Siyuan Ma, Ph.D.

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Academic Appointment

Vanderbilt University Medical Center

Assistant Professor   2022-

Education

Harvard T.H. Chan School of Public Health, Ph.D. in Biostatistics   2019

Thesis: Statistical Methods for Population Structure Discovery in Meta-Analyzed 'Omics Studies

Advisor: Curtis Huttenhower, Ph.D.

Harvard T.H. Chan School of Public Health, M.S. in Biostatistics   2015

Peking University, B.S. in Statistics   2013

Professional Experience

University of Pennsylvania, Postdoctoral Researcher   2020-2022

Advisor: Hongzhe Li, Ph.D.

Harvard T.H. Chan School of Public Health, Postdoctoral Researcher   2019-2020

Advisors: Curtis Huttenhower, Ph.D., Lucas Janson, Ph.D.

Peer-Reviewed Publications

1. **Ma S** and Hongzhe Li., 2022. A Tensor Decomposition Model for Longitudinal Microbiome Studies. *The annals of applied statistics*, in press.

2. **Ma, S.**, Shungin, D., Mallick, H., Schirmer, M., Nguyen, L.H., Kolde, R., Franzosa, E., Vlamakis, H., Xavier, R. and Huttenhower, C., 2022. Population structure discovery in meta-analyzed microbial communities and inflammatory bowel disease using MMUPHin. *Genome biology*, 23(1), pp.1-31.

3. Kondo, A., **Ma, S.**, Lee, M.Y., Ortiz, V., Traum, D., Schug, J., Wilkins, B., Terry, N.A., Lee, H. and Kaestner, K.H., 2021. Highly multiplexed image analysis of intestinal tissue sections in patients with inflammatory bowel disease. *Gastroenterology*, 161(6), pp.1940-1952.

4. Mallick, H., Rahnavard, A., McIver, L.J., **Ma, S.**, Zhang, Y., Nguyen, L.H., Tickle, T.L., Weingart, G., Ren, B., Schwager, E.H. and Chatterjee, S., 2021. Multivariable association discovery in population-scale meta-omics studies. *PLoS computational biology*, 17(11), p.e1009442.

5. **Ma, S.**, Ren, B., Mallick, H., Moon, Y.S., Schwager, E., Maharjan, S., Tickle, T.L., Lu, Y., Carmody, R.N., Franzosa, E.A. and Janson, L., 2021. A statistical model for describing and simulating microbial community profiles. *PLoS computational biology*, 17(9), p.e1008913.

6. Dantzler, K.W., **Ma, S.**, Ngotho, P., Stone, W.J., Tao, D., Rijpma, S., De Niz, M., Nilsson Bark, S.K., Jore, M.M., Raaijmakers, T.K. and Early, A.M.,, 2019. Naturally acquired immunity against immature Plasmodium falciparum gametocytes. *Science translational medicine*, 11(495), p.eaav3963.

7. **Ma, S.***, Ogino, S.*, Parsana, P., Nishihara, R., Qian, Z., Shen, J., Mima, K., Masugi, Y., Cao, Y., Nowak, J.A. and Shima, K., 2018. Continuity of transcriptomes among colorectal cancer subtypes based on meta-analysis. *Genome biology*, 19(1), pp.1-14.

8. Obaldia III, N., Meibalan, E., Sa, J.M., **Ma, S.**, Clark, M.A., Mejia, P., Moraes Barros, R.R., Otero, W., Ferreira, M.U., Mitchell, J.R. and Milner, D.A., 2018. Bone marrow is a major parasite reservoir in Plasmodium vivax infection. *MBio*, 9(3), pp.e00625-18.

9. De Niz, M., Meibalan, E., Mejia, P., **Ma, S.**, Brancucci, N.M., Agop-Nersesian, C., Mandt, R., Ngotho, P., Hughes, K.R., Waters, A.P. and Huttenhower, C., 2018. Plasmodium gametocytes display homing and vascular transmigration in the host bone marrow. *Science advances*, 4(5), p.eaat3775.

10. Mallick, H.*, **Ma, S.***, Franzosa, E.A., Vatanen, T., Morgan, X.C. and Huttenhower, C., 2017. Experimental design and quantitative analysis of microbial community multiomics. *Genome biology*, 18(1), pp.1-16.

