

Yue Li

Assistant Professor
School of Computer Science, McGill University
Associate member of Quantitative Life Science
Associate member of Montreal Institute for Learning Algorithms (MILA)
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<https://www.cs.mcgill.ca/~yueli/>

Education:

12/2018	Postdoc	<i>Machine learning and statistical genetics</i>	Computer science & AI Laboratory Massachusetts Institute of Technology Broad Institute
12/2014	Ph.D.	<i>Computational biology</i>	Department of Computer Science University of Toronto
		Thesis title: <i>Computational Methods of Inferring Context-specific MicroRNA Regulatory Networks</i>	
04/2012	M.Sc.	<i>Computational biology</i>	Department of Computer Science University of Toronto
06/2010	B.Sc.	Honors: <i>Bioinformatics</i> Minors: <i>Statistics</i> GPA: 92%	Department of Computer Science Department of Math. & Stat. University of Saskatchewan

Research interest:

Machine Learning: Latent variable/topic models;
Matrix/tensor decomposition;
Collaborative filtering;
Deep generative models;
Approximate Bayesian inference.

Data Analysis: Next generation sequencing analysis (e.g., RNA/ChIP-seq);
Whole-genome sequencing analysis;
Single-cell multi-omic profiles modeling;
Magnetic resonance imaging (MRI) analysis.

Computational Biology: Electronic health record;
Inference of functional causal mutations;
Expression quantitative traits loci (eQTL);
Regulatory genomics in complex diseases;
Epigenetic regulation by chromatin regulators and histone modifications;
 N^6 -methyladenosine (m⁶A) target site predictions;
Cancer genomics.

Programming: R & Rcpp, C++, Python,, Shell, Matlab, Perl, Awk, C, Java.

Awarded Grants:

- 2019-2023 NSERC Discovery Grant (RGPIN-2019-06216) Probabilistic methods towards understanding complex human phenotypes
- 2019-2021 FRQNT Career Development (FRQ-NT NC-268592) Probabilistic methods towards understanding complex human phenotypes
- 2019-2021 Healthy for Healthy Lives (HBHL) New Investigator (CFREF/HBHL New Invest/Li L3). Computational methods to dissect the genetic, transcriptomic, and phenotypic complexity of the human brain
- 05/2019-05/2020 MiCM ResearchMatch, PI: Yue Li (McGill), co-PI: Audrey Grant (McGill). Integrative approach to dissect regulatory circuitry of pain-related phenotypes
- 04/2020 Canada Foundation for Innovation - Research or technology development funding, Lead PI: Yue Li, co-PI: William Hamilton, co-PI: Reihaneh Rabbany. Fast scalable deep learning for sensitive big data in healthcare and social contexts
- 04/2020-04/2022 CIHR Canadian 2019 Novel Coronavirus (2019-nCoV) Rapid Research, Lead PI: David Buckeridge, co-PI: Yue Li. Using Online News Media to Assess Community and Public Health Responses to COVID-19
- 03/2020-03/2022 NFRF - Exploration (NFRFE-2019-00980) Unravel complex traits by single-cell deconvolution

Refereed Publications:

30. **Li, Y.**[†] et al. (2020). Inferring multimodal latent topics from electronic health records. *Nature Communications* (*accepted*) [†]First and corresponding author
29. Liu, M.* , Jiang, Y.* , Wedow, R.* , **Li, Y.*** , Brazel, D. M., Chen, F., et al. (2019). Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. *Nature Genetics*, 1-13. <http://doi.org/10.1038/s41588-018-0307-5>
28. Wang Y, **Li, Y.**, Yue M, Wang J, Kumar S, Wechsler-Reya RJ, Zhang Z, Ogawa Y, Kellis M, Duester G, Zhao JC. (2018) “N6-methyladenosine RNA modification regulates embryonic neural stem cell self-renewal through histone modifications” *Nature Neuroscience* (Advanced Access)
27. Kreimer, A., Zeng, H., Edwards, M. D., Guo, Y., Tian, K., Shin, S., Welch, R., Wainberg, M., Mohan, R., Sinnott-Armstrong, N. A., **Li, Y.**, Eraslan, G., AMIN, T. B., Goke, J., Mueller, N. S., Kellis, M., Kundaje, A., Beer, M. A., Keles, S., Gifford, D. K. and Yosef, N. (2017), Predicting gene expression in massively parallel reporter assays: a comparative study. *Human Mutation*. Accepted Author Manuscript. doi:10.1002/humu.23197
26. **Li, Y.**, & Kellis, M. (2016). Joint Bayesian inference of risk variants and tissue-specific epigenomic enrichments across multiple complex human diseases. *Nucleic Acids Research*. <http://doi.org/10.1093/nar/gkw627>

