

Justin Silverman

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.	
EDUCATION	MD/PhD Candidate , Duke University <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	2012-2020
	Research Technician , Johns Hopkins University <i>Mentor</i> : Dr. Nina Markovic	2011-2012
	Undergraduate Researcher , Johns Hopkins University <i>Mentor</i> : Dr. Nina Markovic	2008-2011
PUBLICATIONS	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. <i>Microbiome</i> . (<i>Accepted</i>)	
	Shenhav L, Furman O, Barischoe L, Thompson M, Silverman JD , Mizrahi I, Halperin E. (2018) Modeling the temporal dynamics of the gut microbial community in adults and infants. <i>bioRxiv</i> 212993. DOI:10.1101/212993. (<i>Submitted to PLOS Computational Biology</i>)	
	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. <i>Ecological Monographs</i> . (<i>In Press</i>).	
	Silverman JD , Silverman RK. (2018) The Bayesian Sorting Hat: A Decision-Theoretic Approach to Size-Constrained Clustering. arXiv:1710.06047. (<i>In Revision at Journal of Machine Learning Research</i>)	
	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 <i>Vibrio cholerae</i> infection. <i>The Journal of Infectious Diseases</i> . 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. <i>eLife</i> 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. <i>PeerJ</i> 5:e2969 DOI:10.7717/peerj.2969	
PUBLICATIONS IN PREPARATION	[* denotes equal contribution] Silverman JD* , Shenhav L*, David LA, Halperin E, Mukherjee S. Statistical Con-	

siderations in the Design and Analysis of Longitudinal Microbiome Studies (*Invited Review at mSystems*)

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

Silverman JD, Roche K, Shenhav L, David LA, Mukherjee S. A matrix- t marginal Laplace approximation for fast inference in Bayesian multivariate hierarchical linear models. (*In Preparation*)

Silverman JD, David LA, Mukherjee S. There are more than one type of zeros in sequence count data (*In Preparation*)

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*)

PATENTS AND SOFTWARE

Justin D. Silverman (2018) Multinomial logistic-normal linear models using a marginal Laplace approximation (MONGREL)

Justin D. Silverman (2017) Dynamic linear models for microbiota studies (MALLARD)

Justin Silverman (2016) phylr: Phylogenetic partitioning based ILR transform for metagenomics data. R package version 1.0.0. <http://bioconductor.org/packages/phylr/> (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) 2016-2017
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

Statistical and Geometric Methods for the Analysis of Sequence Count Data, Seminar Series in the Center of Statistical Genetics in the Department of Biostatistics at the University of Michigan, Ann Arbor, Michigan. (August 2018)

Quantifying and Controlling for Sources of Technical Variation and Bias in Longitudinal Microbiome Surveys, IMS Invited Session at JSM 2018, Vancouver, British Columbia. (July 2018)

Time-Series Models for Microbiome Data, Probabilistic Microbial Modeling Symposium, San Diego, California. (June 2018)

Geometric methods for modeling time evolution in human microbiota, ENAR 2018 Spring Meeting, Atlanta, Georgia. (March 2018)

Statistical and Geometric Methods for the Analysis of Sequence Count, Wharton Statistics Seminar Series, Philadelphia, Pennsylvania. (March 2018)

Scalable count-compositional models for microbiome time-series data, Seminari d'Estadística I Investigació Operativa, Universitat Politècnica de Catalunya, Spain. (May 2017)

Modeling time evolution in human microbiota, Seminar in Compositional Data, Universitat de Girona, Spain. (May 2017)

A geometric approach to modeling human microbiota dynamics, Health Analytics Workshop, Duke University. (November 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
Austin Hua (Undergraduate)	2017-2018
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	

ACCEPTED ABSTRACTS

Silverman, J, Mukherjee S, David LA. (2017, July). A Phylogenetic Transform Enhances Analysis of Compositional Microbiota Data, JSM 2017. Baltimore, MD.

Silverman, J, Mukherjee S, David LA. (2016, February), A Phylogenetic Approach

to Overcoming Compositional Problems in Microbiome Data, The First Workshop on Challenges in Microbiome Data Analysis. New York, NY.

Roth S, Patel S, Silverman J et al. (2011, September) Association of S. Pyogenes DNA from Throat Swabs of Asymptomatic Children and Very High Prevalence of Rheumatic Heart Disease in Rural South America. 51st ICAAC. Chicago, IL.

Silverman J, et al. (2011, July) Prevalence of Cardiovascular Risk Factors in Guyana, South America, International Academy of Cardiology, 16th World Congress on Heart Disease. Abstract 281.

Silverman J, Jermyn A, Rivera R, Markovic N,. (2010, August), Length Dependent Optical Properties of Ultra-Short Carbon Nanotubes, Johns Hopkins Joint Poster Session: Summer Internship Programs

Szlavecz K, Terzis A, Musaloiu R, Szalay A, Gupchup J, Liang C, Xia L, Cogan J, Silverman J, Swarth C, Matthews S, Ellis E,. (2008), Life Under Your Feet: A Wireless Soil Ecology Sensor Network, Eos Trans. AGU 89(53), Fall Meet. Suppl., Abstract IN23A-10

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 Catalonia, 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

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