

Hakhamanesh Mostafavi

Curriculum Vitae

September 2025

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Academic Positions

Assistant Professor, New York University Grossman School of Medicine (2023-present)

Center for Human Genetics and Genomics

Department of Population Health / Division of Biostatistics

Postdoctoral Scholar, Stanford University (2019-2023)

Department of Genetics

Advisor: Dr. Jonathan Pritchard

Education

PhD in Biological Sciences, Columbia University (2015-2019)

Advisor: Dr. Molly Przeworski

Thesis: "Quantitative Trait Variation and Adaptation in Contemporary Humans"

MPhil in Chemical Engineering, Columbia University (2012-2015)

Advisor: Dr. Ben O'Shaughnessy

Thesis: "Mechanisms of Membrane Fusion during Neurotransmitter Release"

MSc in Macromolecular Materials, Royal Institute of Technology (KTH), Sweden (2010-2012)

Advisor: Dr. Ulf Gedde

Thesis: "Simulation of Semi-Crystalline Polymers"

BSc in Polymer Engineering, Amirkabir University of Technology, Iran (2006-2010)

Advisor: Dr. Fatemeh Goharpey

Thesis: "Rheology of Polymer Nanocomposites"

Publications

17. **Mostafavi H.** Making sense of the polygenicity of complex traits. *Nat. Rev. Genet.* 26, 513 (2025).

16. Lee S., **Mostafavi H.** Missing regulatory effects on complex traits: Contribution of distal variants. *Cell Genomics* 5.3 (2025).

15. Samuel P.S., Olivia S., **Mostafavi H.** et al., A litmus test for confounding in polygenic scores. *bioRxiv* (2025).

14. Spence J.P.*, **Mostafavi H.*** et al., Specificity, length, and luck: How genes are prioritized by rare and common variant association studies. *bioRxiv* (2024). Under revision for *Nature*. *: co-first author.

13. Patel, R., Weiß C., Zhu H., **Mostafavi H.** et al., Characterizing selection on complex traits through conditional frequency spectra. *Genetics*, iyad210 (2024).

12. Zeng T., Spence J.P., **Mostafavi H.**, Pritchard J.K. Bayesian estimation of gene constraint from an evolutionary model with gene features. *Nat. Genet.* 56, 1632-1643 (2024).
11. **Mostafavi H.**, Spence J.P., Naqvi S., Pritchard J.K. Systematic differences in discovery of genetic effects on gene expression and complex traits. *Nat. Genet.* 55, 1866-1875 (2023).
10. Spence J.P., Zeng T., **Mostafavi H.**, Pritchard J.K. Scaling the Discrete-time Wright Fisher model to biobank-scale datasets. *Genetics*, iyad168 (2023).
9. Simons Y., **Mostafavi H.**, Smith C.J., Pritchard J.K., Sella G. Simple scaling laws control the genetic architectures of human complex traits. *bioRxiv* (2022).
8. Patel R., Musharoff S.A., Spence J.P., Pimentel H., Tcheandjieu C., **Mostafavi H.** et al., Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. *Am. J. Hum. Genet.* 109, 1-12 (2022).
7. Venkataraman G.R., DeBoever C., Tanigawa Y., Aguirre M., Ioannidis A.G., **Mostafavi H.** et al., Bayesian model comparison for rare-variant association studies. *Am. J. Hum. Genet.* 108, 2354-2367 (2021).
6. **Mostafavi H.**, Harpak A., Conley D., Pritchard J.K., Przeworski M. Variable prediction accuracy of polygenic scores within an ancestry group. *eLife* 9, e48376 (2020).
5. Berg J.J., Harpak A., Sinnott-Armstrong N., Jorgensen A.M., **Mostafavi H.**, Field Y., Boyle E.A., Zhang X., Racimo F., Pritchard J.K., Coop G. Reduced signal for polygenic adaptation of height in UK Biobank. *eLife* 8, e39725 (2019).
4. Fuller Z., Berg J.J., **Mostafavi H.**, Sella G., Przeworski M. Measuring intolerance to mutation in human genetics. *Nat. Genet.* 51, 772-776 (2019).
3. **Mostafavi H.**, Berisa T., Day F., Perry J., Przeworski M., Pickrell J.K. Identifying genetic variants that affect viability in large cohorts. *PLoS Biol.* 15, e2002458 (2017).
2. **Mostafavi H.**, Thiyagarajan S., Stratton B.S., Warner J.M., Karatekin E., Rothman J.E., O'Shaughnessy B. Entropic forces drive self-organization and membrane fusion by SNARE proteins. *PNAS* 114, 5455-5460 (2017).
1. Moyassari A., **Mostafavi H.**, Gkourmpis T., Hedenqvist M., Gedde U.W., Nilsson F. Simulation of semi-crystalline polyethylene: Effect of short-chain branching on tie chains and entanglements. *Polymer* 72, 177-184 (2015).

