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.

EDUCATION

MD/PhD Candidate, Duke University 2012-2020
Thesis: Bayesian Multivariate Count Models for the Design
 and Analysis of Microbiome Studies
Mentors: Dr. Lawrence David and Dr. Sayan Mukherjee
Research Technician, Johns Hopkins University 2011-2012
Mentor: Dr. Nina Markovic
Undergraduate Researcher, Johns Hopkins University 2008-2011
Mentor: Dr. Nina Markovic

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. *Microbiome. (Accepted)*

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.* (*In Press*).

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 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) 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 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
	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'Estadistica I Investigacio 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: 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

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 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`

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