Jack M. Fu
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[Updated March 17th, 2023]

Education

08/2013-05/2018 — **Johns Hopkins University, Bloomberg School of Public Health**
Ph.D. Biostatistics
Doctoral Advisors:
Ingo Ruczinski, Ph.D.
Jeffrey T. Leek, Ph.D.

08/2009 – 05/2013 — **Duke University**
Major: Statistics with Distinction
Minor: Computational Biology
Summa Cum Laude
Thesis Advisor: Fan Li, Ph.D.

Professional Experience

02/2023 – Current — **Massachusetts General Hospital, Harvard Medical School**
Instructor in Neurology

06/2018 – 02/2023 — **Massachusetts General Hospital, The Broad Institute of MIT and Harvard, Harvard Medical School**
Postdoctoral Research Fellow
Advisor: Michael E. Talkowski, Ph.D.

06/2014 – 05/2018 — **Johns Hopkins Bloomberg School of Public Health**
Ph.D. Researcher
Advisors:
Ingo Ruczinski, Ph.D.
Jeffrey T. Leek, Ph.D.

06/2015 – 08/2015 — **Pacific Biosciences**
Bioinformatics Contractor
Supervisor: Elizabeth Tseng, Ph.D.

06/2012 – 05/2013 — **Duke University**
Undergraduate Researcher
Advisor: Fan Li, Ph.D.

Fellowships and Funding

05/2020 – 04/2022 — **Autism Speaks**
Postdoctoral Fellowship

Research Interest and Narrative

My research interest broadly centers around leveraging existing and emerging genetic sequencing technologies and increasing sample sizes to understand the genetic contribution to human disease and variation. I have extensive training and experience in computational and statistical methodology development for whole-genome, whole-exome, and RNA-seq data. My most recent first-author studies have described the allelic architecture of autism spectrum disorder from a cohort of over 60,000 individuals (ASD; Fu, Satterstrom, Peng, Brand et al., 2022, *Nature Genetics*) and the discovery of high-quality copy number variants (CNVs) in 200,000 samples of the UK Biobank (Bahbadi, Fu et al., 2022, *bioRxiv*).

I also currently lead a sub-team of fellow postdoctoral fellows, PhD students, and technicians for the processing, QC, and analysis of over 700,000 aggregated whole-exome sequenced individuals that will serve as a valuable resource to the research community.

Honors and Awards

Johns Hopkins Department of Biostatistics **2018**
Helen Abbey Award for excellence in teaching

Johns Hopkins Department of Biostatistics **2017**
Jane & Steve Dykacz Award for outstanding student paper in medical biostatistics

Summer Institute in Statistical Genetics at University of Washington **2016**
Travel and tuition award

JHSPH and the Institute for Clinical and Translational Research **2016**
1st place Genomic and Bioinformatics Symposium poster competition

The Maryland Genetics, Epidemiology, and Medicine Training Program **2016**
2nd place poster competition

Teaching Experience

Johns Hopkins Bloomberg School of Public Health

2016-17: Lead Teaching Assistant – Biostatistics 620s
Instructors: Marie Diener-West, Ph.D. and Karen Bandeen-Roche, Ph.D.
Weekly lab instructor for Biostatistics 620s, a core curriculum for MPH students
Substitute lecturer on occasions in front of 200+ students

2015-17: Teaching Assistant -Design of Clinical Experiments
Instructors: Elizabeth Sugar, Ph.D. and Jay Herson, Ph.D.
Weekly office hours and grading

2015-16: Teaching Assistant – Biostatistics for Undergraduates
Instructors: Leah Jager, Ph.D. and Margaret Taub, Ph.D.
Weekly lab instructor

2014-15: Teaching Assistant – Biostatistics 720s
Instructors: Brian Caffo, Ph.D. and Hongkai Ji, Ph.D.
Weekly office hours and grading for Biostatistics 720s, the core Ph.D. curriculum

Selected Publications

Peer reviewed

Fu, Jack M., F. Kyle Satterstrom, Minshi Peng, Harrison Brand, Ryan L. Collins, Shan Dong, Brie Wamsley, et al. 2022. “Rare Coding Variation Provides Insight into the Genetic Architecture and Phenotypic Context of Autism.” *Nature Genetics*, August, 1–12.

Wigdor, Emilie M., Daniel J. Weiner, Jakob Grove, **Jack M. Fu**, Wesley K. Thompson, Caitlin E. Carey, Nikolas Baya, et al. 2022. “The Female Protective Effect against Autism Spectrum Disorder.” *Cell Genomics* 2 (6): 100134.