Invited Seminars and Selected Talks

- “How selection, pleiotropy, and chance shape what we discover in genome-wide associations studies” *European Society for Human Genetics Meeting*, Milan, 2025
- “What genes are prioritized in genetic association studies?” *Columbia University, Biomedical Informatics Department*, 2025
- “Selection, pleiotropy, and chance: why rare and common variant association studies often implicate different genes” *American Society for Human Genetics Meeting*, Denver, 2024
- “What genes are prioritized in genetic association studies?” *Mount Sinai, Department of Genetics and Genomic Sciences*, 2024
- “Natural selection causes association studies to prioritize variant specificity over variant impact”, *Probabilistic Modeling in Genomics Meeting*, Vienna, Austria, 2024

- “Natural selection causes association studies to prioritize variant specificity over variant impact”, *New York Genome Center*, 2024
- “Systematic differences between GWAS hits and eQTLs”, *New York University, Department of Biology*, 2023
- “Limited overlap of eQTLs and GWAS hits due to systematic differences in discovery”, *University of Utah, Rising Stars in Genetics and Genomics Symposium*, 2023
- “An evolutionary perspective on human complex trait genetics”, *Harvard University, Department of Human Evolutionary Biology*, 2023
- “Deconstructing the genetic basis of complex trait variation”, *New York University School of Medicine*, 2023
- “Limited overlap of eQTLs and GWAS hits due to systematic differences in discovery”, *Probabilistic Modeling in Genomics Meeting*, Cold Spring Harbor, 2023
- “Limited overlap of eQTLs and GWAS hits due to systematic differences in discovery”, *Bay Area Population Genomics Meeting*, Berkeley, 2022
- “Identifying genetic variants that affect viability in large cohorts”, *The Biology of Genomes Meeting*, Cold Spring Harbor, 2017
- “Identifying genetic variants that affect viability in large cohorts”, *New York Area Population Genomics Meeting*, New York, 2017

Awards and Honors

- American Society of Human Genetics Meeting, abstract selected as a “Reviewers’ Choice” award, 2020
- John S. Newberry Prize awarded to the “most promising student of the year in the field of vertebrate zoology”, Department of Biological Sciences, Columbia University, 2019
- PhD with distinction, Department of Biological Sciences, Columbia University, 2019
- BSc with honors, Amirkabir University of Technology, 2010

Funding

- NIH R35 (PI), “Deconstructing the Genetic Basis of Complex Trait Variation”

Academic Services

Mentorship

Postdoctoral Fellows

- Yanina Kuzminich (2025-present)
- Sool Lee (2025-present)

Research Associates

- Gouri Rajaram (2024-present)

Graduate Students (MS)

- Rishav Eliyahu Sofer Dasgupta (2024-2025)
- Zoe Shtalryd (2025-present)

PhD Rotation Students

- Mary Casagrande, Epidemiology, NYU (2025)
- Jenisha Stapleton, Epidemiology, NYU (2025)
- Yihao Wang, Biostatistics, NYU (2024)

NTV Students

- Sylvia Dai, Undergraduate Student, NYU Abu Dhabi (2025–present)
- Dylan Guadiz, Undergraduate Student, NYU (2025–present)
- Sofia Alfaro, Summer Student, Sophomore, Stony Brook University (2025)
- Tvisha Bhatnagar, Summer Student, MS, NYU (2025)
- Baback Ghalamsiah, Summer Student, High School Student (2024)

Other Mentorship Roles

- Sandhya Rajkumar, Thesis committee member, NYU SoM (2025-present)
- Ali Sahimi, Thesis committee member, NYU SoM (2025-present)
- Isabel Bojanini, Thesis committee member, NYU Biology (2024-present)
- Shahar Silverman, Thesis committee member, Yale Genetics (2024-present)
- Adam Walker, First-year PhD mentor, Computational Biomedicine, NYU (2024-2025)
- Jennifer Motter, First-year PhD mentor, Computational Biomedicine, NYU (2024-2025)
- Student Advisor (*Egill Richard*), Columbia University, 2017

Teaching

- Lecturer (*Genetics and Genomics: from peas to people*), NYU School of Medicine
- Teaching Assistant (*Statistical Mechanics*), Columbia University, 2014
- Teaching Assistant (*Transport Phenomena II*), Columbia University, 2013
- Teaching Assistant (*Chemical Engineering Control*), Columbia University, 2012

Conferences/Meetings

- Session Chair for “Quantitative Genetics”, Probabilistic Modeling in Genomics Meeting, Vienna, Austria, 2024
- Program Committee Member, New York Area Population Genomics Meeting, 2024
- Organizer, Stanford Genetics department annual retreat (over 300 participants), 2020-2021

Editorial Service

- Associate Editor, GENETICS (Genetics of Complex Traits section), 2024-present

Journal Reviewer

Nature, Nature Genetics, Nature Communications, American Journal of Human Genetics, Science Advances, eLife, Cell Genomics, Molecular Biology and Evolution (MBE), npj Systems Biology and Applications

Grant Reviewer

European Research Council (ERC)