

## Education

- Postdoctoral Fellow     **Harvard Medical School**, May 2014-present  
Department of Immunology  
Advisor: Christophe Benoist, Diane Mathis
- 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 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  
Specialization in Computational Biology and Bioinformatics  
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

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\*. *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. mp.2013.161

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.

Otaegui D, **Mostafavi S**, Bernard CC, de Munain AL, Mousavi P, Oksenberg JR, Baranzini SE. (2007) *Increased transcriptional activity of milk-related genes following the active phase of experimental autoimmune encephalomyelitis and multiple sclerosis*. Journal of Immunology. 179:4074-82.

## Review Papers

**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.

## Papers In Preparation/Submission

**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*. Submitted to Journal of Immunology.

Pierson E., **Mostafavi S**, Battle A, Koller D and the GTEx consortium. *Hierarchical learning of regulatory networks from RNA-sequencing of 35 human tissues*. In preparation (Companion paper as part of the GTEx project).

## Selected Refereed Workshop, Poster and Oral Presentations

**Mostafavi S**, Battle A, Zhu X, Urban AE, Levinson D, Montgomery SB, Koller D. *Normalizing RNA-sequencing data by modeling hidden covariates with prior knowledge*. Neural Information Processing Systems (NIPS) workshop: Computational Biology. Lake Tahoe, USA. 2012. (Poster presentation).

**Mostafavi S**, Battle A, Zhu X, Montgomery S, Potash JB, Weissman, MM, Haudenschild C, McCormick C, Beckman KB, Mei R, Urban AE, Koller D, Levinson DF. *Identifying expression markers of major depressive disorder in a large RNA sequencing study*. World Congress of Psychiatric Genetics (WCPG). Hamburg, Germany. October, 2012. (\*Oral presentation).

**Mostafavi S**, and Koller D. *Using prior biological knowledge when constructing regulatory networks*. International Conference on Machine Learning (ICML) workshop: Machine Learning in Genetics and Genomics. Edinburgh, Scotland. 2012. (\*Oral presentation).

**Mostafavi S**, Goldenberg A, and Morris Q. *Predicting node labels in large networks*. Neural Information Processing Systems (NIPS) Workshop: Networks Across Disciplines---Theory and Applications. Whistler, Canada. 2010. (Extended abstract publication and poster presentation).

**Mostafavi S**, Ray D, Warde-Farley D, Grouios C, Morris Q. *Predicting gene function with multiple data and annotations sources*. Neural Information Processing Systems (NIPS) workshop: Computational Biology. Whistler, Canada. 2007. (\*Oral presentation).

## Teaching Experience

Teaching Assistant	Introduction to Computer Science, Winter 2005, Fall 2006, Fall 2007, and Fall 2008 Duties: lead weekly tutorial sessions, design assignments, mark exams.
Course Assistant	Bioinformatics, Winter 2006 Duties: design and lead weekly tutorials and workshop sessions.
Student Supervision	Supervising two undergraduates and one junior PhD students. Duties: serve as the primary contact for the student; define an appropriate research project, meet weekly with student to guide progress.

## Professional Activities

Organizing Committee	Neural Information Processing Systems (NIPS) Workshop on Computational Biology. December 2013 International Conference on Machine Learning (ICML) Workshop on Machine Learning in Genetics and Genomics, July 2012
Program Committee	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
Reviewing	Molecular Systems Biology, BMC Genomics, PLoS Computational Biology, Bioinformatics
Grants	Contributed to a successful grant application (GTEx Project Statistical Analysis Supplement, under co-I Koller) Served on an NSF review panel (2013)

**Honors and Awards**

Ontario Graduate Scholarship (OGS), 2008-2010  
Queen's Graduate Scholarship, 2004-2006  
Discover McGill Research Fellowship, Summer 2004  
Golden Key Honour Society, 2004-present