Sara Mostafavi, PhD

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CURRENT POSITION

2015-present	Assistant Professor, University of British Columbia, Department of Statistics, Department of Medical Genetics
2015-present	Scientist, Center for Molecular Medicine and Therapeutics
2015-present	Canada Research Chair II in Computational Biology
2015-present	Fellow, Canadian Institute for Advanced Research
2018-present	Faculty member, Vector Institute, Toronto
2018-present	Canada CIFAR AI Chair

ACADEMIC AND TRAINING BACKGROUND

PDF 2014-2015 Harvard Medical School (Computational Immunology)
PDF 2011-2014 Stanford University (Computational Biology and Machine Learning)
PhD 2006-2011 University of Toronto (Computer Science and Computational Biology)
MS   2004-2006 Queen's University (Bioinformatics)
BSc 2001-2004   University of Toronto (Computer Science and Life Sciences)
          1999-2001   Queen's University (Life Sciences) – transferred to UofT in 2001

SELECTED RECENT PUBLICATIONS

Trainees: underlined, co-first or co-senior authorship: *

1. Yoshida H, …, **Mostafavi S*, Buenrostro J*, Benoist C***. The cis-Regulatory Atlas of the Mouse Immune System. (2019). Cell.
2. **Mostafavi S***, Gaiteri C*, Sullivan SE, …, Young-Pearse TL, Bennett DA, De Jager PL. A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease. (2018). Nature Neuroscience.
3. Ng B, White CC, Klein HU, Sieberts SK, McCabe C, Patrick E, Xu J, Yu L, Gaiteri C, Bennett DA, **Mostafavi S*,** De Jager PL*(2017). An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome. Nature Neuroscience.
4. Knowles DA, Davis J, Edgington H, Raj A, … , Mostafavi S, Montgomery SB*, Battle A*. (2017). Allele-specific expression reveals interactions between genetic variation and environment. Nature Methods.
5. **Mostafavi S***, Yoshida H*, Moodley D, …, Mathis D*, Benoist C* and the Immunological Genome Project Consortium. (2016). Parsing the interferon transcriptional network and its disease associations. *Cell.*
6. Pierson E, the GTEx Consortium, Koller D, Battle A*, **Mostafavi S*.** (2015) Sharing and specificity of co-expression networks across 35 human tissues. *PLOS Computational Biology.*
7. The GTEx Consortium. (2015) The Genotype-Tissue Expression (GTEx) pilot analysis: Multi-tissue gene regulation in humans. *Science.*
8. **Mostafavi S**, Ortiz-Lopez A, Hattori K, Pop C, Bogue M, Mathis D, Koller D, Benoist CB. (2014) Variation and genetic control of gene expression in primary immunocytes across inbred mouse strain. *Journal of Immunology.*
9. Raj T, Rothamel K, **Mostafavi S**, Ye C, Lee M, Replogle J, Von Korff A, Imboya S, McCabe C, Okada Y, Patsapolous N, Lee M, Wood I, Mathis D, Hafler D, Koller D, Regev A, Hacohen N, Benoist C*, Stranger BE*, De Jager PL*. (2014). Polarization of the effects of autoimmune and neurodegenerative risk alleles in leukocytes. *Science.*
10. Levinson DF, **Mostafavi S**, Milaneschi, Y, Rivera, M, Ripke S, Wray NR, Sullivan, PF. Genetics studies of major depressive disorder: Why are there no GWAS findings, and what can we do about it? *Biological Psychiatry.*
11. **Mostafavi S**, Battle A, Zhu X, …, , Levinson D. (2013). Type I interferon signaling genes in recurrent major depression: increased expression detected by whole-blood RNA sequencing. *Molecular Psychiatry*

12. Battle A, **Mostafavi S**, Zhu X, Potash JB, Weissman MW, Mc-Cormick C, Haudenschild CD, Beckman K, Shi J, Mei R, Urban AE, Montgomery SB, Levinson D, Koller D. (2013). Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. *Genome Research.*
13. **Mostafavi S**, Battle A, Zhu X, Urban AE, Levinson D, Montgomery SB, Koller D. (2013). Normalizing RNA-sequencing data by modeling hidden covariates with prior knowledge. *PLOS ONE.*
14. Lonsdale J. et al., and the GTEx consortium. (2013). The Genotype-Tissue Expression (GTEx) project. *Nature Genetics.*
15. **Mostafavi S**, Goldenberg A, Morris Q. (2012). Labeling nodes using three degrees of propagation. *PLOS ONE*

RESEARCH FUNDING
2015-2020   Canada Research Chair Program (Tier II Chair in Computational Biology)
2015-2019   CIFAR Catalyst Grant (co-PI). Cell Type Deconvolution Algorithms.
2015-2019   NIH U01 (sub-contract PI). Pathway discovery, validation and compound identification for Alzheimer's disease.
2016-2019   CIFAR research funds (PI). Construction of Epigenetic Growth Chart.
2016-2019   Biogen Inc (PI). Cell-type Specific eQTL Analysis in the Brain. SRA Award.
2016-2020   NSERC Discovery Grant (PI). Multi-Omic Data Integration Methods for Complex Traits.
2017-2022   NIH R24 (sub-contract PI). Computational Methods Inference Gene Regulation Networks in the Immune System.
2018-2023   Genome Canada (co-I). Childhood Asthma and the Microbiome—Precision Health for Life: The Canadian Healthy Infant Longitudinal Development (CHILD) Study
2018-2023   Genome Canada (co-I). Care4Rare-Solve: Multi-omic based diagnosis of rare disease.

SELECTED INVITED PRESENTATIONS
2018   Invited speaker, Princess Margaret Hospital Research Center, Toronto, Canada
2018   Invited speaker, UCLA Human Genetics, Los Angeles, USA
2018   Invited speaker, Women's Brain Initiative Symposium at Brigham Women's Hospital , Boston, USA
2018   Invited speaker, CIFAR and Jacobs Foundation Meeting, Marbach Castle, Germany
2018   Invited speaker, Biogen Inc, Boston, MA, USA
2018   Invited speaker, Statistical Seminar Series, McGill University, Montreal, Canada
2017   Invited speaker, Riken Institute for Integrative Medicine, Tokyo, Japan
2017   Invited speaker, Canadian Human & Statistical Genetics Meeting, Quebec City, Canada
2015   Invited speaker, Mount Sinai School of Medicine, NY, USA
2015   Invited speaker, Aalto University, Computer Science Seminar, Finland
2015   Invited speaker, CIFAR meeting on Brain development, Vancouver, Canada
2015   Invited speaker, Broad Institute, Population Genetics Meeting, Boston, MA

SELECTED ACTIVITIES
2019   Area chair for Proceedings of ISMB
2011-2018   Co-organizer of Machine Learning and Computational Biology Workshop (at NueorIPS)
2015-2019   RECOMB Program Committee member
2011-2017   Pacific Symposium on Biocomputing Program Committee
2012   Co-organizer, Workshop on Genomics and Genetics at ICML
2009-present   Reviewer for Molecular Systems Biology, Bioinformatics, BMC Bioinformatics, Scientific Reports, PLOS Computational Biology, Genome Research, Nature Communications