25. Olsen, J. B., Wong, L., Deimling, S., Miles, A., Guo, H., **Li, Y.**, Zhang, Z., Greenblatt, J., Emili, A., Tropepe, V. (2016). G9a and ZNF644 Physically Associate to Suppress Progenitor Gene Expression during Neurogenesis. *Stem Cell Reports*, 7(3), 454-470.
24. Paul, J., Toosi, B., Vizeacoumar, F., Bhanumathy, K., **Li, Y.**, Gerger, C., Zawily, A., Freywald, T., Anderson, D., Mousseau, D., Kanthan, R., Zhang, Z., Vizeacoumar, F., & Freywald, A. (2016). Targeting synthetic lethality between the SRC kinase and the EPHB6 receptor may benefit cancer treatment. *Oncotarget*, 5.
23. Zhao, D.Y., Gish, G. *, Braunschweig, U.* , **Li, Y.**, Ni, Z., Schmitges, F.W., Zhong, G., Liu, K., Li, W., Moffat, J., Vedadi, M., Min, J., Pawson, T., Blencowe, B., and Greenblatt, J. (2016) SMN and symmetric arginine dimethylation of RNA polymerase II C-terminal domain control termination. *Nature*. 529(7584), pp.48-53.
22. Wong, K. C., **Li, Y.**, Peng, C. (2015) A Comparison Study for DNA Motif Modeling on Protein Binding Microarray. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. doi:10.1109/TCBB.2015.2443782.
21. Wong, K. C., Peng, C., **Li, Y.** (2015) Probabilistic Inference on Multiple Normalized Signal Profiles from Next Generation Sequencing: Transcription Factor Binding Sites. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. doi:10.1109/TCBB.2015.2424421.
20. Wong, K. C., **Li, Y.**, Peng, C. (2015). Identification of coupling DNA motif pairs on long-range chromatin interactions in human K562 cells. *Bioinformatics*, btv555.
19. Wong, K. C., **Li, Y.**, Peng, C., Moses, A. M., Zhang, Z. (2015). Computational learning on specificity-determining residue-nucleotide interactions. *Nucleic acids research*, gkv1134.
18. **Li, Y.***, Wang, Y.* , Zhang, Z., Zamudio, A. V., Zhao, J. C. (2015). Genome-wide detection of high abundance N^6 -methyladenosine sites by microarray. *RNA*.
17. **Li, Y.** & Zhang Z. Computational Biology in microRNA. *WIREs RNA*. 2015. doi: 10.1002/wrna.1286
16. Liang, C. *, **Li, Y.***, Luo, J., Zhang Z. (2015)) A novel motif-discovery algorithm to identify co-regulatory motifs in large transcription factor and microRNA co-regulatory networks in human. *Bioinformatics*
15. **Li, Y.**, Zhang, Z. (2014). Potential microRNA-mediated oncogenic intercellular communication revealed by pan-cancer analysis. *Scientific Reports*. 7(7097).
14. **Li, Y.**, Liang, M., Zhang, Z. (2014). Regression analysis of combined gene expression regulation in acute myeloid leukemia. *PloS Computational Biology*. 10(10): e1003908.
13. **Li, Y.***, Liang, C.* , Easterbrook, S., Luo, J., Zhang Z. (2014). Investigating functional implication of reinforcing feedback loops in transcriptional regulatory network. *Molecular BioSystem* 10(12), 3238–3248.
12. Wong, KC, **Li, Y.**, Peng, C., Zhaolei Z. (2014). SignalSpider: Probabilistic Pattern Discovery on Multiple Normalized ChIP-Seq Signal Profiles. *Bioinformatics*, btu604.

