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KEYWORDS

Computational Biology, Machine Learning, RNA-binding proteins, Cancer and Functional Genomics, Electronic Health Records, Deep Learning, Artificial Intelligence

POSITIONS

2019-	**Member**, Computational and Systems Biology Program, Sloan Kettering Institute
2018-	**Professor (status only)**, Molecular Genetics (Medicine); Computer Science (A&S), University of Toronto
2018-	**Canada CIFAR Artificial Intelligence Chair**
2017-	**Faculty (on leave)**, Vector Institute for Artificial Intelligence

PREVIOUS ACADEMIC POSITIONS

2018-2021	**Professor,** Donnelly Centre, Faculty of Medicine, University of Toronto
2018-2021	**Associate Investigator**, Ontario Institute for Cancer Research
2017-2018	**Visiting Scholar**, New York University, Department of Biology
2014-2018	**Volunteer**, Ontario Institute for Cancer Research, Toronto
2013-2014	**Visiting Researcher**, Centre de Regulació Genòmica (CRG), Barcelona, Spain
2011-2018	**Associate Professor**, Donnelly Centre, Faculty of Medicine, cross-appointed Molecular Genetics (Medicine); Computer Science (A&S) and Electrical and Computer Engineering (Applied Sciences), University of Toronto
2011-2016	**Director of Collaborative Graduate Program in Genome Biology and Bioinformatics**, University of Toronto
2005-2010	**Assistant Professor**, Banting & Best Department of Medical Research, Faculty of Medicine, cross-appointed Molecular Genetics and Computer Science, University of Toronto

ACADEMIC AND TRAINING BACKGROUND

2003-2005	**Post-Doctoral Fellow**, Banting & Best Department of Medical Research and Electrical and Computer Engineering, University of Toronto
2002-2003	**Post-Doctoral Fellow**, Ontario Cancer Institute, Princess Margaret Hospital
1996-2002	**PhD in Computational Neuroscience**, in Department of Brain and Cognitive Sciences, Massachusetts Institute of Technology, Cambridge, USA
1999-2001	**Graduate training and research in machine learning**, Gatsby Computational Neuroscience Unit, University College London, England
1991-1996	**Honours B.Sc.,** Computer Science, University of Toronto

PUBLICATIONS

H-index 60, 22,773 citations, 12,496 since 2016, source: Google Scholar

* indicates equal contribution; † indicates co-senior; underline indicates trainee or staff

Manuscripts in review or revision

1. Kimberly Skead, Armande Ang Houle, Sagi Abelson, Mawusse Agbessi, Vanessa Bruat, Boxi Lin, David Soave, Liran Shlush, Stephen Wright, John Dick, **Quaid Morris**†, and Philip Awadalla†. *Interacting evolutionary pressures drive mutation dynamics and health outcomes in aging blood* (in review for Nature Communications)

Peer-reviewed journal articles (105)

1. Stefan C. Dentro*, Ignaty Leshchiner*, Kerstin Haase*, Maxime Tarabichi*, Jeff Wintersinger*, Amit G. Deshwar*, Kaixian Yu*, Yulia Rubanova*, Geoff Macintyre*, [33 co-authors], Wenyi Wang†, **Quaid D. Morris**†, David C. Wedge†, Peter Van Loo†, PCAWG Evolution and Heterogeneity Working Group, PCAWG network. *Characterizing genetic intra-tumor heterogeneity across 2,658 human cancers.* Cell 2021

   Contributions: My lab co-led the project, produced subclonal reconstructions for ~3,000 tumours, and developed new principled probabilistic methods to: (i) optimally combine subclonal and copy number reconstructions from 6-11 different independent methods, (ii) correct for winner's curse in variant allele estimates, (iii) use read pairs spanning multiple SNV loci, (iv) track changes in mutation signature exposure over evolutionary time (see TrackSig below)

2. Ha KCH, Sterne-Weiler T, **Morris Q**, Weatheritt RJ, Blencowe BJ. *Differential contribution of transcriptomic regulatory layers in the definition of neuronal identity*. Nat Commun. 2021 Jan 12;12(1):335. doi: 10.1038/s41467-020-20483-8. PMID: 33436550; PMCID: PMC7804943.

3. Rehman SK, Haynes J, Collignon E, Brown KR, Wang Y, Nixon AML, Bruce JP, Wintersinger JA, Singh Mer A, Lo EBL, Leung C, Lima-Fernandes E, Pedley NM, Soares F, McGibbon S, He HH, Pollet A, Pugh TJ, Haibe-Kains B, **Morris Q**, Ramalho-Santos M, Goyal S, Moffat J, O'Brien CA. *Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy*. Cell. 2021 Jan 7;184(1):226-242.e21. doi: 10.1016/j.cell.2020.11.018. PMID: 33417860.

4. Tarabichi, Maxime*; Salcedo, Adriana*; Deshwar, Amit G*; Leathlobhair, Máire Ni*; Wintersinger, Jeff; Wedge, David C†; Van Loo, Peter†; **Morris, Quaid D**†; Boutros, Paul C†, *A practical guide to cancer subclonal reconstruction from DNA sequencing.*

5. Linda K Sundermann, Jeff Wintersinger, Gunnar Rätsch, Jens Stoye, **Quaid Morris**, *Reconstructing tumor evolutionary histories and clone trees in polynomial-time with SubMARine.* PLoS Computational Biology, 2021

6. Liu LY, Bhandari V, Salcedo A, Espiritu SMG, **Morris QD**, Kislinger T, Boutros PC, *Quantifying the influence of mutation detection on tumour subclonal reconstruction*. Nat Commun. 2021 Jan 15

7. Kosti A, de Araujo PR, Li WQ, Guardia GDA, Chiou J, Yi C, Ray D, Meliso F, Li YM, Delambre T, Qiao M, Burns SS, Lorbeer FK, Georgi F, Flosbach M, Klinnert S, Jenseit A, Lei X, Sandoval CR, Ha K, Zheng H, Pandey R, Gruslova A, Gupta YK, Brenner A, Kokovay E, Hughes TR, **Morris QD**, Galante PAF, Tiziani S, Penalva LOF, *The RNA-binding protein SERBP1 functions as a novel oncogenic factor in glioblastoma by bridging cancer metabolism and epigenetic regulation.* Genome Biol. 2020 Aug 6

8. Arttu Jolma, Jilin Zhang, Estefania Mondragón, Teemu Kivioja, Yimeng Yin, Fangjie Zhu, **Quaid Morris**, Timothy R. Hughes, L. James Maher III, Jussi Taipale. *Binding specificities of human RNA binding proteins towards structured and linear RNA sequences. Genome Research 2020 Jul*

9. Mojca Mattiazzi Usaj*, Nil Sahin*, Helena Friesen, Carles Pons, Matej Usaj, Myra Paz Masinas, Ermira Shuteriqi, Aleksei Shkurin, Patrick Aloy, **Quaid Morris**†, Charlie Boone†, and Brenda Andrews†, *Exploring endocytic*

compartment morphology with systematic genetics and single cell image analysis. Molecular Systems Biology 2020 Feb

Contributions: My lab is the main computational lead and we developed the cell image classification pipeline.