11. Sinha, R., Abu-Ali, G., Vogtmann, E., Fodor, A.A., Ren, B., Amir, A., Schwager, E., Crabtree, J., **Ma, S.**, Abnet, C.C. and Knight, R., 2017. Assessment of variation in microbial community amplicon sequencing by the Microbiome Quality Control (MBQC) project consortium. *Nature biotechnology*, 35(11), pp.1077-1086.

12. Pelle KG, Oh K, Buchholz K, Narasimhan V, Joice R, Milner DA, Brancucci N, **Ma S**, Voss TS, Ketman K, Seydel KB. Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection. *Genome medicine*. 2015 Dec;7(1):1-20.

Invited Talks and Presentations

1. A Tensor Factorization Model for Longitudinal Microbiome Data. Dec 2022. CMStatistics Conference. Virtual Seminar.

2. Modeling the Joint Distribution of Compositional Microbiome Data. Dec 2022. Biostatistics Branch, National Cancer Institute. Virtual Seminar.

3. Modeling the Joint Distribution of Compositional Microbiome Data. Aug 2022. Department of Statistics, University of Pittsburgh. Virtual Seminar.

4. A Tensor Factorization Model for Longitudinal Microbiome Data. Aug 2022. Joint Statistical Meetings. Washington, DC.

5. A Tensor Factorization Model for Longitudinal Microbiome Data. May 2022. New England Statistics Symposium. Virtual Seminar.

6. Modeling the Joint Distribution of Compositional Microbiome Data. Feb 2022. Department of Biostatistics, Columbia University. Virtual Seminar.

7. Modeling the Joint Distribution of Compositional Microbiome Data. Feb 2022. Department of Biostatistics, New York University School of Global Public Health. Virtual Seminar.

8. Modeling the Joint Distribution of Compositional Microbiome Data. Jan 2022. Department of Biostatistics, Vanderbilt University Medical Center. Virtual Seminar.

9. A Statistical Model for Simulating and Testing for Microbiomes. Oct 2021. Department of Biostatistics, Epidemiology, and Informatics, University of Pennsylvania. Virtual Semniar.

10. Testing Cell-Cell Interactions in Imaging Mass Cytometry Data. Feb 2021. Perelman School of Medicine, University of Pennsylvania. Virtual Semniar.

11. Meta-Analysis of Population Structure in the IBD Gut Microbiome. Feb 2019. Microbiome Working Group, Harvard T.H. Chan School of Public Health. Boston, MA.

12. Meta-Analysis of Population Heterogeneity in IBD Patients' Gut Microbiome. Oct 2017. The Center for Microbiome Informatics and Therapeutics, Massachusetts Institute of Technology. Cambridge, MA.

13. Subtype Continuity Revealed by Meta-analysis of the Colorectal Cancer Transcriptome. Oct 2015. Department of Biostatistics, Dana-Farber Cancer Institute. Boston, MA.

Softwares

microTensor: Tensor Decomposition of Longitudial Microbiome Studies. github.com/syma-research/microTensor

SparseDOSSA 2: A Statistical Model for Describing and Simulating Microbial Community Profiles. github.com/biobakery/SparseDOSSA2

MMUPHin: Meta-analysis Methods with Uniform Pipeline for Heterogeneity in Microbiome Studies. www.bioconductor.org/packages/release/bioc/html/MMUPHin.html

Teaching

Guest Lecturer. BST 272: Introduction to Programming. Harvard T.H. Chan School of Public Health.

Teaching assistant. BST 235: Advanced Regression. Harvard T.H. Chan School of Public Health.

Teaching assistant. BST 254: Special Topics in Biostatistics (Structural Equations and Causal Inference). Harvard T.H. Chan School of Public Health.

Teaching assistant. BST 244: Analysis of Failure Time Data. Harvard T.H. Chan School of Public Health.

Teaching assistant. BST 215: Linear and longitudinal regression. Harvard T.H. Chan School of Public Health.

Teaching assistant. BST 508: Genomic data manipulation. Harvard T.H. Chan School of Public Health.

Professional Activities

Journal Referee

Nature communications, mSystems, Biometrics, The annals of applied statistics, PLOS Computational Biology, Bioinformatics, Frontiers in genetics, GigaScience, Journal of molecular biology, Plos One

Membership

American Statistical Association   2017-

Eastern North America Region of the IBS   2019-