11. **Li, Y.***, Liang, C.*, Wong, KC., Luo, J., Zhang Z. (2014). Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. *Bioinformatics* **30**(18), 2627–2635.
10. Wong, KC., Peng, C., **Li, Y.**, Chan, TM. (2014). Herd Clustering: A synergistic approach using collective intelligence. *Applied Soft Computing*
9. **Li, Y.**, Liang, C., Wong, KC, Jin, K., and Zhang, Z. (2014) Inferring probabilistic miRNA-mRNA interaction signatures in cancers: a role-switch approach. *Nucleic Acids Research*, **42**(9), e76. doi: 10.1093/nar/gku182
8. Wang, Y., **Li, Y.**, Toth, JI., Petroski, MD., Zhang, Z., and Zhao J. (2014). *N*⁶-methyladenosine modification destabilizes developmental regulators in embryonic stem cells. *Nature Cell Biology*, **16**(2), 1-10. doi:10.1038/ncb2902
7. **Li, Y.**, Goldenberg, A., Wong, KC., Zhang Z. (2013). A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. *Bioinformatics*. (Oxford, England), **30**(5), 621–628. doi:10.1093/bioinformatics/btt599 doi:10.1093/bioinformatics/btt599
6. Wong, KC., Chan, TM., Peng, C., **Li, Y.**, and Zhang, Z. (2013). DNA motif elucidation using belief propagation. *Nucleic Acids Research*, **41**(16), e153. doi:10.1093/nar/gkt574
5. **Li, Y.**, Zhao, D. Y., Greenblatt, J. F., and Zhang, Z. (2013). RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-seq experiments. *Nucleic Acids Research*, **41**(8), e94. doi:10.1093/nar/gkt142
4. Arsenault, R. J., **Li, Y.**, Maattanen, P., Scruten, E., Doig, K., Potter, A., Griebel, P., Kusalik, A., and Napper, S. (2013) Altered Toll-like receptor 9 signaling in *Mycobacterium avium* subsp. *paratuberculosis*-infected bovine monocytes reveals potential therapeutic targets. *Infection and immunity*, **81**(1), 226237.
3. Arsenault, R. J., **Li, Y.**, Potter, A., Griebel, P. J., Kusalik, A., and Napper, S. (2012) Induction of ligand-specific PrPC signaling in human neuronal cells. *Prion*, **6**(5), 477-488.
2. Arsenault, R. J., **Li, Y.**, Bell, K., Doig, K., Potter, A., Griebel, P. J., Kusalik, A., and Napper, S. (2012) *Mycobacterium avium* subsp. *paratuberculosis* Inhibits Interferon Gamma-Induced Signaling in Bovine Monocytes. Insights into the Cellular Mechanisms of Johnes Disease. *Infection and immunity*, **80**, 3039-3048.
1. **Li, Y.**, Arsenault, R. J., Trost, B., Slind, J., Griebel, P. J., Napper, S., and Kusalik, A. (2012) A Systematic Approach for Analysis of Peptide Array Kinome Data. *Science Signaling*, **5**(220), pl2-pl2.

(*equal contribution)

Book chapters:

Wong, K. C., **Li, Y.**, & Zhang, Z. (2015). Unsupervised Learning in Genome Informatics. arXiv preprint arXiv:1508.00459.

Zhao, D., **Li, Y.**, Greenblatt, J., & Zhang, Z. (2014). ncRNA-Protein Interactions in Development and Disease from the Perspective of High-Throughput Studies. In A. Emili, J. Greenblatt, & S. Wodak (Eds.), *Systems Analysis of Chromatin-Related Protein Complexes in Cancer* (pp. 87-115). Springer New York. doi:10.1007/978-1-4614-7931-4_5

Technical reports:

Li, Y. Exploring the Power and Flexibility of Generative Neural Network with Contrastive Back-propagation. (2011) University of Toronto.

Li, Y., Pajon, R., Bickis, M., & Kusalik, A. (2009) Regression After Stratification to Predict Immunogenicity Responses using Proteome Microarray. University of Saskatchewan.

Manuscripts under revision:

Li, Y., Davila, J., and Kellis, M. (2017). A probabilistic framework to dissect functional cell-type-specific regulatory elements and risk loci underlying the genetics of complex traits. bioRxiv <http://doi.org/10.1101/059345>

Li, Y., Shi, A., Tewhey, R., Sabeti, P., Ernst, J., & Kellis, M. (2017). Genome-wide regulatory model from MPRA data predicts functional regions, eQTLs, and GWAS hits. bioRxiv <http://doi.org/10.1101/110171>

Manuscripts under review:

Li, Y.[†] et al. Partitioning gene-based variance of complex traits by gene score regression.

