

Siyuan Ma, Ph.D. 🏠 University of Pennsylvania • Philadelphia, PA • United States
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EDUCATION AND TRAINING

University of Pennsylvania Philadelphia, PA, United States
Postdoctoral researcher 2020-now
Advisor: Dr. Hongzhe Li
Research focus: *longitudinal microbiome statistics, spatial proteomics modelling*

Harvard T.H. Chan School of Public Health Boston, MA, United States
Postdoctoral researcher 2019-2020
Advisors: Dr. Curtis Huttenhower, Dr. Lucas Janson
Research focus: *high-dimensional conditional associations in microbiome data*

Ph.D. in Biostatistics 2015-2019
Advisor: Dr. Curtis Huttenhower
Dissertation: *Statistical methods for population structure discovery in 'omics Studies*

M.S. in Biostatistics 2013-2015

Peking University Beijing, China
SAS programmer internship 2013
B.S. in Mathematics and Statistics 2009-2013

PUBLICATIONS

- [10] Ma, S., Ren, B., Mallick, H., et al. (2021), A statistical model for describing and simulating microbial community profiles. *PLOS Computational Biology*
- [9] Kondo, A., Ma, S., Lee, M.M.Y., et al. (2021), Highly multiplexed image analysis of intestinal tissue sections in patients with inflammatory bowel disease. *Gastroenterology*
- [8] Mallick, H., Rahnavard, A., McIver, L.J., Ma, S., et al. (2021), Multivariable Association Discovery in Population-scale Meta-omics Studies. *PLOS Computational Biology*
- [7] Dantzler, K., Ma, S., Ngotho, P., et al. (2019), Naturally acquired immunity against immature *Plasmodium falciparum* gametocytes. *Science Translational Medicine*
- [6] Ma, S.*, Ogino, S.*, Parsana, P., et al. (2018), Continuity of transcriptomes among colorectal cancer subtypes, based on meta-analysis. *Genome Biology*
- [5] Obaldia, N., Meibalan, E., Sa, J. M., Ma, S., et al. (2018), Bone marrow is a major parasite reservoir in *Plasmodium vivax* infection. *MBio*
- [4] De Niz, M., Meibalan, E., Mejia, P., Ma, S., et al. (2018), *Plasmodium* gametocytes display homing and vascular transmigration in the host bone marrow. *Science advances*
- [3] Mallick, H.*, Ma, S.*, Franzosa, E.A., et al. (2017). Experimental design and quantitative analysis of microbial community multi'omics. *Genome Biology*
- [2] Sinha, R., Abu-Ali, G., Vogtmann, E., Fodor, A.A., Ren, B., Amir, A., Schwager, E., Crabtree, J., Ma, S., et al (2017), Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium, *Nature Biotechnology*
- [1] Pelle, K.G., Oh, K., Buchholz, K., Narasimhan, V., Joice, R., Milner, D.A., Brancucci, N.M.B., Ma, S., et al (2015), Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection, *Genome Medicine*

WORKING PAPERS

- [4] Ma, S., Li, H., A tensor decomposition model for longitudinal microbiome studies, *revision invited at Annals of Applied Statistics*

- [3] Ma, S., Shungin, D., Mallick, H., et al., Population structure discovery in meta-analyzed microbial communities and inflammatory bowel disease, *resubmitted at Genome Biology*
- [2] Ma, S., Li, H., Flexible Ising modeling for co-colonization in longitudinal microbiomes, *in preparation*
- [1] Ma, S., Huttenhower, C., Janson, L., A flexible framework for novel health-microbiome associations and controlling false discoveries, *in preparation*

INVITED TALKS

- [5] "A Statistical Model for Simulating and Testing for Microbiomes", Biostatistics Seminar Series, Department of Biostatistics, Epidemiology, and Informatics, University of Pennsylvania. Philadelphia, PA, 2021
- [4] "Testing Cell-Cell Interactions in Imaging Mass Cytometry Data", IMC Working Group Meeting, Perelman School of Medicine, University of Pennsylvania. Philadelphia, PA, 2021
- [3] "Meta-Analysis of Population Structure in the IBD Gut Microbiome", Microbiome Working Group Meeting, Harvard Chan Microbiome in Public Health Center. Boston, MA, 2019
- [2] "Meta-Analysis of Population Heterogeneity in IBD Patients' Gut Microbiome", CMIT Work-in-Progress Meeting, Center for Microbiome Informatics and Therapeutics, Massachusetts Institute of Technology. Cambridge, MA, 2017
- [1] "Subtype Continuity Revealed by Meta-analysis of the Colorectal Cancer Transcriptome", Department of Biostatistics Genomics Meeting, Dana-Farber Cancer Institute. Boston, MA, 2015

CONFERENCE PRESENTATIONS

- [5] "Tensor Decomposition of Longitudinal Microbiomes", Joint Statistical Meetings. Virtual Conference, 2021
- [4] "Tensor Decomposition of Longitudinal Microbiomes", ENAR Spring Meeting. Virtual Conference, 2021
- [3] "SparseDOSSA: A Statistical Model for Simulating Realistic Microbial Community Profiles", Joint Statistical Meetings. Virtual Conference, 2020
- [2] "Population Structure Discovery in Meta-Analyzed Microbial Communities", Conference on Intelligent Systems for Molecular Biology. Chicago, IL, 2018
- [1] "Population Structure Discovery in Meta-Analyzed Microbial Communities", Joint Statistical Meetings. Baltimore, MD, 2017

MENTORING AND TEACHING

Harvard T.H. Chan School of Public Health	Boston, MA, United States
Student Mentor	2020
• Supervised summer research student on developing, implementing, and validating hierarchical hypothesis testing methods for high-dimensional microbiome data	
Guest Lecturer	2019
• <i>Genomic Data Manipulation</i>	
Teaching Assistant	2014-2019
• <i>Advanced Regression, Causal Inference, Biomedical Informatics, Failure Time Analysis, Longitudinal Regression, Genomic Data Manipulation</i>	

HONORS & AWARDS

Correlation One with Citadel LLC	New York, NY
Global Datathon Championship Third Place	2017
Boston Datathon Championship Winner	2017
Harvard T.H. Chan School of Public Health	Boston, MA
Certificate of Distinction in Teaching	2017
Robert B. Reed Prize for Best Qualifying Examination	2016