10. Stephanie M. Dobson, Robert J. Vanner, Esmé Waanders, Jeffrey Wintersinger, [19 co-authors] **Quaid Morris**, Charles G. Mullighan, and John E. Dick, *Latent diagnosis subclones in acute B leukemia are drug tolerant and initiate evolution to relapse.* Cancer Discovery 2020 Feb 21

    Contributions: My lab is the main computational lead and we developed new cancer evolution reconstruction algorithms.

11. Moritz Gerstung*, Clemency Jolly*, Ignaty Leshchiner*, Stefan C. Dentro*, Santiago Gonzalez, Thomas J. Mitchell, Yulia Rubanova, Pavana Anur, Daniel Rosebrock, Kaixan Yu, Maxime Tarabichi, Amit Deshwar, Jeff Wintersinger, [28 co-authors], **Quaid D. Morris**, Paul T. Spellman†, David C. Wedge†, Peter Van Loo†, PCAWG Evolution and Heterogeneity Working Group, PCAWG network. *The evolutionary history of 2,658 cancers.* Nature 2020 Feb 5

12. Yulia Rubanova, Ruian Shi, Roujia Li, Jeff Wintersinger, Nil Sahin, Amit Deshwar, **Quaid Morris**, PCAWG-11 working group. *TrackSig: reconstructing evolutionary trajectories of mutation signature exposure.* Nat Commun. 2020 Feb 5

13. Wei Jiao*, Gurnit Atwal*, Paz Polak*, Rosa Karlic, Edwin Cuppen, Alexandra Danyi, Jeroen de Ridder, Carla van Herpen, Martijn P Lolkema, Neeltje Steeghs, Gad Getz, **Quaid D Morris**†, Lincoln D Stein†, PCAWG Pathology & Clinical Correlates Working Grp, ICGC/TCGA Pan-cancer Analysis of Whole Genomes Net. *A deep learning system can accurately classify primary and metastatic cancers based on patterns of passenger mutations.* Nat Commun. 2020 Feb 5

    Contributions: My lab developed the deep neural network that the system is based on.

14. Adriana Salcedo*, Maxime Tarabichi*, Shadrielle Melijah G Espiritu*, Amit G Deshwar*, Matei David, Nathan M Wilson, Stefan Dentro, Jeff A Wintersinger, [18 co-authors], Kyle Ellrott†, David C Wedge†, **Quaid D Morris**†, Peter Van Loo†, Paul C Boutros†, DREAM SMC- Het Participants. *Creating Standards for Evaluating Tumour Subclonal Reconstruction.* Nat Biotechnol. 2020 Jan

    Contributions: My lab co-led the project and developed new principled statistical techniques to compare subclonal reconstructions.

15. Rodrigues DC, Mufteev M, Weatheritt RJ, Djuric U, Ha KCH, Ross PJ, Wei W, Piekna A, Sartori MA, Byres L, Mok RSF, Zaslavsky K, Pasceri P, Diamandis P, **Morris Q**, Blencowe BJ, Ellis J. *Shifts in Ribosome Engagement Impact Key Gene Sets in Neurodevelopment and Ubiquitination in Rett Syndrome.* Cell Rep. 2020 Mar 24
16. Laver JD, Ly J, Winn AK, Karaiskakis A, Lin S, Nie K, Benic G, Jaberi-Lashkari N, Cao WX, Khademi A, Westwood JT, Sidhu SS, **Morris Q**, Angers S, Smibert CA, Lipshitz HD. *The RNA-Binding Protein Rasputin/G3BP Enhances the Stability and Translation of Its Target mRNAs.* Cell Rep. 2020 Mar 10

17. Simon W.M. Eng* , Florence A. Aeschlimann* , Mira van Veenendaal* , Roberta A. Berard, Alan M. Rosenberg, **Quaid Morris†** , and Rae S.M. Yeung† on behalf of the ReACCh- Out Research Consortium. *Patterns of joint involvement in juvenile idiopathic arthritis are predictive of disease course: A prospective study with multilayer non-negative matrix factorization.* PLoS Med. 2019 Feb 26
18. Magomedova L, Tiefenbach J, Zilberman E, Le Billan F, Voisin V, Saikali M, Boivin V, Robitaille M, Gueroussov S, Irimia M, Ray D, Patel R, Xu C, Jeyasuria P, Bader GD, Hughes TR, **Morris QD**, Scott MS, Krause H, Angers S, Blencowe BJ, Cummins CL. *ARGLU1 is a transcriptional coactivator and splicing regulator important for stress hormone signaling and development.* Nucleic Acids Res. 2019 Jan 30.
19. Samuel A. Lambert, Ally W.H. Yang, Alexander Sasse, Gwendolyn Cowley, Mihai Albu, Mark X. Caddick, **Quaid D. Morris**, Matthew T. Weirauch, and Timothy R. Hughes. *Similarity regression predicts evolution of transcription factor sequence specificity.* Nat Genet. 2019 Jun
20. Franz M, Rodriguez H, Tannus Lopes C, Zuberi K, Montojo J, Bader G†, **Morris Q**†. *GeneMANIA prediction server 2018 update.* Nucleic Acids Research. 2018 NAR-00370-Web-B- 2018.R1
21. Espiritu SMG*, Liu LY*, Rubanova Y*, Bhandari V*, Holgersen EM, Szyca LM, Fox NS, Chua MLK, Yamaguchi TN, Heisler LE, Livingstone J, Wintersinger J, Yousif F, Lalonde E, Rouette A, Salcedo A, Houlahan KE, Li CH, Huang V, Fraser M, van der Kwast T, **Morris QD**†, Bristow RG†, Boutros PC†. *The Evolutionary Landscape of Localized Prostate Cancers Drives Clinical Aggression.* Cell 2018 May 3;173(4):1003-1013.e15. doi:

10.1016/j.cell.2018.03.029.