Wen, Z., . . . , **Li, Y.**[†] Mining heterogeneous clinical notes by multi-modal latent topic model.

Lu, X., . . . , **Li, Y.**[†] Recurrent Disease Progression Networks for Modelling Risk Trajectory of Heart Failure.

Bahrami, M., . . . , **Li, Y.**[†] Deep feature extraction of single-cell transcriptomes by generative adversarial network.

[†]corresponding author

Teaching Experience:

McGill University:

01/01/2019 - 04/30/2019 COMP 204 Winter 2019 Computer programming for Life Sciences

Massachusetts Institute of Technology:

10/21/2017 Lecturer on deep learning in genomics for class 6.878

- 01/09–04/30 2017 Lecturer of Machine learning for Computational Biology for class 6.888
- 12/01/2016 Lecturer on phenome-wide association studies for class 6.878
- 10/21/2016 Lecturer on deep learning in genomics for class 6.878
- 04/21/2016 Laboratory assignment on microRNA-mediated expression clustering in cancer for class 6.881
- 03/07/2016 Laboratory assignment on Bayesian fine-mapping GWAS for class 6.881

University of Toronto:

- 01/15–04/30 2012,2014 Teaching Assistant for CSC321: Introduction to Neural Networks and Machine Learning, Mississauga, Winter 2012,2014, all of the tutorials (including developing & delivering presentation slides) and all of the markings
- 09/10 2012–04/30 2013 Teaching Assistant for CSC209: Software Tools and Systems Programming, St. George, Fall 2012 & Winter 2013, tutorials and markings
- 09/10 2011–04/30 2012 Teaching Assistant for CSC343: Introduction to Databases, St. George, Winter 2011 & Fall 2012, markings
- 09/10–12/20 2010 Teaching Assistant for CSC236: Introduction to Theory of Computation at St. George, St. George, Fall 2010, tutorial (including blackboard demonstration of concepts and proofs) and markings

University of Saskatchewan:

- 05/13–06/30 2009 Teaching Assistant for CMPT214 Programming Principles and Practice

Supervision Experience at McGill University:

- 04/01/2019 - 07/01/2019 Theophile Pierre Henri Buffiere, (summer internship from France Polytechnique, April-July)
- 05/07/2019 - 09/07/2019 Wan-Chun Su, (summer internship from MiCM and Computer science and Biology U2, May-August)
- 05/01/2019 - 08/01/2019 Yan Miao, (summer internship from SURA, May-August)
- 05/01/2019 - 05/01/2020 Amir Ardalan Kalantari Dehaghi, (McGill 2nd year Master student, started)
- 05/01/2019 - 08/01/2020 Si Yi Li, (RA for the summer, and new Master student this Fall)
- 05/01/2019 - 08/01/2019 Joseph Szymborski, (QLS program rotation student May-August)
- 05/01/2019 - 08/01/2019 Amanda Liu (volunteer McGill Computer science and Biology U2 student)
- 02/01/2019 - now Ziyang song (current Concordia MSc student)
- 02/01/2019 - now Xavier Sumba Toral (current Concordia-McGill MSc student)

02/01/2019 - Xing Han Lu (McGill U3 student)

Mentor Experience:

MIT

- 01/01/2017–08/01/2018 Mentor of graduate student Peter Nguyen
- 05/01/2016–05/01/2017 Mentor of graduate student Alvin Shi
- 05/01/2016–05/01/2017 Mentor of graduate student Isabel Chien
- 05/01/2016–12/01/2018 Mentor of MD student Yuri Ahuja from Harvard Medical School
- 06/20/2016–09/01/2016 Mentor of undergraduate student Daniel Sosa
- 03/01/2016–09/01/2016 Mentor of undergraduate student Ajay Saini
- 10/01/2015–01/01/2016 Mentor of undergraduate student Uma Roy

University of Toronto

- 07/04/2014–08/31/2014 Mentor of senior undergraduate visiting student Shengcheng Dong from Tsinghua University, China
- 10/13/2013–03/11/2014 Mentor of junior graduate student Minggao Liang from Molecular Genetic, University of Toronto
- 05/27/2013–08/27/2013 Mentor of third year undergraduate Quanxin Zhou from Computer Science, University of Toronto
- 09/10–12/20/2011 Mentor of fourth year undergraduate Alharith Hussin from Computer Science, University of Toronto

