

Employment

Assistant Professor **University of British Columbia (UBC)** Jan 2015-present
Canada Research Chair in Computational Biology
Department of Statistics, Department of Medical Genetics

Research Fellow **Harvard Medical School**, May 2014-Dec 2014
Department of Immunology
Advisors: Christophe Benoist, Diane Mathis

Education

Postdoctoral Fellow **Stanford University**, March 2011-April 2014
Department of Computer Science
Advisor: Daphne Koller

Ph.D. **University of Toronto**, 2006-2011
Department of Computer Science
Specialization in Machine Learning and Computational Biology
Advisor: Quaid Morris
Dissertation: Computational Prediction of Gene Function from High-Throughput Data Sources.

M.Sc **Queen's University**, 2004-2006
Department of Computer Science
Advisor: Parvin Mousavi
Thesis: A Computational Approach for Predicting Therapy Response in Multiple Sclerosis.

B.Sc Honors **University of Toronto**, 1999-2004
Dual Major in Computer Science and Life Sciences
Graduated with High Distinction

Research Interest

My research focus is to understand the interrelationship between genotype and phenotype in the context of common human clinical traits. In particular, my interest lies in developing and applying statistical and machine learning techniques to study the genetic basis of complex diseases, by combining association evidence across multiple genome-wide data sources, such as gene expression and genotype data, and by modeling prior biological pathways and networks for disentangling spurious from meaningful correlations.

Refereed Publications

Mostafavi S*, Yoshida H*, Moodley D, LeBoité H, Rothamel K, Raj T, Ye CJ, Chevrier N, Zhang SY, Feng T, Lee M, Casanova JL, Clark JD, Hegen M, Telliez JP, Hacoheh N, De Jager PL, Regev A, Mathis D*, Benoist C* and the Immunological Genome Project Consortium. Parsing the interferon transcriptional network and its disease associations. *Cell* (In press). 2016.

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

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

Mostafavi S, Ortiz-Lopez A, Hattori K, Pop C, Bogue M, Mathis D, Koller D, Benoist CB. *Variation and genetic control of gene expression in primary immunocytes across inbred mouse strain*. Journal of Immunology. 2014.

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, Hacoheh N, Benoist C*, Stranger BE*, De Jager PL*. *Polarization of the effects of autoimmune and neurodegenerative risk alleles in leukocytes*. Science 344(6183).

Mostafavi S, Battle A, Zhu X, Potash JB, Weissman MW, Shi J, Beckman K, Haudenschild C, McCormick C, Mei R, Gamberoff MJ, Gindes H, Adams P, Goes FS, Mondimore FM, MacKinnon D, Notes L, Schweizer B, Furman D, Montgomery SB, Urban AE, Koller D, 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. gr.155192.113.

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. 8 (7): e68141.

Lonsdale J. et al., and the GTEx consortium. (2013). *The Genotype-Tissue Expression (GTEx) project*. Nature Genetics. 45: 580-585.

Mostafavi S, Goldenberg A, Morris Q. (2012). *Labeling nodes using three degrees of propagation*. PLoS ONE 7(12): e51947.

Goldenberg A, **Mostafavi S**, Quon G, Boutros P, Morris Q. (2011) *Unsupervised detection of genes of influence in lung cancer using biological networks*. Bioinformatics. 27: 3166-3172.

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

Warde-Farley D, Donaldson S, Comes O, Zuberi K, Badrawi R, Chao P, Franz M, Grouios C, Kazi F, Tannus Lopes C, Maitland A, **Mostafavi S**, Montojo J, Shao Q, Wright G, Bader GD, Morris Q. (2010) *The GeneMANIA prediction server: Biological network integration for gene prioritization and predicting gene function*. Nucleic Acids Research. 38 Suppl: W214-220.

Costanzo M, Baryshnikova A, Bellay J, Kim Y, Spear ED, Sevier CS, Ding H, Koh JL, Toufighi K, **Mostafavi S**, Prinz J, St Onge RP, Vander Sluis B, Makhnevych T, Vizeacoumar FJ, Alizadeh S, Bahr S, Brost RL, Chen Y, Cokol M, Deshpande R, Li Z, Lin ZY, Liang W, Marback M, Paw J, San Luis BJ, Shuteriqi E, Tong AH, van Dyk N, Wallace IM, Whitney JA, Weirauch MT, Zhong G, Zhu H, Houry WA, Brudno M, Ragibizadeh S, Papp B, Pál C, Roth FP, Giaever G, Nislow C, Troyanskaya OG, Bussey H, Bader GD, Gingras AC, Morris QD, Kim PM, Kaiser CA, Myers CL, Andrews BJ, Boone C. (2010) *The genetic landscape of a cell*. Science. 327:425-431.