22. Ha KCH, Blencowe BJ†, **Morris Q**†. *QAPA: a new method for the systematic analysis of alternative polyadenylation from RNA-seq data*. Genome Biol. 2018 Mar 28;19(1):45. doi: 10.1186/s13059-018-1414-4.
23. Davis GM, Tu S, Anderson JWT, Colson RN, Gunzburg MJ, Francisco MA, Ray D, Shrubsole SP, Sobotka JA, Seroussi U, Lao RX, Maity T, Wu MZ, McJunkin K, **Morris QD**, Hughes TR, Wilce JA, Claycomb JM, Weng Z, Boag PR. *The TRIM-NHL protein NHL-2 is a co-factor in the nuclear and somatic RNAi pathways in C. elegans.* Elife. 2018 Dec 21;7. pii: e35478. doi: 10.7554/eLife.35478. [Epub ahead of print] PMID: 30575518.
24. Maxime Tarabichi, Inigo Martincorena, Moritz Gerstung, Florian Markowetz, Paul T Spellman, **Quaid D Morris**, Ole Christian Lingjaerde, David C Wedge, Peter Van Loo, - PCAWG Evolution and Heterogeneity Working Group. *Neutral tumor evolution?* Nature Genetics (in press), bioRxiv version: doi: https://doi.org/10.1101/158006)
25. Francois-Moutal, Liberty; Jahanbakhsh, Shahriyar; Nelson, Andrew ; Ray, Debashish; Scott, David; Hennefarth, Matthew; Moutal, Aubin; Ambrose, Andrew; Perez-Miller, Samantha; Al- Shamari, Ahmed; Coursodon, Philippe; Meechoovet, Bessie; Reiman, Rebecca; Lyons, Eric; Beilstein, Mark; Chapman, Eli; **Morris, Quaid**; Van Keuren-Jensen, Kendall; Hughes, Tim; Khanna, Rajesh; Koehler, Carla; Jen, Joanna; Gokhale, Vijay; Khanna, May. *A Chemical Biology Approach to Model Pontocerebellar Hypoplasia Type 1B (PCH1B)* ACS Chem Biol. 2018 Sep 6.
26. Youn JY, Dunham WH, Hong SJ, Knight JDR, Bashkurov M, Chen GI, Bagci H, Rathod B, MacLeod G, Eng SWM, Angers S, **Morris Q**, Fabian M, Côté JF, Gingras AC. High-Density Proximity Mapping Reveals the Subcellular Organization of mRNA-Associated Granules and Bodies. Mol Cell. 2018 Feb 1;69(3):517-532.e11.
27. Cook K, Vembu S, Ha KC, Zheng H, Laverty KU, Hughes TR, Ray D, **Morris Q**. RNAcompete-S: combined RNA sequence/structure preferences for RNA binding proteins derived from a single- step *in vitro* selection. Methods. 2017 Jun 24
28. Dang H, Takai A, Forgues M, Pomyen Y, Mou H, Xue W, Ray D, Ha KCH, **Morris QD**, Hughes TR, Wang XW. Oncogenic Activation of the RNA Binding Protein NELFE and MYC Signaling in Hepatocellular Carcinoma. Cancer Cell. 2017 Jul 10
29. Collins KM, Kainov YA, Christodolou E, Ray D, **Morris Q**, Hughes T, Taylor IA, Makeyev EV, Ramos A. An RRM-ZnF RNA recognition module targets RBM10 to exonic sequences to promote exon exclusion. Nucleic Acids Res. 2017 Apr 4.
30. Frost DW, Vembu S, Wang J, Tu K, **Morris Q**, Abrams HB. Using the Electronic Medical Record to Identify Patients at High Risk for Frequent Emergency Department Visits and High System Costs. Am J Med. 2017 Jan 5.
31. Ray D, Ha KC, Nie K, Zheng H, Hughes TR, **Morris QD**. RNAcompete methodology and application to determine sequence preferences of unconventional RNA-binding proteins. Methods. 2016 Dec 10.
32. Rodrigues DC, Kim DS, Yang G, Zaslavsky K, Ha KC, Mok RS, Ross PJ, Zhao M, Piekna A, Wei W, Blencowe BJ, **Morris Q**, Ellis J. MECP2 Is Post-transcriptionally Regulated during Human Neurodevelopment by Combinatorial Action of RNA-Binding Proteins and miRNAs. Cell Rep. 2016 Oct 11
33. Solana J, Irimia M, Ayoub S, Orejuela MR, Zywitza V, Jens M, Tapial J, Ray D, **Morris Q**, Hughes TR, Blencowe BJ, Rajewsky N. Conserved functional antagonism of CELF and MBNL proteins controls stem cell-specific alternative splicing in planarians. Elife. 2016 Aug 9
34. Cui A, Quon G, Rosenberg AM, Yeung RS, **Morris Q**; BBOP Study Consortium. Gene Expression Deconvolution for Uncovering Molecular Signatures in Response to Therapy in Juvenile Idiopathic Arthritis. PLoS One. 2016 May 31
35. Loedige I, Jakob L, Treiber T, Ray D, Stotz M, Treiber N, Hennig J, Cook KB, **Morris Q**, Hughes TR, Engelmann JC, Krahn MP, Meister G. The Crystal Structure of the NHL Domain in Complex with RNA Reveals the Molecular Basis of Drosophila Brain-Tumor-Mediated Gene Regulation. Cell Rep. 2015 Nov 10
36. Anghel CV, Quon G, Haider S, Nguyen F, Deshwar AG, **Morris QD**, Boutros PC. ISOpureR: an R implementation of a computational purification algorithm of mixed tumour profiles. BMC Bioinformatics. 2015 May 14