Research Experience:

- 01/01 2019–now Assistant Professor at McGill University
- 02/01 2015–12/15/2018 Postdoctoral research associate at Prof. Manolis Kellis Lab, Computer Science and Artificial Intelligence Laboratory, MIT
- 09/01 2010–12/01 2014 Research Assistant at Prof. Zhaolei Zhang Lab, Donnelly Centre for Cellular and Biomolecular Research, University of Toronto
- 09/01–10/30 2009 Research Assistant for Prof. Anthony Kusalik, Bioinformatics Laboratory, University of Saskatchewan
- 05/04–08/28/2009 NSERC Undergraduate Research in *Machine-learning in Prediction of Immunogenicity Response*, Bioinformatics Laboratory, University of Saskatchewan

Presentations:

Oral presentations:

- 05/09/2019 **Li, Y.** (2019) Clinical Updates by Means of Artificial Intelligence: The Example of MixEHR, Medicine without Doctors, Jewish General Hospital, Montreal
- 04/25/2019 **Li, Y.** (2019) Multiomic learning of disease regulatory networks, Advances and Thoughts Genome Center, McGill University, Montreal
- 10/18/2017 **Li, Y.** (2018) Dissecting the genetic, transcriptomic, and phenotypic complexity of PTSD across 9400 individuals and 30 million phenotypic observations, *American Society of Human Genetics* (ASHG) 2018
- 05/18/2017 **Li, Y.** (2017) Imputation-based modeling of electronic health records for disease and patient classification. Medical and Population Genetics., Broad Institute, MA.
- 02/29/2017 **Li, Y.** (2017) A Bayesian method to infer disease networks using electronic health records. Statistical Genetics Meeting, Broad Institute, MA.
- 02/29/2017 **Li, Y.** (2017) A Bayesian method to infer disease networks using electronic health records. Statistical Genetics Meeting, Broad Institute, MA.
- 02/28/2017 **Li, Y.** (2017) A Bayesian method to infer disease networks using electronic health records. Google, Cambridge, MA.
- 12/06/2016 **Li, Y.** (2016) Bayesian inference of risk variants using genetic and epigenomic annotations and phenotypic imputation using electronic health records. Tsinghua University, Beijing, China
- 11/07/2016 **Li, Y.** (2016) Joint Bayesian inference of risk variants using summary statistics and epigenomic annotations across multiple traits. Program in Quantitative Genomics Work Group seminar series. Harvard TH Chan School of Public Health, Cambridge, MA
- 10/20/2016 **Li, Y.** (2016) Joint Bayesian inference of risk variants using summary statistics and epigenomic annotations across multiple traits. *American Society of Human Genetics* (ASHG) 2016. (Selected abstract for Epstein Trainee Award for Excellence in Human Genetics Research). Platform Presentation, Vancouver Convention Centre, Canada.
- 09/24/2015 **Li, Y.** (2015) Joint Bayesian inference of causal variants across multiple traits using epigenomic annotations and linkage disequilibrium information. Medical and Population Genetics. Broad Institute. Cambridge, MA
- 08/06/2015 **Li, Y.** (2015) Joint Bayesian inference of driver variants in nine immune disorders using epigenomic annotations. Statistical and Computational Challenges In Bridging Functional Genomics, Epigenomics, Molecular QTLs, and Disease Genetics Workshop. Banff International Research Station, Canada. (talk

video link: <http://www.birs.ca/events/2015/5-day-workshops/15w5142/videos/watch/201508061445-Li.html>)

