
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 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