37. Laver JD, Li X, Ray D, Cook KB, Hahn NA, Nabeel-Shah S, Kekis M, Luo H, Marsolais AJ, Fung KY, Hughes TR, Westwood JT, Sidhu SS, **Morris Q**, Lipshitz HD, Smibert CA. Brain tumor is sequence-specific RNA-binding protein that directs maternal mRNA clearance during the Drosophila maternal-to-zygotic transition. Genome Biol. 2015 May 12
38. Deshwar AG, Vembu S, Yung C, Jang GH, Stein L, **Morris Q**. PhyloWGS: Reconstructing subclonal composition and evolution from whole genome sequencing of tumors. Genome Biology 2015 Feb.
39. Xiong HY, Alipanahi B, Lee LJ, Bretschneider H, Merico D, Yuen RK, Hua Y, Gueroussov S, Najafabadi HS, Hughes TR, **Morris Q**, Barash Y, Krainer AR, Jojic N, Scherer SW, Blencowe BJ, Frey BJ. RNA splicing. The human splicing code reveals new insights into the genetic determinants of disease. Science. 2015 Jan 9
40. Montojo J, Zuberi K, Rodriguez H, Bader GD, **Morris Q**. GeneMANIA: Fast gene network construction and function prediction for Cytoscape. F1000Res. 2014 Jul 1
41. Vlasblom J, Zuberi K, Rodriguez H, Arnold R, Gagarinova A, Deineko V, Kumar A, Leung E, Rizzolo K, Samanfar B, Chang L, Phanse S, Golshani A, Greenblatt JF, Houry WA, Emili A, **Morris Q**, Bader G, Babu M. Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in Escherichia coli. Bioinformatics. 2014 Oct 13
42. Montojo J, Zuberi K, Shao Q, Bader GD, **Morris Q**. Network Assessor: an automated method for quantitative assessment of a network's potential for gene function prediction. Front Genet. 2014 May 16
43. Eng SW, Duong TT, Rosenberg AM, **Morris Q**†, Yeung RS†; on behalf of the REACCH OUT and BBOP Research Consortia. The biological basis for clinical heterogeneity in childhood arthritis. Arthritis Rheumatol. 2014 Sep 8.
44. Norris AD, Gao S, Norris ML, Ray D, Ramani AK, Fraser AG, **Morris Q**, Hughes TR, Zhen M, Calarco JA. A pair of RNA-binding proteins controls networks of splicing events contributing to specialization of neural cell types. Mol Cell. 2014 Jun 19
45. Jiao W*, Vembu S*, Deshwar AG, Stein L, **Morris Q**. Inferring clonal evolution of tumors from single nucleotide somatic mutations. BMC Bioinformatics. 2014 Feb 1
46. Chen L*, Dumelie JG*, Li X, Cheng MH, Yang Z, Laver JD, Siddiqui NU, Westwood JT, **Morris Q**, Lipshitz HD, Smibert CA. Global regulation of mRNA translation and stability in the early Drosophila embryo by the Smaug RNA-binding protein. Genome Biol. 2014 Jan 7
47. Musso G, Tasan M, Mosimann C, Beaver JE, Plovie E, Carr LA, Chua HN, Dunham J, Zuberi K, Rodriguez H, **Morris Q**, Zon L, Roth FP, Macrae CA. Novel cardiovascular gene functions revealed via systematic phenotype prediction in zebrafish. Development. 2014 Jan
48. de Boer CG, van Bakel H, Tsui K, Li J, **Morris QD**, Nislow C, Greenblatt JF, Hughes TR. A unified model for yeast transcript definition. Genome Res. 2014 Jan
49. Heraud-Farlow JE, Sharangdhar T, Li X, Pfeifer P, Tauber S, Orozco D, Hörmann A, Thomas S, Bakosova A, Farlow AR, Edbauer D, Lipshitz HD, **Morris QD**, Bilban M, Doyle M, Kiebler MA. Staufen2 Regulates Neuronal Target RNAs. Cell Rep. 2013 Dec 26
50. Laver JD*, Li X*, Ancevicius K*, Westwood JT†, Smibert CA†, **Morris QD**†, Lipshitz HD†. Genome-wide analysis of Staufen-associated mRNAs identifies secondary structures that confer target specificity. Nucleic Acids Res. 2013 Nov 1
51. Deshwar AG, **Morris Q**. PLIDA: Cross-platform gene expression normalization using perturbed topic models. Bioinformatics. 2013 Oct 11.
52. Mezlini AM, Wang B, Deshwar A, **Morris Q**, Goldenberg A. Identifying cancer specific functionally relevant miRNAs from gene expression and miRNA-to-gene networks using regularized regression. PLoS One. 2013 Oct 2
53. Radfar H, Wong W, **Morris Q**. BayMiR: inferring evidence for endogenous miRNA-induced gene repression from mRNA expression profiles. BMC Genomics. 2013 Aug 30
54. Ray D*, Kazan H*, Cook KB*, Weirauch MT*, Najafabadi HS*, Li X, Gueroussov S, Albu M, Zheng H, Yang A, Na

H, Irimia M, Matzat LH, Dale RK, Smith SA, Yarosh CA, Kelly SM, Nabet B, Mecenas D, Li W, Laishram RS, Qiao M, Lipshitz HD, Piano F, Corbett AH, Carstens RP, Frey BJ, Anderson RA, Lynch KW, Penalva LO, Lei EP, Fraser AG, Blencowe BJ, **Morris QD**†, Hughes TR†. A compendium of RNA-binding motifs for decoding gene regulation. Nature. 2013 Jul 11

55. Zuberi K, Franz M, Rodriguez H, Montojo J, Lopes CT, Bader GD, **Morris Q**. GeneMANIA prediction server 2013 update. Nucleic Acids Res. 2013 Jul;41(Web Server issue)
56. Kazan H, **Morris Q**. RBPmotif: a web server for the discovery of sequence and structure preferences of RNA-binding proteins. Nucleic Acids Res. 2013 Jul;41(Web Server issue)
57. Quon G, Haider S, Deshwar AG, Cui A, Boutros PC, **Morris Q**. Computational purification of individual tumor gene expression profiles leads to significant improvements in prognostic prediction. Genome Med. 2013 Mar 28
58. Weirauch MT, Cote A, Norel R, Annala M, Zhao Y, Riley TR, Saez-Rodriguez J, Cokelaer T, Vedenko A, Talukder S; DREAM5 Consortium, Bussemaker HJ, **Morris QD**, Bulyk ML, Stolovitzky G, Hughes TR. Evaluation of methods for modeling transcription factor sequence specificity. Nat Biotechnol. 2013 Feb
59. Alshalalfa M, Bader GD, Goldenberg A, **Morris Q**, Alhajj R. Detecting microRNAs of high influence on protein functional interaction networks: a prostate cancer case study. BMC Syst Biol. 2012 Aug 28
60. Chen CY, **Morris Q**, Mitchell JA. Enhancer identification in mouse embryonic stem cells using integrative modeling of chromatin and genomic features. BMC Genomics. 2012 Apr 26
61. Siddiqui NU, Li X, Luo H, Karaiskakis A, Hou H, Kislinger T, Westwood JT, **Morris Q**†, Lipshitz HD†. Genome-wide analysis of the maternal-to-zygotic transition in Drosophila primordial germ cells. Genome Biol. 2012 Feb 20
62. Qiao W*, Quon G*, Csaszar E, Yu M, **Morris Q**†, Zandstra PW†. PERT: a method for expression deconvolution of human blood samples from varied microenvironmental and developmental conditions. PLoS Comput Biol. 2012 Dec
63. Mostafavi S, Goldenberg A, **Morris Q**. Labeling nodes using three degrees of propagation. PLoS One. 2012
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65. Goldenberg A, Mostafavi S, Quon G, Boutros PC, **Morris Q**. Unsupervised detection of genes of influence in lung cancer using biological networks. Bioinformatics. 2011 Nov 15
66. Radfar MH, Wong W, **Morris Q**. Computational prediction of intronic microRNA targets using host gene expression reveals novel regulatory mechanisms. PLoS One. 2011
67. Schimmer BP, Tsao J, Cordova M, Mostafavi S, **Morris Q**, Scheys JO. Contributions of steroidogenic factor 1 to the transcription landscape of Y1 mouse adrenocortical tumor cells. Mol Cell Endocrinol. 2011 Apr 10
68. Ramani AK, Calarco JA, Pan Q, Mavandadi S, Wang Y, Nelson AC, Lee LJ, **Morris Q**, Blencowe BJ, Zhen M, Fraser AG. Genome-wide analysis of alternative splicing in Caenorhabditis elegans. Genome Res. 2011 Feb
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biological network integration for gene prioritization and predicting gene function. Nucleic Acids Res. 2010 Jul 1