- 10/02/2014 **Li, Y.** (2014) New computational methods to the roles of microRNAs in cancer, The Donnelly Seminar Series, The Donnelly Centre (CCBR), University of Toronto
- 01/08/2014 **Li, Y.** (2014) ORF-GL2 Meeting Report on RIP-Seq analysis, The Donnelly Centre (CCBR), University of Toronto
- 02/20/2013 **Li, Y.** (2013) ORF-GL2 Meeting Report on RIP-Seq analysis, The Donnelly Centre (CCBR), University of Toronto
- 06/23/2012 **Li, Y.** (2012) Computational Identification of Protein-Associated Functional Noncoding RNA from High-throughput Sequencing Data. Presented to Dr. Xiaohua Shens laboratory members at Tsinghua University and to Zhaos laboratory members at Institute of Computing Technology, Chinese Academy of Sciences, Beijing, China
- 05/16/2012 **Li, Y.** (2012) ORF-GL2 Meeting Report on RIP-Seq analysis and colorectal cancer projects, The Donnelly Centre (CCBR), University of Toronto
- 11/02/2011 **Li, Y.** (2011) An Integrative Computational Approach to Elucidate Protein-Associated Non-coding RNA Regulators using High-throughput Sequencing Data. One-hour oral technical report at the ORF-GL2 Meeting, Donnelly Centre for Cellular & Biomolecular Research (CCBR), University of Toronto
- 05/10/2011 **Li, Y.** (2011) RIP-Seq Analysis and Preliminary Results. One-hour oral technical report at the ORF-GL2 Meeting, The Donnelly Centre (CCBR), University of Toronto
- 08/29/2009 **Li, Y.** (2009) Machine-learning using Antibody Profiles. Individual presentations to group leaders Drs. Sylvia van den Hurk, Volker Gerdts, Scott Napper, and Volker Gerdtss research team from Vaccine and Infectious Disease Organization (VIDO) for potential collaboration, University of Saskatchewan
- 08/26/2009 **Li, Y., Kusalik, A., Trost, B.** (2009) Machine-learning and Infectious Disease Research. This invited talk was delivered at the Research Alliance for the Prevention of Infectious Disease (RAPID) Annual General Meeting in Saskatoon

Poster Presentations:

- 10/07/2015 **Li, Y.** (2015) Joint Bayesian inference of causal variants across multiple traits using epigenomic annotations and linkage disequilibrium information. American society of human genetics 2015. Baltimore Convention Center. Baltimore, MD
- 07/11/2014 **Li, Y., Liang, C., Wong, KC, Jin, K., and Zhang, Z.** (2014) Inferring probabilistic miRNA-mRNA interaction signatures in cancers: a role-switch approach. Poster for ISMB 2014 - International Society for Computational Biology at Boston

- 08/20/2012 **Li, Y.**, Zhao, D., Greenblatt, J., and Zhang, Z. (2012) RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-Seq experiments. Poster presented at Scientific Advisory Board Meeting at The Donnelly Centre (CCBR) & at International Conference of System Biology (ICSB) 2012, Hart House, University of Toronto
- 08/29/2011 **Li, Y.**, Zhao, D., Greenblatt, J., and Zhang, Z. (2011) Constructing Protein-RNA Interactome using RIP-Seq. Poster presented in McGill-Toronto Computation Molecular and System Biology Retreat held at the McGill University
- 08/29/2010 Arsenault, R. J., **Li, Y.**, Griebel, P., Potter, A., Babiuk, L., Kusalik, A., and Napper, S. (2010) Prion Signaling in Human Neuronal Cells. Poster presented at PrP Canada PrioNet Conference in Ottawa
- 03/10/2010 PrP Canada PrioNet Conference in Ottawa, Arsenault, R. J., **Li, Y.**, Griebel, P., Potter, A., Babiuk, L., Kusalik, A., and Napper, S. (2010) *Prion Signaling in Human Neuronal Cells*, University of Saskatchewan
- 08/29/2009 NSERC Undergraduate Research Poster, **Li, Y.**, Pajon, R., Bickis, M. and Kusalik, A. (2009). *Comparisons of Machine-Learning Methods to Predict Diagnostic Values for Leprosy Infection Based on Protein Microarray Data.*, University of Saskatchewan

Attended Conferences:

- 10/15–18/2018 American Society of Human Genetics Annual Meeting, San Diego, CA, USA
- 10/18–22/2016 American Society of Human Genetics Annual Meeting, Vancouver, BC, Canada
- 10/6–10/2015 American Society of Human Genetics Annual Meeting, Baltimore, MD, USA
- 07/11–15/2014 The 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2014), Boston, MA, USA
- 08/19–23/2012 The 13th International Conference on System Biology (ICSB 2012), Toronto, ON, Canada
- 07/14–17/2012 The 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2012), Long Beach, CA, USA

Honours, Awards & Fellowship:

- 2016 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research – Semifinalist. Value: \$750
- 2012–2015 Natural Sciences and Engineering Research Council of Canada (NSERC) Alexander Graham Bell Canada Graduate Scholarship (CGS) at Doctoral's Level. Level: National. Type: Academic and Research. Value: \$105,000.

