

# Sara Mostafavi, PhD

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## CURRENT POSITION

2018-present Faculty member, Vector Institute, Toronto, Canada  
2015-present Assistant Professor, University of British Columbia (UBC), Department of Statistics, Department of Medical Genetics, Vancouver, Canada  
2015-present Scientist, Center for Molecular Medicine and Therapeutics at UBC

## HONORS

2018-present Canada CIFAR Artificial Intelligence (AI) Chair  
2015-present Canada Research Chair (CRC II) in Computational Biology  
2015-present Fellow, Canadian Institute for Advanced Research, Child and Brain Development

## ACADEMIC AND TRAINING BACKGROUND

PDF 2014 Harvard Medical School (Computational Immunology)  
PDF 2011-2014 Stanford University (Dept. Computer Science; mentor: Daphne Koller)  
PhD 2006-2011 University of Toronto (Dept. Computer Science; advisor: Quaid Morris)  
MS 2004-2006 Queen's University (Dept. Computing Sciences)  
BSc 2001-2004 University of Toronto (Dual major—Computer Science, Life Sciences)  
1999-2001 Queen's University (Life Sciences) – transferred to UofT in 2001

## SELECTED PUBLICATIONS

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

Under review:

Patrick E, Taga M, Ergun A, ..., Bradshaw E\$, **Mostafavi S\$**. (2019). *Deconvolving the contributions of cell-type heterogeneity on cortical gene expression*. bioRxiv. (Under review at Nature Communications)

Published:

Klein H, ..., **Mostafavi S**, ..., Philip L De Jager. (2019) *Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimer's human brains*. Nature Neuroscience.

Sieberts SK, ..., **Mostafavi S**, ..., Amp-Ad Consortium, CommonMind Consortium. (2019) Large eQTL meta analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Science Scientific Data.

Yuan V, ..., **Mostafavi S**, ..., Wendy P Robinson (2019). *Accurate ethnicity prediction from placental DNA methylation data*. Epigenetics & Chromatin.

Graham E, Vermeulen M, ..., Young-Pearse T\$, **Mostafavi S\$**. (2019) *Somatic mosaicism of sex chromosomes in the blood and brain*. Brain Research.

Ng B, Casazza W, ..., **Mostafavi S**. (2019). *Using transcriptomic hidden variables to infer context-specific genotype effects in the brain*. AJHG

Yoshida H, Lareau C, ..., **Mostafavi S\$**, Buenrostro J\$, Benoist C\$. (2019). *The cis-Regulatory Atlas of the Mouse Immune System*. Cell.

**Mostafavi S\***, Gaiteri C\*, Sullivan SE, ..., Young-Pearse TL, Bennett DA, De Jager PL. (2018). *A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease*. Nature Neuroscience.

Ng B, White CC, Klein HU, Sieberts SK, McCabe C, Patrick E, Xu J, Yu L, Gaiteri C, Bennett DA, **Mostafavi S**<sup>§</sup>, De Jager PL<sup>§</sup> (2017). *An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome*. Nature Neuroscience.

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.

**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.

Pierson E, the GTEx Consortium, Koller D, Battle A<sup>§</sup>, **Mostafavi S**<sup>§</sup>. (2015) *Sharing and specificity of co-expression networks across 35 human tissues*. PLOS Computational Biology.

The GTEx Consortium. (2015) *The Genotype-Tissue Expression (GTEx) pilot analysis: Multi-tissue gene regulation in humans*. Science.

**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.

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.

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.

**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

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.

**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.

**Mostafavi S**, Goldenberg A, Morris Q. (2012). *Labeling nodes using three degrees of propagation*. PLOS ONE

**Mostafavi S**, and Morris Q. (2010) *Fast integration of heterogeneous data sources for predicting gene function with limited annotation*. Bioinformatics. 26:1759-1765.

**Mostafavi S**, Ray D, Warde-Farley D, Grouios C, Morris Q. (2008) *GeneMANIA: A real-time multiple association network integration algorithm for predicting gene function*. Genome Biology.

### **ACTIVE RESEARCH FUNDING**

- 2019-2021 Jacob Foundation (co-PI). Developing epigenetic measurements to forecast long term benefits of early-life interventions.
- 2018-2021 NIH U01 (sub-contract PI). Multi-omic network-directed proteoforom discovery, dissection and functional validation to prioritize novel AD therapeutic targets.
- 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.
- 2017-2022 NIH R24 (sub-contract PI). ImmGen: Gene Expression in Immune Cells
- 2016-2021 NSERC Discovery Grant (PI). Integrating multiple types of genomics data to identify meaningful associations.
- 2016-2019 Canadian Institute for Advanced Research (CIFAR) (co-PI). Construction of Epigenetic Growth Chart.
- 2016-2019 Biogen Inc (PI). Cell-type Specific eQTL Analysis in the Brain. SRA Award.
- 2015-2020 Canada Research Chair Program (Tier II Chair in Computational Biology)
- 2015-2019 Canadian Institute for Advanced Research (CIFAR) (PI). Cell Type Deconvolution Algorithms.
- 2015-2019 NIH U01 (sub-contract PI). Pathway discovery, validation and compound identification for Alzheimer's disease.

### **SELECTED INVITED PRESENTATIONS**

- 2019 Nature Next Generation Genomics Conference, NY, USA.
- 2019 Department of Computer Science, Boston University. Boston, MA, USA.
- 2019 ImmunoBC Symposium, UBC, Vancouver, Canada.
- 2019 Biostatistics Seminar Series, University of Washington, Seattle, WA, USA
- 2019 EMBL-EBI Industry and academia partnership program: Neuroinformatics. San Diego, CA, USA.
- 2018 Departmental seminars, Princess Margaret Hospital Research Center, Toronto, Canada
- 2018 Human genetics seminar, UCLA, Los Angeles, USA
- 2018 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 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 Seminar series, Mount Sinai School of Medicine, NY, USA
- 2015 Computer science seminar series, Aalto University, Computer Science Seminar, Finland

### **SELECTED ACTIVITIES**

- 2019 Organizer, Machine Learning in Computational Biology (MLCB), co-located with NeurIPS
- 2019 Area chair, Studies of Phenotypes and Clinical Applications at ISMB
- 2018 Canadian Institute for Health Research (CIHR), grant review panel
- 2017-present NeurIPS Program Committee
- 2015-present RECOMB Program Committee
- 2012 Co-organizer, Workshop on Genomics and Genetics at ICML
- 2012 National Science Foundation (NSF), grant review panel
- 2011-2018 Co-organizer of Machine Learning and Computational Biology Workshop (at NeurIPS)
- 2011-2017 Pacific Symposium on Biocomputing Program Committee