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85. L Peña-Castillo, [37 co-authors including S Mostafavi, D Ray, D Warde-Farley, C Grouios, **QD Morris**], TR Hughes, F Roth (2008) *A critical assessment of M. musculus gene function prediction using integrated genomics evidence.* Genome Biology 9 Suppl 1:S2.
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88. E Walker, M Ohishi, RE Davey, W Zhang, PA Cassar, TS Tanaka, SD Der, **QD Morris**, TR Hughes, PW Zandstra, and WL Stanford Novel Networks Regulating Embryonic Stem Cell Self- Renewal and Commitment, Cell Stem Cells 2007 Jun7
89. J Huang, **QD Morris**, and BJ Frey Bayesian Inference of microRNA targets from sequence and expression data, Journal of Computational Biology 2007 Jun
90. J Huang, T Babak, TW Corson, G Chua, BL Gallie, TR Hughes, BJ Blencowe, †BJ Frey and †**QD Morris**, Tissue expression profiling identifies human microRNA targets, Nature Methods 2007 Dec
91. O Shai, **QD Morris**, BJ Blencowe, BJ Frey. Inferring global levels of alternative splicing isoforms using a generative model of microarray data. Bioinformatics. 2006 Mar 1
92. BJ Frey, **QD Morris**, TR Hughes. GenRate: a generative model that reveals novel transcripts in genome-tiling

microarray data. J Comput Biol. 2006 Mar

93. T Kislinger, B Cox, A Kannan, C Chung, P Hu, A Ignatchenko, MS Scott, AO Gramolini, **QD Morris**, MT Hallett, J Rossant, TR Hughes, B Frey, A Emili. Global survey of organ and organelle protein expression in mouse: combined proteomic and transcriptomic profiling. Cell. 2006
94. BP Schimmer, M Cordova, H Cheng, A Tsao, AB Goryachev, AD Schimmer, **QD Morris**. Global profiles of gene expression induced by adrenocorticotropin in Y1 mouse adrenal cells. Endocrinology. 2006 May
95. G Chua, **QD Morris**, R Sopko, MD Robinson, O Ryan, ET Chan, BJ Frey, BJ Andrews, C Boone. TR Hughes. Identifying transcription factor functions and targets by phenotypic activation, Proc. Natl. Acad. Sci. USA. 2006 Aug 8
96. Dueck D, **QD Morris**, BJ Frey (2005) Multi-way clustering of microarray data using probabilistic sparse matrix factorization. Bioinformatics 21 Suppl 1:i144-i151
97. J Huang, **QD Morris**, BJ Frey (2005) GenXHC: A probabilistic generative model for cross- hybridization compensation in high-density genome-wide microarray data. Bioinformatics 21 Suppl 1:i222-i231
98. B Frey***,** N Mohammad***,** **QD Morris*,** W Zhang***,** MD Robinson, S Mnaimneh, R Chang, Q Pan, E Sat, J Rossant, J Aubin, BJ Blencowe, and TR Hughes (2005) Genome-wide analysis of mouse transcripts using exon microarrays and factor graphs. Nature Genetics 37(9):991-6
99. S Mnaimneh, AP Davierwala, J Haynes, J Moffat, WT Peng, W Zhang, X Yang, J Pootoolal, G Chua, A Lopez, M Trochesset, D Morse, NJ Krogan, SL Hiley, Z Li, **QD Morris**, J Grigull, N Mitsakakis, CJ Roberts, JF Greenblatt, C Boone, CA Kaiser, BJ Andrews, TR Hughes, (2004) Exploration of essential gene functions via titratable promoter alleles. Cell. 118(1): 31-44**.**
100. W Zhang*, **QD Morris***, R Chang, O Shai, MA Bakowski, N Mitsakakis, N Mohammad, M Robinson, R Zirnglibl, E Somogyi, N Laurin, WT Peng, N Krogan, E Eftekharpour, E Sat, J Grigull, Q Pan, J Greenblatt, M Fehlings, D van der Kooy, J Aubin, BG Bruneau, J Rossant, BJ Blencowe, BJ. Frey, and TR Hughes (2004) The functional landscape of mouse gene expression. Journal of Biology 3(5): 21-43
101. T Babak, W Zhang, **QD Morris**, BJ Blencowe, and TR Hughes (2004) Probing microRNAs with microarrays: tissue specificity and functional inference. RNA 10(11):1813-9.
102. S Hiley, J Jackman, T Babak, M Trochesset, **QD Morris**, E Phizicky, TR Hughes (2004) Detection and discovery of RNA modifications using microarrays. Nucleic Acids Research 33(1):e2
103. Q Pan, O Shai, C Misquitta, N Mohammed, W Zhang, T Babak, H Siu, TR Hughes, **QD Morris**, B Frey, and BJ Blencowe (2004) *Global regulatory properties of mammalian alternative splicing revealed by quantitative microarray profiling.* Molecular Cell 16(6)
104. Q Pan, MA Bakowski, **QD Morris**, W Zhang, B Frey, TR Hughes, and BJ Blencowe (2004) Frequent species-specific alternative splicing of conserved human and mouse exons. Trends in Genetics 21(2):73-7
105. Peng WT, Robinson MD, Mnaimneh S, Krogan NJ, Cagney G, **Morris Q**, Davierwala AP, Grigull J, Yang X, Zhang W, Mitsakakis N, Ryan OW, Datta N, Jojic V, Pal C, Canadien V, Richards D, Beattie B, Wu LF, Altschuler SJ, Roweis S, Frey BJ, Emili A, Greenblatt JF, Hughes TR. A panoramic view of yeast noncoding RNA processing. Cell. 2003 Jun 27

Peer-reviewed computer science conference papers (19) (OUT OF DATE)

1. Khasahmadi A, Hassani K, Moradi P, Lee L, **Morris Q**. Memory-based Graph Networks. ICLR 2020. arXiv:2002.09518
2. Young A, Chmura J, Park Y, **Morris Q**, Atwal G. Genome Gerrymandering: optimal division of the genome into regions with cancer type specific differences in mutation rates. Pac Symp Biocomput. 2020;25:274-285. PubMed PMID: 31797603.
3. Harrigan CF, Rubanova Y, **Morris Q**, Selega A. TrackSigFreq: subclonal reconstructions based on mutation signatures and allele frequencies. Pac Symp Biocomput. 2020;25:238-249. PubMed PMID: 31797600; PubMed Central PMCID: PMC6905203.
4. Zhang H, Candido E, Wilton AS, Duchen R, Jaakkimainen L, Wodchis W, **Morris Q**. Identifying Transitional High Cost Users from Unstructured Patient Profiles Written by Primary Care Physicians. Pac Symp Biocomput. 2020;25:127-

