

# SHIYANG MA

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Department of Biostatistics  $\diamond$  Columbia University

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## EDUCATION

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### University of Rochester; Rochester, NY

2016 – 2019

Ph.D. in Statistics, Department of Biostatistics and Computational Biology

– Advisors: Dr. Michael P. McDermott and Dr. David Oakes

– Dissertation: Methods for Improving Efficiency in Clinical Trials

### University of Rochester; Rochester, NY

2014 – 2016

M.A. in Statistics, Department of Biostatistics and Computational Biology

### Sichuan University; Chengdu, China

2009 – 2014

B.S. in Mathematics, Department of Mathematics

## EXPERIENCE

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### Columbia University; New York, NY

2019/10 – Present

Postdoctoral Research Scientist, Department of Biostatistics

– Supervisor: Dr. Iuliana Ionita-Laza

### President, Chinese Students and Scholars Association at University of Rochester

2017 – 2018

### Biostatistics Intern, Mayo Clinic; Rochester, MN

2017

## AWARDS AND HONORS

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Gold Medal, Best student research awards, Theory and methodology, UP-STAT

2018

## RESEARCH INTEREST

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### statistical genetics; clinical trials

- developing statistical and computational methods for the analysis of genetic data
- dose-response studies and adaptive designs

## PUBLICATIONS

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- Ma, S., Wang, C., Khan, A., Liu, L., Dalglish, J., Kiryluk, K., He, Z. and Ionita-Laza, I. (2022) Fine-mapping gene-based associations via knockoff analysis of biobank-scale data with applications to UK Biobank. Submitted.
- He, Z., Liu, L., Belloy, M. E., Guen, Y. L., Sossin, A., Liu, X., Qi, X., Ma, S., Wyss-Coray, T., Tang, H., Sabatti, C., Cands, E., Greicius, M. D. and Ionita-Laza, I. (2022) Summary statistics knockoff inference empowers identification of putative causal variants in genome-wide association studies. Submitted.
- Ma, S. and McDermott, M. P. (2022) Adaptive dose-response studies to establish proof-of-concept in learning-phase clinical trials. *Biometrical Journal*, **64**, 146-164.
- Ma, S., Dalglish, J., Lee, J., Wang, C., Liu, L., Gill, R., Buxbaum, J. D., Chung, W. K., Aschard, H., Silverman, E. K., Cho, M. H., He, Z. and Ionita-Laza, I. (2021) Powerful gene-based testing by integrating long-range chromatin interactions and knockoff genotypes. *Proceedings of the National Academy of Sciences of the United States of America*, **118**, e2105191118.

- He, Z., Guen, Y. L., Liu, L., Lee, J., **Ma, S.**, Yang, A. C., Liu, X., Rutledge, J., Losada, P. M., Song, B., Belloy, M. E., Butler, R. R., Longo, F. M., Tang, H., Mormino, E. C., Wyss-Coray, T., Greicius, M. D. and Ionita-Laza, I. (2021) Genome-wide analysis of common and rare variants via multiple knockoffs at biobank scale, with an application to Alzheimer disease genetics. *American Journal of Human Genetics*, **108**, 2336-2353.
- Prasad, P., Brown, L., **Ma, S.**, McDavid, A., Rudmann, A., Lent, D., Reagan-Webster, P., Valcin, K. E., Graman, P. and Apostolakis, M. (2021) “If the glove fits”: Hospital-wide universal gloving is associated with improved hand hygiene and may reduce *Clostridioides difficile* infection. *Infection Control and Hospital Epidemiology*, **42**, 1351-1355.
- **Ma, S.** and McDermott, M. P. (2020) Generalized multiple contrast tests in dose-response studies. *Statistics in Medicine*, **39**, 757-772.
- Andrzejewski, K. L., **Ma, S.**, Owens, A., Bull, M. T., Biglan, K. M., Kanchana, S., Mink, J. W., McDermott, M. P., Crane, B. T., Barbano, R. (2018) Alterations in vestibular function in individuals with cervical dystonia and the effects of botulinum toxin treatment. *Basal Ganglia*, **13**, 1-6.
- Schobel, S. A., Palermo, G., Auinger, P., Long, J. D., **Ma, S.**, Khwaja, O. S., Trundell, D., Cudkowicz, M., Hersch, S., Sampaio, C., Dorsey, E. R., Leavitt, B. R., Kieburtz, K. D., Seigny, J. J., Langbehn, D. R., Tabrizi, S. J.; TRACK-HD, COHORT, CARE-HD, and 2CARE Huntington Study Group Investigators. (2017) Motor, cognitive, and functional declines contribute to a single progressive factor in early HD. *Neurology*, **89**, 2495-2502.
- Couderc, J. P., **Ma, S.**, Page, A., Besaw, C., Xia, J., Chiu, W. B., de Bie, J., Vicente, J., Vaglio, M., Badilini, F., Babaeizadeh, S., Chien, C. S., Baumert, M. (2017) An evaluation of multiple algorithms for the measurement of the heart rate corrected JTpeak interval. *Journal of Electrocardiology*, **50**, 769-775.

## PRESENTATIONS

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- The 34th New England Statistics Symposium (NESS); Hybrid conference. “Powerful gene-based testing by integrating long-range chromatin interactions and knockoff genotypes” (Invited talk), October 2021.
- Eighth Annual Conference of the Upstate chapters of the American Statistical Association (UP-STAT); Rochester, NY. “Adaptive dose-response studies with generalized multiple contrast tests”, April 2019.
- 2018 Joint Statistical Meetings; Vancouver, British Columbia, Canada. “Does it Pay to Repeat the Baseline?” August 2018.
- Seventh Annual Conference of the Upstate chapters of the American Statistical Association (UP-STAT); Rochester, NY. “Generalized Multiple Contrast Tests in Proof-of-Concept Dose-Response Studies,” April 2018.
- International Society for Computerized Electrocardiology 42nd Annual Conference; St. Simons Island, GA. The 2017 ISCE “JTpeak” Initiative, April 2017.

## JOURNAL REVIEW

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*Journal of Applied Statistics; Clinical Trials: Journal of the Society for Clinical Trials; Statistics in Biopharmaceutical Research; Biostatistics and Epidemiology*

## SOFTWARE DEVELOPED

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- **BIGKnock**: An R package of performing biobank-scale gene-based association test via knockoffs.
- **GeneScan3DKnock**: An R package for performing improved gene-based testing by integrating long-range chromatin interactions, along with knockoff-enhanced tests.
- **GeneScan3D - UK Biobank Gene-based Results**: Browser of the GeneScan3D gene-based results for 1,403 UK biobank binary phecodes, 42 BioBank Japan binary phenotypes and 5 psychiatric phenotypes.