Weiner, Daniel, Emi Ling, Serkan Erdin, Derek J. C. Tai, Rachita Yadav, Jakob Grove, **Jack M. Fu**, et al. 2022. “Statistical and Functional Convergence of Common and Rare Variant Risk for Autism Spectrum Disorders at Chromosome 16p.” *Nature Genetics*. In Press.

Collins, Ryan L., Harrison Brand, Konrad J. Karczewski, Xuefang Zhao, Jessica Alföldi, Laurent C. Francioli, Amit V. Khera, …, **Jack M. Fu**, … et al. 2020. “A Structural Variation Reference for Medical and Population Genetics.” *Nature* 581 (7809): 444–51.

Collins, Ryan L., Harrison Brand, Konrad J. Karczewski, Xuefang Zhao, Jessica Alföldi, Laurent C. Francioli, Amit V. Khera, …, **Jack Fu**, …, et al. 2020. "A Structural Variation Reference for Medical and Population Genetics." *Nature* 581 (7809): 444–51.

Collins, Ryan L., Joseph T. Glessner, Eleonora Porcu, Maarja Lepamets, Rhonda Brandon, Christopher Lauricella, Lide Han, Theodore Morley, Lisa-Marie Niestroj, Jacob Ulirsch, Selin Everett, …, **Jack M. Fu**, … et al. 2022. "A Cross-Disorder Dosage Sensitivity Map of the Human Genome." *Cell* 185 (16): 3041-3055.e25.

Zhao, Xuefang, Ryan L. Collins, Wan-Ping Lee, Alexandra M. Weber, Yukyung Jun, Qihui Zhu, Ben Weisburd, …, **Jack Fu**, … et al. 2021. "Expectations and Blind Spots for Structural Variation Detection from Long-Read Assemblies and Short-Read Genome Sequencing Technologies." *American Journal of Human Genetics* 108 (5): 919–28

Fu, Jack, Terri H. Beaty, Alan F. Scott, Jacqueline Hetmanski, Margaret M. Parker, Joan E. Bailey Wilson, Mary L. Marazita, et al. 2017. "Whole Exome Association of Rare Deletions in Multiplex Oral Cleft Families." *Genetic Epidemiology* 41 (1): 61–69.

Fu, Jack M., Elizabeth J. Leslie, Alan F. Scott, Jeffrey C. Murray, Mary L. Marazita, Terri H. Beaty, Robert B. Scharpf, and Ingo Ruczinski. 2019. "Detection of de Novo Copy Number Deletions from Targeted Sequencing of Trios." *Bioinformatics* 35 (4): 571–78.

Manuscripts

Babadi, Mehrtash, **Jack M. Fu***, Samuel K. Lee, Andrey N. Smirnov, Laura D. Gauthier, Mark Walker, David I. Benjamin, et al. 2022. "GATK-GCNV: A Rare Copy Number Variant Discovery Algorithm and Its Application to Exome Sequencing in the UK Biobank." *BioRxiv*. https://doi.org/10.1101/2022.08.25.504851.

*Joint first author

Presentations

Regional

2021	Integrative Gene Discovery in ASD and NDD / Invited presentation Program in Medical and Population Genetics Cambridge, MA
2021	Integrative Rare Variant Discovery Across the NDD Spectrum / Invited presentation The Stanley Center for Psychiatric Research Cambridge, MA
2022	The Genetics of Neuropsychiatric Disorders: Recent Work and Next Steps / Invited presentation NeuroDevelopment Variability Initiative Cambridge, MA

National

2020	Integrative and Comparative Analysis of Autism Spectrum Disorder and Developmental Delay from Over 200,000 Exome Sequenced Individuals / Selected platform presentation American Society of Human Genetics Annual Meeting 2020 Virtual
2022	The Impact of Rare Coding CNVs in 197,306 UK Biobank Exomes / Selected platform presentation American Society of Human Genetics Annual Meeting 2022 Los Angeles, CA

International

2020	Integrative analysis of autism and comparisons to developmental delay from 165,000 individuals / Invited presentation World Congress of Psychiatric Genetics 2020 Virtual

Professional Contributions
Reviewer: Biological Psychiatry
Ad hoc reviewer: Cell, Genome Biology

Professional Societies
American Statistical Association
The American Society of Human Genetics