- 05/14/2012 Ontario Graduate Scholarship (OGS) Award Doctoral's Level 2012-2013. Level: Provincial. Type: Academic and Research. Value: \$15,000. (declined)
- 06/30/2011 C.C. Gotlieb (Kelly) Graduate Fellowship from The Department Of Computer Science, University of Toronto. Level: Institutional. Type: Academic. Value: \$500.
- 05/14/2011 Ontario Graduate Scholarship (OGS) Award Master's Level 2011-2012. Level: Provincial. Type: Academic and Research. Value: \$15,000.
- 06/01 2010 Most Distinguished Graduate Award in Bioinformatics, University of Saskatchewan. Level: Institutional. Type: Academic. Value: \$100.
- 03/19 2010 Natural Sciences and Engineering Research Council of Canada (NSERC) Alexander GrahamBell Canada Graduate Scholarship (CGS) at Master's Level. Level: National. Type: Academic and Research. Value: \$17,500.
- 04/27 2009 Researcher of Tomorrow Fellowship, University of Saskatchewan. Level: Institutional. Type: Academic. Value: \$1,000.
- 03/02 2009 Natural Sciences and Engineering Research Council of Canada (NSERC) Undergraduate Student Research Award. Level: Institutional. Type: Academic. Value: \$4,500.
- 2007–2008 Named to Dean's Honour List that recognizes students who rank in top 5% of all students in the College of Arts and Science, University of Saskatchewan. Level: Institutional. Type: Academic. Value: \$0.

Patents:

- 2012 Cortese, R., Petronis, A., Zanke, B., Zhang, Z., **Li, Y.**, Kwan, A. Diagnostic Markers and Methods for Identifying Subjects Predisposed to Colorectal Cancer
- 2010 **Li, Y.**, Arsenault, R. J., Griebel, P., Napper, S., and Kusalik, A. Methods Of Kinome Analysis. Approved by Canadian Intellectual Property Office.

Academic services as reviewer (42 papers reviewed in total):

- 2019 *AJHG* (papers reviewed 1)
- 2019 *ISMB 2019* (papers reviewed 5)
- 2019 *ICIC* (papers reviewed 1)
- 2019 *PloS One* (papers reviewed 1)
- 2013-2015,2017,2018 *Bioinformatics* (papers reviewed: 7)
- 2018 *Computational Biology and Chemistry* (papers reviewed: 2)
- 2014-2017 *PloS Computational Biology* (papers reviewed: 4)
- 2018 *Nature Genetics*(papers reviewed: 1)

2014,2016,2018 *Nucleic Acid Research* (papers reviewed: 3)
2014 *Genome Biology* (papers reviewed: 2)
2016-2017 *IEEE Transactions* (papers reviewed: 2)
2016,2018 *PloS One* (papers reviewed: 2)
2018 *Neural Computing and Applications (NCAA)* (papers reviewed: 1)
2015,2019 *Scientific reports* (papers reviewed: 2)
2017 *Biodata Mining* (papers reviewed: 1)
2017 *Nature molecular psychiatry* (papers reviewed: 1)
2016 *RECOMB 2017* (papers reviewed: 1)
2016 *Journal of Biomedical Informatics* (papers reviewed: 1)
2016 *BMC Bioinformatics* (papers reviewed: 1)
2016 *Computers in Biology and Medicine* (papers reviewed: 1)
2016 *Big Data Analytics in Genomics* (chapter reviewed: 1)
2016 *The 27th International Conference on Genome Informatics 2016* (papers reviewed: 1)
2016 *BMC Biology* (papers reviewed: 1)
2015 *Pacific Symposium on Biocomputing 2016* (papers reviewed: 1)
2014 *BMC System Biology* (papers reviewed: 1)
2015 *Computational Biology and Bioinformatics: Gene Regulation, CRC Press* (chapters reviewed: 3)

References:

Prof. Manolis Kellis
CSAIL & Broad Institute
Massachusetts Institute of Technology
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Prof. Zhaolei Zhang
Department of Molecular Genetics
University of Toronto
zhaolei.zhang@utoronto.ca

Prof. Anna Goldenberg
Department of Computer Science
University of Toronto
anna.goldenberg@utoronto.ca

Prof. Crystal Jing Zhao
Tumor Initiation and Maintenance Program
Sanford-Burnham Medical Research Institute
czhao@sanfordburnham.org