138. PubMed PMID: 31797592.

5. Cremer C, **Morris Q**, Duvenaud D. Reinterpreting Importance-Weighted Autoencoders. ICLR Workshop 2017. arXiv:1704.02916
6. Deshwar AG, Vembu S, **Morris Q**. Compa nonparametric Bayesian tree priors for clonal reconstruction of tumors. Pac Symp Biocomput. (PSB) 2015;20:20-31. PubMed PMID: 25592565.
7. Vembu S, **Morris Q**. An efficient algorithm to integrate network and attribute data for gene function prediction. Pac Symp Biocomput. (PSB) 2014;19:388-99. PubMed PMID: 24297564.
8. Warde-Farley D, Brudno M, **Morris Q**, Goldenberg A. Mixture model for sub-phenotyping in GWAS. Pac Symp Biocomput. 2012:363-74. PubMed PMID: 22174291.
9. Radfar MH, Wong W, **Morris Q**. Conf Proc IEEE Eng Med Biol Soc. 2010;2010:791-4. PubMed PMID: 21096111.
10. S Mostafavi, **Q Morris**, (2009) Using hierarchical information in predicting gene function. Proceedings of the Association for Uncertainty in Artificial Intelligence (UAI) Conference 2009
11. G Quon, YW Teh, E Chan, T Hughes, M Brudno, **Q Morris**, (2008) A Mixture Model for the Evolution of Gene Expression in Non-homogeneous Datasets, Proceedings of Advances in Neural Information Processing Systems (NIPS) 21
12. JC Huang, BJ Frey, **QD Morris**. (2008) Comparing sequence and expression for predicting microRNA targets using GenMiR3. Pac Symp Biocomput. (PSB) 2008:52-63. PubMed PMID: 18229676.
13. J Huang, **QD Morris**, BJ Frey (2006) Predicting MicroRNA Targets by Integrating Sequence and Expression Data using Factor Graphs. Tenth International Conference for Research in Computational Molecular Biology (RECOMB) 2006
14. BJ Frey, **QD Morris**, W Zhang, N Mohammad, TR Hughes (2005) Genrate: a generative model that finds and scores new genes and exons in genomic microarray data. Pac Symp Biocomput. (PSB) 2005:495-506. PubMed PMID: 15759654.
15. BJ Frey, **QD Morris**, W Zhang, MD Robinson, N Mohammad, TR Hughes (2005) GenRate: A generative model that finds and scores new gene structures in genome-wide microarray data. Ninth International Conference for Research in Computational Molecular Biology (RECOMB) 2005
16. O Shai, B Frey, **QD Morris**, Q Pan, C Misquitta, BJ Blencowe (2004*)* Probabilistic inference of alternative splicing events in microarray data. Proceedings of Advances in Neural Information Processing Systems (NIPS) 17
17. **Q Morris**, BJ Frey, CJ Paige (2003) Denoising and untangling graphs using degree priors. Proceedings of Advances in Neural Information Processing Systems (NIPS) 16
18. **Q Morris** (2001) Recognition networks for approximate inference in BN20 networks. Proceedings of the Association for Uncertainty in Artificial Intelligence (UAI) Conference 2001
19. J Siskind, **Q Morris** (1996) A maximum-likelihood approach to visual event classification. Proceedings of Fourth European Conference on Computer Vision, Cambridge, UK

Review articles (13)

1. Eng SWM, Yeung RSM, **Morris Q**. *The promise of machine learning to inform the management of juvenile idiopathic arthritis*. Expert Rev Clin Immunol. 2021 Jan;17(1):1-3. doi: 10.1080/1744666X.2020.1850268. Epub 2021 Jan 26. PMID: 33475006; PMCID: PMC7944407.

2. Sasse A, Laverty K, Hughes TR, **Morris Q**. Motif models for RNA-binding proteins. Current Opinion in Structural Biology. 2018 Aug 29;53:115-123. doi:10.1016/j.sbi.2018.08.001.

3. Grys BT, Lo DS, Sahin N, Kraus OZ, **Morris Q**, Boone C, Andrews BJ. Machine learning and computer vision approaches for phenotypic profiling. J Cell Biol. 2017 Jan 2.
4. Cook KB, Hughes TR, **Morris QD**. High-throughput characterization of protein-RNA interactions. Brief Funct Genomics. 2015 Jan.
5. Re A, Joshi T, Kulberkyte E, **Morris Q**, Workman CT. RNA-protein interactions: an overview. Methods Mol Biol. 2014;1097
6. Listgarten J, Stegle O, **Morris Q**, Brenner SE, Parts L. Personalized medicine: from genotypes and molecular phenotypes towards therapy- session introduction. Pac Symp Biocomput. 2014; 19:224-8. PubMed PMID: 24297549.
7. Li X*, Kazan H*, Lipshitz HD, **Morris QD**. Finding the target sites of RNA-binding proteins. Wiley Interdiscip Rev RNA. 2014 Jan;5(1):111-30. doi: 10.1002/wrna.1201. Epub 2013 Nov 11.
8. **Morris Q**, Brenner SE, Listgarten J, Stegle O. The future of genome-based medicine. Pac Symp Biocomput. 2013:456-8. PubMed PMID: 23424151.
9. Mostafavi S, **Morris Q**. Combining many interaction networks to predict gene function and analyze gene lists. Proteomics. 2012 May
10. **Morris Q,** Bulyk ML, Hughes TR. Jury remains out on simple models of transcription factor specificity. Nat Biotechnol. 2011 Jun 7
11. BP Schimmer, M Cordova, H Cheng, A Tsao, **QD Morris**, (2007) A genome-wide assessment of adrenocorticotropin action in the Y1 mouse adrenal tumor cell line. Mol Cell Endocrinol. Feb 26
12. Roy P, **QD Morris** (2005) Network News: Functional Modules Revealed during Early Embryogenesis in C. elegans. Developmental Cell 9(3):307-8
13. G Chua, MD Robinson, **QD Morris**, TR Hughes (2004) Transcriptional networks: reverse- engineering gene regulation on a global scale. Current Opinion in Microbiology 7(5): 638-46.

Not shown: Scientific abstracts (>100)

SUPERVISORY ACTIVITIES

(Co-supervisor indicated in parentheses, unless otherwise noted, school is University of Toronto).

