

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

Refereed Publications

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 (In Press)

Knowles DA, Davis J, Edgington H, Raj A, Favé MJ, Zhu X, Potash JB, Weissman MM, Shi J, Levinson DF, Awadalla P, **Mostafavi S**, Montgomery SB*, Battle A*. (2017). *Allele-specific expression reveals interactions between genetic variation and environment*. Nature Methods.

Del Bel KL, Ragotte RJ, Saferali A, Lee S, Vercauteren SM, **Mostafavi S**, Schreiber RA, Prendiville JS, Phang MS, Halperin J, Au N, Dean JM, Jewels E, Junker AK, Rogers PC, Seear M, McKinnon ML, Turvey SE. (2017). *JAK1 gain-of-function causes an autosomal dominant immune dysregulatory and hypereosinophilic syndrome*. Journal of Allergy and Clinical Immunology.

Moodley D, Yoshida H, **Mostafavi S**, Asinowski N, Ortiz-Lopez A, Symanowicz P, Telliez JB, Hegen M, Clark JD, Mathis D, Benoist C. (2016). *Network pharmacology of JAK inhibitors*. Proceedings of National Academy of Science (PNAS).

Kukurba KR, Parsana P, Balliu B, Smith KS, Zappala Z, Knowles DA, Favé MJ, Davis JR, Li X, Zhu X, Potash JB, Weissman MM, Shi J, Kundaje A, Levinson DF, Awadalla P, **Mostafavi S**, Battle A*, Montgomery SB*. (2016). *Impact of the X Chromosome and sex on regulatory variation*. Genome Research.

Clifford RL, Jones MJ, MacIsaac JL, McEwen LM, Goodman SJ, **Mostafavi S**, Kobor MS*, Carlsten C*. (2016). *Inhalation of diesel exhaust and allergen alters human bronchial epithelium DNA methylation*. Journal of Allergy Clinical Immunology.

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, Hacohen N, De Jager PL, Regev A, 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*, **Mostafavi S***. (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.

Mostafavi S, Battle A, Zhu X, Potash JB, Weissman MW, Shi J, Beckman K, Haudenschild C, McCormick C, Mei R, Gameroff 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.

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.

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

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

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

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

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.

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.

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.

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.

Review Papers

Gaiteri C, **Mostafavi S**, Honey CJ, De Jager PL, Bennett DA. (2016) *Genetic variants in Alzheimer disease - molecular and brain network approaches.* Nature Reviews Neurology.

Levinson DF, **Mostafavi S**, Milaneschi, Y, Rivera, M, Ripke S, Wray NR, Sullivan, PF (2014). *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.

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

Recent Selected Talks

- 10/2016 “Integrating genomics data to identify meaningful associations”. University of British Columbia and NTU joint meeting. Vancouver, BC, Canada.
- 09/2016 “Network biology”. University of Pittsburgh and Carnegie Mellon University. Pittsburgh, PA, USA.
- 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.
- 11/2015 “From complex regulatory networks to complex disease”. Invited Lecture: Centre for Heart Lung Innovation. Vancouver, Canada.
- 04/2015 “Integrating multiple types of genomics data to disentangle meaningful associations.” Invited speaker: Annual Canadian Human and Statistical Genetics Meeting. Vancouver, Canada.
- 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.

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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.

Details of Teaching Activity

January 2016-April 2016

University of British Columbia

Course coordinator: Statistical Methods for High Dimensional Biology (STAT540)

Course consisted of 49 graduate students of from varied backgrounds (Statistics, Computer Science, Bioinformatics, Biology).

Duties: design and deliver 14 lectures, design course evaluation scheme, supervise TAs in delivering seminars.

January 2015-April 2015

University of British Columbia Co-instructor: Statistical Methods for High Dimensional Biology (STAT540)

Course consisted of ~45 graduate students of from varied backgrounds (Statistics, Computer Science, Bioinformatics, Biology).

Duties: deliver 6 lectures, design assignments, guide student projects.

September 2006- December 2008

Teaching Assistant (4 semesters) for the course “Introduction to Computer Science” at University of Toronto

January 2006- April 2006

Queen’s University

Course Assistant: Bioinformatics

Professional Activities

Organizing Committee	Neural Information Processing Systems (NIPS) Workshop on Computational Biology. December 2013-2017 (yearly workshop) International Conference on Machine Learning (ICML) Workshop on Machine Learning in Genetics and Genomics, July 2012
Program Committee	Neural Information Processing Systems (NIPS), Dec 2016, Dec 2017 Great Lakes Bioinformatics and the Canadian Computational Biology Conference (GLBIO/CCBC), May 2016 Intelligent Systems for Molecular Biology (ISMB), July 2016 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 2012-2016

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Journal Reviewing Scientific Reports, Molecular Systems Biology, PLoS Computational Biology, Bioinformatics, Genome Research, Cell Systems, Nature Communication

Grants Reviewing
NIH review panel (2017)
Research Foundation Flanders (2017)
Research Councils UK (RCUK) (2015)
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