

Hakhamanesh Mostafavi

Curriculum Vitae

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Academic Positions

Assistant Professor, New York University 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

12. **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).
11. Spence J.P., Zeng T., **Mostafavi H.**, Pritchard J.K. Scaling the Discrete-time Wright Fisher model to biobank-scale datasets. *Genetics* 225, iyad168 (2023).
10. Zeng T., Spence J.P., **Mostafavi H.**, Pritchard J.K. Bayesian estimation of gene constraint from an evolutionary model with gene features. *bioRxiv* (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

- “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*, 2024
- “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” (Pending)

Academic Services

Teaching and Mentoring

- Lecturer (*Genetics and Genomics: from peas to people*), NYU School of Medicine
- Thesis Committee Member (*Isabel Bojanini*), NYU Biology, 2024-
- Student Advisor (*Egill Richard*), Columbia University, 2017
- 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

Journal Reviewer

Nature, Nature Genetics, Science Advances, eLife, Cell Genomics, Molecular Biology and Evolution (MBE), npj Systems Biology and Applications