Current

PhDs

Tam, Cyrus – Computational Biology and Medicine (CBM), Weill-Cornell Med School (WCMC) -- 2021
Darmofal, Madison – CBM, WCMC – 2021 (M Berger)
Lyudovyk, Olga – CBM, WCMC – 2021 (B Greenbaum)
Shi, Ruian (Ian)– Computer Science – 2021
Harrigan, Caitlin– Computer Science – 2021 (K Campbell)
Qiao, Jingping – Molecular Genetics (Computational Biology track) – 2019 (L. Stein)
von Krosigk, Nik – Molecular Genetics (Computational Biology track) – 2019 (L. Stein)
Barber, Jarry – Molecular Genetics (Computational Biology track) – 2019 (P. Awadalla)
Laverty, Kaitlin – Molecular Genetics – 2017 (T. Hughes)
Sasse, Alexander – Molecular Genetics (Computational Biology track) – 2017
Wintersinger, Jeff -- Computer Science – 2016
Sahin, Nil – Molecular Genetics – 2016 (B. Andrews)
Niu, Kun -- Molecular Genetics – 2015

PDFs

Bretschneider, Hannes – Donnelly Centre, University of Toronto -- 2019 (B Blencowe)

Not shown: Undergraduates and non-research staff, incl. software developers and system administrators

Completed
(current status indicated)

PhDs

Atwal, Gurnit – Molecular Genetics (Computational Biology track) – 2017-2021 (G. Bader)
Postdoctoral Research Fellow, Memorial Sloan Kettering Cancer Center, New York, USA
Rubanova, Yulia – Computer Science – 2016-20
Research Scientist, Deep Mind, London, England
Cremer, Chris – Computer Science – 2016-20 (D. Duvenaud)
Research Intern, Facebook AI, Pittsburgh
Eng, Simon – Immunology – 2011-18 (R. Yeung)
Research Associate in Yeung lab at SickKids, Toronto
Ha, Kevin -- Molecular Genetics – 2012-18 (delay due to medical leave) (B. Blencowe)
Data Scientist, BioSymetrics, Toronto
Deshwar, Amit – Electrical and Computer Engineering – 2012-18 (delay due to multi-year leave)
Research Scientist, Deep Genomics
Radfar, Mohammed (Martin) Hossein – Electrical and Comp Eng – 2008-13 (W. Wong)
Research Assistant Professor in Computer Science, Stony Brook University
Li, Xiao – Molecular Genetics – 2007-13 (H. Lipshitz)
Assistant Professor, Case Western University
Kazan, Hilal – Computer Science – 2007-12
Associate Professor, Computer Science, Antalya Bilim University
Quon, Gerald – Computer Science – 2006-12
Assistant Professor in Computer Science at University of California Davis
Mostafavi, Sara – Computer Science – 2006-11
Associate Professor, Computer Science, University of Washington, Canada CIFAR AI chair

MSc

Shi, Ruian (Ian)– Computer Science – 2019-21
PhD student, University of Toronto
Harrigan, Caitlin– Computer Science – 2019-21
PhD student, University of Toronto
Young, Adamo– Computer Science – 2018-20
PhD student, University of Toronto
Ahmadi, Amir – Electrical and Computer Engineering – 2018-20 (B. Frey)
Research Scientist, Autodesk AI lab
Cremer, Chris – Computer Science – 2014-16
Research Intern, Facebook AI, Pittsburgh
Wintersinger, Jeff – Computer Science – 2014-16
PhD student, University of Toronto
Deshwar, Amit – Electrical and Computer Engineering – 2010-12
Research Scientist, Deep Genomics
Jiao, Wei – Molecular Genetics – 2011-3 (L. Stein)
Research Scientist at Ontario Institute for Cancer Research
Warde-Farley, David – Computer Science – 2007-09
Research Scientist at DeepMind, London, England
Mavandadi, Sepand – Electrical and Computer Engineering – 2006-08
Software engineer at Amazon.com

PDF

Goldenberg, Anna – Computer Science – 2008-11 (incl. maternal leave) (T. Hughes)
Senior Scientist in Genetics and Genome Biology, SickKids, Toronto
Associate Professor in Computer Science, Univ Toronto
Associate Director for Health Research, Vector Institute
Vembu, Shankar – Computer Science – 2011-2017 (part-time)
Founder: argmix a technology consulting firm specializing in machine learning
Gray, Gavin, PhD – Computer Science – 2019-2020
Postdoctoral Research Fellow, Vector Institute

Sundermann, Linda, PhD – Computer Science – 2019-2021
Research Scientist, Silicon Valley start-up
Selega, Alina, PhD – Computer Science – 2019-2021
Postdoctoral Research Fellow, Lunenfeld Research Institute, Toronto
Jolma, Arttu, PhD – Molecular Biology – 2016-2018 (T. Hughes)
Postdoctoral Research Fellow, Hughes Lab, Toronto

Research Associates
Razasi, Rozita, PhD – Molecular Biology – 2017-2019 (T. Hughes)
Ray, Debashish, PhD – Molecular Biology – 2011-2019 (T. Hughes)

Not shown: Non-research staff, incl. software developers and system administrators (>10), undergraduate researchers (>30)

ACTIVITIES AND CONTRIBUTIONS

Selected Awards:

Canada CIFAR chair, 2018-present
Clarivate Highly Cited Researcher, 2018-present
Early Researcher Award, Ontario Ministry of Research and Innovation, 2010-14
Information Processing Laboratory Postdoctoral Fellowship, 2002-03
NSERC PDF Fellowship, 2003-05

Invited Seminar & Conference Presentations (out-of-date, only shown up to 2017):

Keynote 1 hour seminars: RECOMB Cancer Computational Biology (2017), EBI Functional Genomics workshop, Hinxton (2014), RECOMB AS-SIG (2014), McGill-Toronto Bioinformatics Workshop (2013), ORNL Bioinformatics conference (Memphis, Tennessee) (2011), RECOMB Cancer Computational Biology (2011)

Invited 1 hour seminars (>75): in Canada, China, Denmark, France, Germany, Italy, India, and Singapore, Spain, Switzerland, USA, and UK including European Bioinformatics Institute, Fields Institute Toronto, Broad Institute, Crick Institute, UC Berkeley, Harvard Medical School, Yale, UPenn/CHOP, CMU, Weill-Cornell Medical School, CRG Barcelona, University of Edinburgh, University of Freiburg, University of Washington, Microsoft Research Redmond and Cambridge

Invited conference or workshop presentations: RECOMB Cancer Computational Biology (2015), Pacific Symposium on Biocomputing (2012, 2014), RECOMB Regulatory Genomics satellite (2010, 2011, 2012), Riboclub Sherbrooke (2010), ISMB AS-SIG (2009, 2010), ISMB Techtrack (2010), ISMB Workshops (2013 x2), McGill Barbados Bioinformatics Conference (2005, 2008, 2012-2017), ISMB (2007, 2014), Cold Spring Harbor Laboratory mRNA processing conference (2009, 2013), CIHR integrating physical and biological sciences workshop (2008), NHGRI Proteomic Sequence & Function Workshop (2008)

Editorial and Advisory Boards: Deputy Editor: PLoS Computational Biology (2018-present), Associate Editor: PLoS Computational Biology (2013-2018), BMC Bioinformatics (2010-2013); Guest Associate Editor: PLoS Computational Biology (2009); Co-editor of BMC Bioinformatics Special Issue (2006); Scientific Advisory Board: Univ of Sherbrooke Genome Canada project (2007-2009)

