Silverman JD**, Washburne A, Edlund A, Zaramela L, Zengler K, Knight R. Establishing microbial measurement standards with reference frames (*In Preparation*)

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

Bloom, RJ, **Silverman JD**, Villa MM, Durand HK, David LA. Growth rate and successional stage in an artificial gut system. (*In Preparation*)

Villa MM, Bloom RJ, **Silverman JD**, Durand HK, Midani FS, David LA, Droplet culture of human gut microbiota reveals primary degraders of dietary polysaccharides. (*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/philr/ (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 2016-2017
and Clinical Sciences, Pilot Grant ($50,000)
Authored (Submitting PIs: Lawrence David and Sayan Mukherjee)
"A geometric approach to modeling human microbiota dynamics"

HONORS AND AWARDS		
	Best Young Presentation (Compositional Data Analysis Workshop)	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		
	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 7th 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:	Summer 2018
	Stochastic Properties of Dynamical Systems: Project Manager	
	Human Microbiome Seminar	Spring 2017
	Guest Lecturer, University of North Carolina, Chapel Hill	
	Statistical Methods in Computational Biology	Spring 2017
	Teaching Assistant and Guest Lecturer, Duke University	
	Spectroscopy (Quantum Mechanics for Biophysics)	Fall 2011
	Teaching Assistant, Johns Hopkins University	

REFERENCES **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`

GRADUATE / MEDICAL COURSEWORK

- Statistical Methods for Computational Biology
- Bayesian and Modern Statistics
- Time Series and Dynamic Models
- Genome Tools and Technologies
- Intro Computational Genomics
- Molecular Biology

- Biochemistry
- Physiology
- Pathology
- Neuroscience
- Immunology
- Medical Microbiology

CLINICAL ROTATIONS

- Medicine
- Surgery
- Pediatrics
- Neurology
- Psychiatry

- Obstetrics and Gynecology
- Pediatric Intensive Care
- Emergency Medicine
- Family Medicine
- Radiology

STANDARDIZED TESTING

270	USMLE Step 1	2014
263	USMLE Step 2 CK	2015
Pass	USMLE Step 2 CS	2015