Mostafavi S and Morris Q. *Using the Gene Ontology hierarchy when predicting gene function*. (2009) In Proceedings of Conference on Uncertainty in Artificial Intelligence (UAI). Montreal, Canada.

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. 9 (Suppl 1):S4.

Peña-Castillo L, Tasan M, Myers CL, Lee H, Joshi T, Zhang C, Guan Y, Leone M, Pagnani A, Kim WK, Krumpelman C, Tian W, Obozinski G, Qi Y, **Mostafavi S**, Lin GN, Berriz GF, Gibbons FD, Lanckriet G, Qiu J, Grant C, Barutcuoglu Z, Hill DP, Warde-Farley D, Grouios C, Ray D, Blake JA, Deng M, Jordan MI, Noble WS, Morris Q, Klein-Seetharaman J, Bar-Joseph Z, Chen T, Sun F, Troyanskaya OG, Marcotte EM, Xu D, Hughes TR, Roth FP. (2008) *A critical assessment of Mus musculus gene function prediction using integrated genomic evidence*. Genome Biology. 9 (Suppl 1):S2.

Review Papers

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, and Morris Q. (2012) *Combining many interaction networks to predict gene function and analyze gene lists*. Journal of Proteomics. 12 (10): 1687-1696.

Mostafavi S, Goldenberg A, Morris Q. (2011) *Predicting node characteristics from molecular networks*. *Methods in Molecular Biology*. 781:399-414.

Recent Selected Talks

- 12/2015 “Modeling genes and pathways in a genomic study of major depression.” Mount Sinai School of Medicine. NY, USA.
- 10/2015 “Modeling tissue-specific co-expression networks in 35 human tissues.” CSHL Probabilistic Modeling in Genomics, Cold Spring Harbor Lab, NY, USA.
- 09/2015 “Transcriptomic analysis of dementia in Alzheimer’s disease.” Harvard Medical School, Boston, USA.
- 09/2015 “Integrating multiple types of genomics data to disentangle meaningful associations.” Department of Computer Science, Aalto University, Helsinki, Finland.
- 01/2014 “Integrating multiple types of genomics data to disentangle meaningful associations.” Guest lecture for the “Applied Computational Immunology” course, Stanford University, CA, USA.
- 01/2014 “Integrating multiple types of genomics data to disentangle meaningful associations.” Invited talk, Department of Statistics, and the CMMT, University of British Columbia, Canada.
- 10/2012 “Identifying expression markers of major depressive disorder in a large RNA sequencing study”. World Congress of Psychiatric Genetics (WCPG). Hamburg, Germany.
- 08/2012 “Using prior biological knowledge when constructing regulatory networks”. International Conference on Machine Learning (ICML) workshop: Machine Learning in Genetics and Genomics. Edinburgh, Scotland.

Teaching Experience

- Instructor Statistical Methods for High Dimensional Biology (STAT540), Winter 2015, Winter 2016
Department of Statistics, University of British Columbia, Vancouver, CA
- Teaching Assistant Introduction to Computer Science, Winter 2005, Fall 2006, Fall 2007, and Fall 2008
Department of Computer Science, University of Toronto, CA
- Course Assistant Bioinformatics, Winter 2006
Department of Computing, Queen’s University, CA

Professional Activities

Organizing Committee	Neural Information Processing Systems (NIPS) Workshop on Computational Biology, December 2013-2015 (yearly workshop) International Conference on Machine Learning (ICML) Workshop on Machine Learning in Genetics and Genomics, July 2012
Program Committee	International Conference on Research in Computational Molecular Biology (RECOMB), April 2016 International Conference on Machine Learning (ICML), July 2015 Pacific Symposium on Biocomputing (PSB) Workshop on Personalized Medicine, January 2012, January 2013, January 2014 Neural Information Processing Systems (NIPS) Workshop on Computational Biology, December 2012
Journal Reviewing	Scientific Reports, Molecular Systems Biology, PLoS Computational Biology, Bioinformatics
Grants Reviewing	CIHR external reader (2015) NSF review panel (2013)

Honors and Awards

Canada Research Chair in Computational Biology 2015-2020
Research Fellow of Canadian Institute for Advanced Research (CIFAR) 2015-present
Ontario Graduate Scholarship (OGS), 2008-2010
Queen's Graduate Scholarship, 2004-2006
Discover McGill Research Fellowship, Summer 2004
Golden Key Honour Society, 2004-present