Gerald Quon

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Academic Summary

(2016-present) Assistant Professor, Department of Molecular and Cellular Biology, University of California, Davis.

(2012-2015) Postdoctoral Research Associate, MIT Computer Science and Artificial Intelligence Laboratory.
Advisor: Professor Manolis Kellis.

(2006-2012) Ph.D. Computer Science, University of Toronto, Canada.
Dissertation: Probabilistic models for the analysis of gene expression profiles.
Advisor: Professor Quaid Morris.

(2011) Research Intern, Microsoft Research, USA.
Project: Patterns of methylation heritability in a genome-wide analysis of four brain regions.
Advisor: Dr. Jennifer Listgarten.

(2004-2006) M.Sc. Biochemistry, University of Toronto, Canada.
Dissertation: The landscape of false-positive transcription factor binding site predictions in yeast.
Advisor: Professor Shoshana Wodak.

(1999-2004) B. Math, Computer Science with Bioinformatics Option, University of Waterloo, Canada.

Manuscripts in review

Quon, G., Feizi, S., Marbach, D., Claussnitzer, M., Kellis, M. Diverse enhancer networks reveal the regulatory architecture of complex traits.

Refereed Publications

(*) indicates joint first authorship.

(2016) Marbach, D., Lamparter, D., **Quon, G.**, Kellis, M., Kutalik, Z., Bergmann, S. Tissue-specific regulatory circuits reveal variable modular perturbations across complex diseases. Nature Methods, 13, 366-370.

(2016) Batmanghelich, N.K., Dalca, A., **Quon, G.**, Sabuncu, M., Golland, P., for the Alzheimer's Disease Neuroimaging Initiative. Probabilistic Modeling of Imaging, Genetics and Diagnosis. IEEE Transactions on Medical Imaging. **35**(7):1765-79.

(2016) Cui, A.*, **Quon, G.***, Rosenberg, A., Yeung, R., Morris, Q. Gene expression deconvolution for uncovering molecular signatures in response to therapy in juvenile idiopathic arthritis. PLOS ONE. **11**(5):e0156055.

(2015) Claussnitzer, M., Dankel, S.N., Kim, K., **Quon, G.**, *et al.* FTO obesity variant circuitry and adipocyte browning in humans. New England Journal of Medicine, **373**:895-907.

(2015) Roadmap Epigenomics Consortium *et al.* Integrative analysis of 111 reference human epigenomes. Nature, **518**:317-330. (co-integrative analysis lead)

(2015) Gjoneska, E., Pfenning, A.R., Mathys, H., **Quon, G.**, Kundaje, A., Tsai, L., Kellis, M. Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimer's disease. Nature, **518**:365-369.

(2013) **Quon, G.**, Haider, S., Deshwar, A.G., Cui, A., Boutros, P.C., Morris, Q. Computational purification of individual tumor gene expression profiles leads to significant improvements in prognostic prediction. Genome Medicine, **5**:29.

(2013) **Quon, G.**, Lippert, C., Heckerman, D., Listgarten, J. Patterns of methylation heritability in a genome-wide analysis of four brain regions. Nucleic Acids Research, **41**: 2095-2104.

(2013) Lippert, C., **Quon, G.**, Kang, E.Y., Kadie, C.M., Listgarten, J., Heckerman, D. The benefits of selecting phenotype-specific variants for applications of mixed models in genomics. Scientific Reports, **3**:1815.

(2012) Qiao, W.*, **Quon, G.***, Csaszar, E., Yu, M., Morris, Q.D., Zandstra, P.W. PERT: a method for expression deconvolution of human blood samples from varied microenvironmental and developmental conditions. PLoS Computational Biology, 8(12): e1002838.

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

(2010) Li, X., **Quon, G.**, Lipshitz, H.D., Morris, Q. Predicting in vivo binding sites of RNA-binding proteins using mRNA secondary structure. RNA, **16**:1096-1107.

(2009) **Quon, G.**, Morris, Q. ISOLATE: a computational strategy for identifying the primary origin of cancers using high-throughput sequencing. Bioinformatics, **25**:2882-2889.

(2009) Chan, E.T., **Quon, G.T.** *et al.* Conservation of core gene expression in vertebrate tissues. J. Biol., **8**:33.

(2009) **Quon, G.**, Teh, Y.W., Chan, E., Brudno, M., Hughes, T., Morris, Q.D. A mixture model for the evolution of gene expression in non-homogeneous datasets. Advances in Neural Information Processing Systems, 21, 1297-1304.

(2005) Thiruv, B., **Quon, G.**, Saldanha, A., Steipe, B. Nh3D: A reference dataset of structures of non-homologous proteins. BMC Structural Biology, **5**:12.

(2004) Stromer, J., **Quon, G.**, Gordon, P., Turinsky, A., Sensen, C.W. JABIRU: Harnessing Java 3D behaviors for device and display portability. IEEE Computer Graphics and Applications, **25**:70-80.

(2004) Shah, S.P., He, D., Sawkins, J., Druce, J., **Quon, G.**, Lett, D., Zheng, G., Xu, T., Ouellette, B.F. Pegasys: software for executing and integrating analyses of biological sequences. BMC Bioinformatics, **5**:40.

