Yue Li

Massachusetts Institute of Technology
Postdoctoral Research Associate
Computational Biology Group
Computer Science & Artificial Intelligence Laboratory
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Education:

12/2014	Ph.D.	*Computational biology*	Department of Computer Science University of Toronto
	Thesis title: *Computational Methods of Inferring Context-specific MicroRNA Regulatory Networks*		
04/2012	M.Sc.	*Computational biology*	Department of Computer Science University of Toronto
06/2010	B.Sc.	Honors: *Bioinformatics* Minors: *Statistics* GPA: 92%	Department of Computer Science Department of Math. & Stat. University of Saskatchewan

Research Background:

Computational methods: Bayesian inference, probabilistic graphical models, generalized linear models, parametric and nonparametric testing, neural networks

Programming skills: R (developed and contributed **eight** R/Bioconductor packages), Rcpp, Matlab, Python, Shell, Perl, Awk, C, C++, Java.

Data analysis: Microarray, tiling array analysis;
Next generation sequencing analysis including RNA-seq, ChIP-seq, RIP-seq, CLIP-seq, PAR-CLIP, etc.

Biological problems of interest:

Genome-wide association studies;
Electronic health record;
Epigenetics in complex diseases;
Cancer genomics;
Transcriptional regulatory network
Epigenetic regulation by chromatin regulators and histone modifications;
RNA epigenetics (N^6-methyladenosine or m6A target site predictions);
Post-transcriptional regulation by microRNAs;
Function characterization of long noncoding RNAs;
Functional genomics.

Refereed Publications:

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 Backpropagation. (**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 in preparation:

Li, Y., Ahuja, Y. & Kellis, M. Imputation-based Bayesian inference of electronic health records.

Teaching Experience:

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

Mentor Experience:

01/01/2017–now Mentor of graduate student Peter Nguyen at MIT

05/01/2016–now Mentor of graduate student Alvin Shi at MIT

05/01/2016–now Mentor of graduate student Isabel Chien at MIT

05/01/2016–now Mentor of MD student Yuri Ahuja from Harvard Medical School

06/20/2016–09/01/2016 Mentor of undergraduate student Daniel Sosa at MIT

03/01/2016–09/01/2016 Mentor of undergraduate student Ajay Saini at MIT

10/01/2015–01/01/2016 Mentor of undergraduate student Uma Roy at MIT

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:

02/01 2015–present 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:

05/18/2017 **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:

10/18–22/2016 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 GrahamBell 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 (33 papers reviewed in total):

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 *Scientific reports* (papers reviewed: 1)

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