Grant Review Panels: NIH GCAT (Feb 2018); CIHR (guest 2008, full member 2009-present); NSF (2007, 2013); Canadian Breast Cancer Foundation, Panel A (Feb 2012); Ad hoc reviewer: NSERC (various); Burroughs Wellcome Fund, W.M. Keck, Israel Research Fund, MITACS

Symposium and Workshop Organization (out-of-date, only shown to 2017): Co-organizer: RNA regulation @ Pacific Symposium on Biocomputing (2015), Personalized medicine session @ Pacific Symposium on Biocomputing (2012-2014), Machine Learning in Computational Biology workshop @ NIPS (2006-2008), Post-transcriptional regulation workshop @ Pacific Symposium on Biocomputing 2009, Session Chair: International Conference on Machine Learning 2006

Reviewing for Journals and Conferences (>250 manuscripts): Nature, Science, Nature Biotechnology, Nature Structural and Molecular Biology, Nature Genetics, Nature Methods, Molecular Systems Biology, Genome Biology, Genome Research, PLoS Computational Biology, Bioinformatics, BMC Bioinformatics, IEEE Transactions on Pattern Analysis and Machine Intelligence. Conferences include Pacific Symposium on Biocomputing (PSB), International Conference on Intelligent Systems for Molecular Biology (ISMB), Artificial Intelligence and Statistics (AISTATS), Advances in Neural Information Processing Systems (NIPS), International Conference of Machine Learning (ICML), RECOMB regulatory genomics and systems biology satellite.

Outreach: Faculty lecturer for Canadian Bioinformatics Workshop (1 or 2 workshops / year since 2008 in Toronto, and Vancouver), faculty lecturer for Cold Spring Harbor Workshops (1 / year, 2016-19)

RESEARCH FUNDING (OUT OF DATE)

Ongoing

Comprehensive Analysis of RNA binding proteins and their cellular function.
Canadian Institute of Health Research (CIHR)
Total funding: $1.1 million; Period: 2020-25
Role: PI; co-investigator: Timothy Hughes.

Machine learning and biology
National Sciences and Engineering Research Council of Canada (NSERC)
Total funding: $210,000; Period: 2019-25
Role: PI

Translating genomic test to the clinic
MITACS
Total funding: $120,000; Period: 2019-2021
Role: PI

Computational models of cancer evolution
Ontario Institute of Cancer Research Associate Investigator Award
Total funding: $1.4 million; Period: 2018-23
Role: PI

UCAN CAN-DU: Canada-Netherlands Personalized Medicine Network in Childhood Arthritis.
CIHR & Netherlands Org for Health Research & Dutch Arthritis Foundation
Total funding: $8 million; Period: 2017-22
Role: Co-investigator; co-PIs: Rae Yeung and Nico Wulffraat

Improving cancer treatment by reconstructing the evolutionary history of tumours
Compute Canada's Resources for Research Groups
Total funding: ~$750,000 (cloud compute services, estimated value); Period 2015-21
Role: PI

Systematic characterization of unconventional RNA binding proteins
National Institutes of Health R01 HG008613
Total Funding: $1.59 million; Period 2015-20 (NCE)
Role: Co-investigator, computational lead; PI: Timothy Hughes

Completed

The eukaryotic RNA-protein recognition code.
Canadian Institute of Health Research (CIHR)
Total funding: $1.4 million; Period: 2013-20 (NCE)
Role: PI; co-investigator: Timothy Hughes.

Canadian Centre for Computational Genomics (C3G).
Genome Canada
Total funding: $7.05 million; Period: 2017-20
Role: Co-investigator, Cancer genomics pipeline development and research; co-PIs: G Bourque and M Brudno
Regulatory network control of neural stem cells for endogenous repair.
Canada First Research Excellence Funding
Total funding: $240,000; Period: 2017-19
Role: PI

Pathways to enhance the clinical utility of hematopoietic stem cell transplantation.
Canada First Research Excellence Funding
Total funding: $224,000; Period: 2017-19
Role: PI

Post-transcriptional gene regulatory modules that control stem cell differentiation.
Canada First Research Excellence Funding
Total funding: $100,000; Period: 2017-19
Role: PI

Systematic analysis of cooperativity between RNA-binding proteins.
Canadian Institute of Health Research (CIHR)
Total funding: $100,000; Period: 2016-18 (NCE)
Role: PI; co-investigator: Timothy Hughes

Machine learning to support biological discovery.
Natural Sciences and Engineering Research Council of Canada (NSERC)
Total funding: $280,000; Period: 2011-17 (NCE)
Role: PI

Medicine-by-design: Cell population analysis. Transitional funding
Canada First Research Excellence Funding
Total funding: $70,000; Period: 2016-17
Role: PI

CGEP: Computationally optimized characterization of cancer genes, proteins, their structure, function and interactions
Ontario Research Fund
Total funding: $10 million; Period 2010-16
Role: Co-investigator, GeneMANIA development. co-PIs: Igor Jurisica, Gary Bader.

Computer-assisted cancer diagnosis and treatment planning.
Ontario Research Fund: Early Researcher Award
Total funding: $140,000 (with UToronto match); Period 2010-14
Role: PI

Determining the sequence and structure specificities of RNA-binding proteins.
National Institutes of Health 1R01HG005700 – 01
Total funding: $1.19 million; Period 2010-13
Role: Co-investigator, computational lead; PI: Timothy Hughes

Deciphering the cis-regulatory code of Drosophila mRNA regulation using integrative computational and biochemical genomic analyses.
Canadian Institutes of Health Research
Total funding: $556,686; Period 2009-13
Role: PI; co-investigator: Timothy Hughes

Software tools to simplify gene function prediction.
Genome Canada & Ontario Research Fund
Total funding: $1.43 million; Period 2008-10
Role: co-PI; co-PI: Gary Bader

Integrative Biology Team Grant.
Genome Canada
Total funding: $55 million; Period: 2007-10
Role: Co-investigator; Principal Investigator: Brenda Andrews

Enabling systems biology through machine learning: intelligent software to automatically summarize and combine large-scale biological databases.
National Sciences and Engineering Research Council of Canada (NSERC)
Total funding: $72,000; Period: 2006-10
Role: PI

Start-up funding.
University of Toronto, Faculty of Medicine
Total funding: $250,000; Period: 2005-10
Role: PI

Systems biology through machine learning: adaptive computer programs for denoising, interpreting, and integrating large-scale biological databases.
Canadian Foundation for Innovation & Ontario Research Fund
Total funding: $257,746 (equipment grant); Period: 2006-09
Role: PI

<u>Not shown:</u> *Grants < $50,000 total funding incl. various 1-year grants and industrial fellowships*