Technical reports

(2015) Feizi, S., **Quon, G.**, Medard, M., Kellis, M., Jadbabaie, A. Spectral Alignment of Networks, Available on MIT DSpace: http://hdl.handle.net/1721.1/94606

(2014) Batmanghelich, N.K., **Quon, G.**, Kulesza, A., Kellis, M., Golland, P., Bornn, L. Diversifying Sparsity Using Variational Determinantal Point Processes. arXiv preprint arXiv:1411.6307.

Selected talks

(2017) (**invited**) Computational integration of epigenomic and functional genomic data for fine-mapping complex trait loci. International Plant and Animal Genome XXV.

(2016) (**invited**) Predicting combinatorial therapies using drug gene networks. UC Davis Cancer Center Symposium.

(2016) (**invited**) ENCODE-CHARGE collaboration for Anthropometric Traits. CHARGE Investigators Meeting.

(2015) (**invited**) Machine learning approaches to personalized medicine and genomics. Harvey Mudd College Computer Science Colloquium.

(2015) (**invited, plenary**) Tissue-specific enhancer networks underlying complex traits. BIRS 15w5142: Statistical and Computational Challenges In Bridging Functional Genomics, Epigenomics, Molecular QTLs, and Disease Genetics.

(2015) (**plenary**) Predicting novel GWAS loci based on shared regulatory architecture inferred from ENCODE and Roadmap Epigenomics Consortium datasets. CHARGE Investigators Meeting.

(2014) (**invited**) Body mass index variants localize in regulatory modules specific to adipocyte progenitor cells. CHARGE Investigators Meeting.

(2014) Enhancer-centric networks identify regulatory processes, target genes, and driver regulatory elements underlying complex traits. RECOMB Regulatory Genomics.

(2014) Context-specific regulatory networks identify key regulators of complex traits. American Society of Human Genetics.

(2014) Context-specific regulatory networks identify key regulators of complex traits. ISMB Network Biology.

(2014) Investigating the functional role of variance-eQTL in transcriptional variation. ISMB Regulatory Genomics.

(2013) Regulatory networks reveal directed pathways enriched in disease-associated SNPs in complex diseases. ENCODE Consortium Meeting 2013.

(2011) Computational purification of tumor gene expression profiles leads to predictive models of patient outcome. RECOMB Satellite Workshop on Computational Cancer Biology.

(2010) Tumour heterogeneity is a central obstacle to predictive models of patient prognosis in lung cancer. NIPS Workshop on Predictive Models in Personalized Medicine.

(2010) A probabilistic topic model for the analysis of blood disease disorders. NIPS Workshop on Machine Learning in Computational Biology.

(2009) ISOLATE: a computational strategy for identifying the primary origin of cancers using high-throughput sequencing. Intelligent Systems for Molecular Biology.

(2007) Reconstructing the ancestral regulome of conserved orthologs across vertebrate organisms. CSHL Systems Biology: Global Regulation of Gene Expression.

Honors & Awards

(2014) $750 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Semifinalist (top 60 / 550 applicants)

(2011) $2,000 AACR-GlaxoSmithKline Outstanding Clinical Scholar Award

(2008-2010) $42,000 NSERC Postgraduate Scholarship Doctoral

(2007-2010) $33,000 University of Toronto Fellowship

(2007-2008) $15,000 Ontario Graduate Scholarship

(2004-2006) $34,600 NSERC Postgraduate Scholarship Masters

(2004) $7,500 NSERC Undergraduate Summer Research Assistantship

(2004) Honourable Mention, Computing Research Association Outstanding Undergraduate

Patents

Quon, G., Haider, S., Cui, A., Boutros, P.C., Morris, Q.D., ”Method for Identifying a Target Molecular Profile Associated with a Target Cell Population,” U.S. Patent: 20150294062, publication date October 15, 2015.

Teaching

(2011) Faculty, Canadian Bioinformatics Workshops. Invited to lecture course modules and labs on applying clustering and dimensionality reduction to functional genomics data. **Ranked most effective instructor by students**.

(2006-2010) Teaching Assistant, Canadian Bioinformatics Workshops. Invited to help instruct students on techniques for analyzing genomics and functional genomics data.

(2006-2010) Teaching Assistant, University of Toronto: 7 undergraduate courses (Algorithms, Software Engineering, Algorithms, Systems Programming), 2 graduate courses (Machine Learning in Computational Biology, Software Engineering).

(2009) Mentor, The Saturday Program. Tutored underprivileged children on math and science.

Service

(2016) Program Committee - PSB 2016 Precision Medicine

(2015) Organizer - NIPS Machine Learning in Computational Biology workshop

(2015) Program Committee - PSB 2015 Precision Medicine

(2012) Program Committee - Machine Learning in Genetics and Genomics workshop (ICML 2012)

Reviewer: Nature Communications, Bioinformatics, Journal of Machine Learning Research, PNAS, PLoS Computational Biology, Genomic Medicine